

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KLVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48483
2	29	100.0	6	4	AAB48474
3	29	100.0	6	4	AAB82623
4	29	100.0	6	4	AAB82631
5	29	100.0	6	5	AAB96819
6	29	100.0	6	5	AAB96811
7	29	100.0	6	5	AAB11657
8	29	100.0	6	5	AAB11648
9	29	100.0	6	6	AAB35446
10	29	100.0	6	6	AAB35438
11	29	100.0	6	8	ADQ37322
12	29	100.0	6	8	ADQ37270
13	29	100.0	6	8	ADQ37313
14	29	100.0	6	8	ADQ37262
15	29	100.0	6	9	ADY37921
16	29	100.0	6	9	ADY37929
17	29	100.0	99	4	ABG32598
18	28	96.6	6	4	AAB48482
19	28	96.6	6	4	AAB48490
20	28	96.6	6	4	AAB82630
21	28	96.6	6	4	AAB82638
22	28	96.6	6	5	AAB96818
23	28	96.6	6	5	AAB96826
24	28	96.6	6	5	AAB11664

25	28	96.6	6	5	AAU11656	Aau11656	Peptide #
26	28	96.6	6	6	ABE35452	Aae35452	Abeta pep
27	28	96.6	6	8	ADQ37277	Adq37277	Vaccine a
28	28	96.6	6	8	ADQ37321	Adq37321	Antifibri
29	28	96.6	6	8	ADQ37329	Adq37329	Antifibri
30	28	96.6	6	9	ADY37928	Ady37928	Amyloid-t
31	28	96.6	6	9	ADY37936	Ady37936	Amyloid-t
32	28	96.6	22	8	ADQ09761	Adq09761	Rice 26kD
33	28	96.6	23	8	ADY37938	Ady37938	Rice 26 k
34	28	96.6	37	3	AAB05910	Aab05910	Mouse ind
35	28	96.6	37	8	ADK34080	Adk34080	Human nNO
36	28	96.6	37	8	ADL70727	Adl70727	Mouse iNO
37	28	96.6	77	3	AAG02840	Aag02840	Human sec
38	28	96.6	175	4	AAO11219	Aao11219	Human pol
39	28	96.6	186	7	ADC07962	Adc07962	Rice prot
40	28	96.6	186	7	ADC07948	Adc07948	Rice prot
41	28	96.6	190	4	AAM83792	Aam83792	Human imm
42	28	96.6	564	4	ABE61977	AbE61977	Drosophila
43	28	96.6	854	8	ADQ66704	AdQ66704	Novel hum
44	28	96.6	922	8	ABM83252	Abm83252	Human dia
45	28	96.6	925	7	ADF76335	Adf76335	Novel hum
46	28	96.6	925	7	ADJ70225	Adj70225	Human hea
47	28	96.6	925	8	ADJ75428	Adj75428	Marker ge
48	28	96.6	925	8	ADJ75495	Adj75495	Marker ge
49	28	96.6	925	8	ADN04860	Adn04860	Antipsori
50	28	96.6	925	8	ADR14233	Adr14233	Human NF-
51	28	96.6	925	8	ADR25011	Adr25011	PRO polyp
52	28	96.6	925	8	ADR97294	Adr97294	Human RIG
53	28	96.6	925	9	AEA23525	Aea23525	PRO polyp
54	28	96.6	925	9	AEA23525	Aea23525	Human PRO
55	28	96.6	1144	2	AAR77360	Aar77360	Inducible
56	28	96.6	1144	2	AAS51246	Aas51246	Inducible
57	28	96.6	1144	4	AAG64500	Aag64500	Mouse ind
58	28	96.6	1144	4	ABU79138	Abu79138	Inducible
59	28	96.6	1144	7	ADF74304	Adf74304	INOS poly
60	28	96.6	1144	7	ADF77632	Adf77632	Mouse ind
61	28	96.6	1144	8	ADJ76212	Adj76212	Marker ge
62	28	96.6	1144	8	ADJ76136	Adj76136	Marker ge
63	28	96.6	1144	9	AEA03075	Aea03075	VEGF amin.
64	28	96.6	1443	4	ABE68472	AbE68472	Drosophila
65	27	93.1	6	2	AAW02314	Aaw02314	Beta-amyl
66	27	93.1	6	2	AAW89378	Aaw89378	Beta-amyl
67	27	93.1	6	4	AB48484	Aab48484	Antifibri
68	27	93.1	6	4	AB48476	Aab48476	Antifibri
69	27	93.1	6	4	AB82632	Aab82632	Antifibri
70	27	93.1	6	5	ABG71009	Abg71009	Long form
71	27	93.1	6	5	ABO5157	Abo05157	Beta amyl
72	27	93.1	6	5	AAU96820	Aau96820	Amyloid t
73	27	93.1	6	5	AB883305	Abb83305	Amyloid-b
74	27	93.1	6	5	AAU11658	Aau11658	Peptide #
75	27	93.1	6	5	AAU11650	Aau11650	Peptide #
76	27	93.1	6	6	AAE35445	Aae35445	Abeta pep
77	27	93.1	6	6	AAE35434	Aae35434	Abeta pep
78	27	93.1	6	6	ADJ64060	Adj64060	Human bet
79	27	93.1	6	8	ADQ37271	Adq37271	Vaccine a
80	27	93.1	6	8	ADQ37315	Adq37315	Antifibri
81	27	93.1	6	8	ADQ37368	Adq37368	Beta-amyl
82	27	93.1	6	8	ADQ37269	Adq37269	Vaccine a
83	27	93.1	6	8	ADQ37292	Adq37292	Vaccine a
84	27	93.1	6	8	ADQ37258	Adq37258	Vaccine a
85	27	93.1	6	8	ADQ37353	Adq37353	Beta-amyl
86	27	93.1	6	8	ADQ37323	Adq37323	Antifibri
87	27	93.1	6	9	ADY37930	Ady37930	Amyloid-t
88	27	93.1	6	9	ADY37948	Ady37948	Amyloid-t
89	27	93.1	6	9	ADY37947	Ady37947	Amyloid-t
90	27	93.1	6	9	AEA23039	Aea23039	Human bet
91	27	93.1	7	2	AAR88300	Aar88300	Non-amnes
92	27	93.1	7	2	AAR87921	Aar87921	Test pept
93	27	93.1	7	2	AAW02312	Aaw02312	Beta-amyl
94	27	93.1	7	2	AAW89376	Aaw89376	Beta-amyl
95	27	93.1	7	4	AAW67281	Aab67281	Residues
96	27	93.1	7	4	AB48475	Aab48475	Antifibri
97	27	93.1	7	4	AB48492	Aab48492	Antifibri

98	27	93.1	7	4	AA848491	Ab48491 Antifibri	171	27	93.1	10	4	AA846226	Ab46226 Human APP
99	27	93.1	7	4	AA82624	Ab82624 All-D pep	172	27	93.1	10	4	AA846225	Ab46225 Human APP
100	27	93.1	7	4	AA82624	Ab82624 All-D pep	173	27	93.1	10	4	AA846228	Ab46228 Human APP
101	27	93.1	7	4	AA82639	Ab82639 All-D pep	174	27	93.1	10	4	AA846224	Ab46224 Human APP
102	27	93.1	7	5	AB871007	Abg71007 Long form	175	27	93.1	10	4	AA846227	Ab46227 Human APP
103	27	93.1	7	5	AB805155	Ab805155 Beta amyl	176	27	93.1	10	4	AA882641	Ab882641 All-D pep
104	27	93.1	7	5	AAU96827	Aau96827 Amyloid t	177	27	93.1	10	5	AAU96829	Aau96829 Amyloid t
105	27	93.1	7	5	AAU96812	Aau96812 Amyloid t	178	27	93.1	10	6	ABP57511	Abp57511 Different
106	27	93.1	7	5	AAU96828	Aau96828 Amyloid t	179	27	93.1	10	6	AAE35455	Aae35455 Abeta pep
107	27	93.1	7	5	AB804920	Ab804920 Human amy	180	27	93.1	10	8	ADQ37280	Adq37280 Vaccine a
108	27	93.1	7	5	AAU11665	Aau11665 Peptide #	181	27	93.1	10	8	ADQ37371	Adq37371 Amyloid-b
109	27	93.1	7	5	AAU11649	Aau11649 Peptide #	182	27	93.1	10	8	ADQ37374	Adq37374 Amyloid-b
110	27	93.1	7	5	AAU11666	Aau11666 Peptide #	183	27	93.1	10	9	ADY37939	Ady37939 Amyloid-t
111	27	93.1	7	6	AB882630	Ab882630 Abeta fib	184	27	93.1	11	2	AAW32560	Aaw32560 Anti-amyl
112	27	93.1	7	6	AAE35439	Aae35439 Abeta pep	185	27	93.1	11	4	AAW52586	Aaw52586 Peptide #
113	27	93.1	7	6	AAE35454	Aae35454 Abeta pep	186	27	93.1	11	5	AAU99431	Aau99431 Human amy
114	27	93.1	7	6	AAE35453	Aae35453 Abeta pep	187	27	93.1	11	5	AAE29504	Aae29504 Amyloid b
115	27	93.1	7	6	ADA90937	Ada90937 Solid-pha	188	27	93.1	11	6	ABU79013	Abu79013 Amyloidog
116	27	93.1	7	6	ADA90154	Ada90154 Anti-Abet	189	27	93.1	11	7	ABR84683	Abr84683 Aggreca
117	27	93.1	7	7	AD20746	Ad20746 Human bet	190	27	93.1	11	7	ABW00147	Abw00147 Amyloid-b
118	27	93.1	7	7	ADF50855	Adf50855 Human cal	191	27	93.1	12	6	AAE35464	Aae35464 Abeta pep
119	27	93.1	7	8	ADJ64058	Adj64058 Human bet	192	27	93.1	12	6	AAE35435	Aae35435 Abeta pep
120	27	93.1	7	8	ADP64922	Adp64922 Beta-amyl	193	27	93.1	12	6	AAE35466	Aae35466 Abeta pep
121	27	93.1	7	8	ADQ37278	Adq37278 Vaccine a	194	27	93.1	12	7	ADD20745	Add20745 Human bet
122	27	93.1	7	8	ADQ37314	Adq37314 Antifibri	195	27	93.1	12	7	ADD20744	Add20744 Human bet
123	27	93.1	7	8	ADQ37263	Adq37263 Vaccine a	196	27	93.1	12	8	ADJ71476	Adj71476 N-termina
124	27	93.1	7	8	ADQ37279	Adq37279 Vaccine a	197	27	93.1	12	8	ADQ37407	Adq37407 Amyloid-b
125	27	93.1	7	8	ADQ37330	Adq37330 Antifibri	198	27	93.1	12	8	ADQ37289	Adq37289 Vaccine a
126	27	93.1	7	8	ADQ37331	Adq37331 Antifibri	199	27	93.1	12	8	ADQ37259	Adq37259 Vaccine a
127	27	93.1	7	8	ADQ37351	Adq37351 Beta-amyl	200	27	93.1	12	9	ADZ08890	Adz08890 Human bet
128	27	93.1	7	9	ADY37922	Ady37922 Amyloid-t	201	27	93.1	12	9	ADZ08892	Adz08892 Human bet
129	27	93.1	7	9	ADY37938	Ady37938 Amyloid-t	202	27	93.1	13	6	AAE35465	Aae35465 Abeta pep
130	27	93.1	7	9	ADY37937	Ady37937 Amyloid-t	203	27	93.1	13	6	AAE35467	Aae35467 Abeta pep
131	27	93.1	7	9	ADZ08903	Adz08903 Human bet	204	27	93.1	13	6	ADA37467	Ada37467 Human amy
132	27	93.1	8	2	AAW02310	Aaw02310 Beta-amyl	205	27	93.1	13	8	ADJ71477	Adj71477 N-termina
133	27	93.1	8	2	AAW45967	Aaw45967 Peptide d	206	27	93.1	13	8	ADJ71464	Adj71464 N-termina
134	27	93.1	8	2	AAW32551	Aaw32551 Amyloidog	207	27	93.1	13	8	ADQ37408	Adq37408 Amyloid-b
135	27	93.1	8	2	AAW89374	Aaw89374 Beta-amyl	208	27	93.1	13	8	ADQ37290	Adq37290 Vaccine a
136	27	93.1	8	4	AAE10663	Aae10663 Human amy	209	27	93.1	14	6	ADA89887	Ada89887 Beta-A4 s
137	27	93.1	8	4	AAE02615	Aae02615 Human amy	210	27	93.1	14	6	ADJ71452	Adj71452 N-termina
138	27	93.1	8	5	ABG71005	Abg71005 Long form	211	27	93.1	14	8	ADJ71465	Adj71465 N-termina
139	27	93.1	8	5	ABB78624	Abb78624 Human alp	212	27	93.1	14	8	ADJ71478	Adj71478 N-termina
140	27	93.1	8	5	ABB05153	Abb05153 Beta amyl	213	27	93.1	14	9	ADZ08889	Adz08889 Human bet
141	27	93.1	8	5	ABU09765	Abu09765 Amyloidog	214	27	93.1	15	2	AAW02334	Aaw02334 Beta-amyl
142	27	93.1	8	6	ABR61959	Abr61959 Human amy	215	27	93.1	15	2	AAW89358	Aaw89358 Beta-amyl
143	27	93.1	8	7	ABW00134	Abw00134 Beta-amyl	216	27	93.1	15	2	AAW89354	Aaw89354 Beta-amyl
144	27	93.1	8	8	ADJ64056	Adj64056 Human bet	217	27	93.1	15	5	ABG71014	Abg71014 Long form
145	27	93.1	8	8	ADQ37385	Adq37385 Antifibri	218	27	93.1	15	5	ABB05162	Abb05162 Beta amyl
146	27	93.1	8	8	ADQ37349	Adq37349 Beta-amyl	219	27	93.1	15	5	AAE26271	Aae26271 Human bet
147	27	93.1	8	9	ADZ08900	Adz08900 Human bet	220	27	93.1	15	6	ABU79057	Abu79057 Aggregati
148	27	93.1	8	9	AEA51423	Aea51423 C-Abeta 1	221	27	93.1	15	6	ABU79064	Abu79064 Aggregati
149	27	93.1	8	9	AEA51420	Aea51420 A 16-22-C	222	27	93.1	15	6	ABU79059	Abu79059 Aggregati
150	27	93.1	8	9	AEA62831	Aea62831 Immunocon	223	27	93.1	15	6	ABU79060	Abu79060 Aggregati
151	27	93.1	8	9	AEA62834	Aea62834 Immunocon	224	27	93.1	15	6	ABU79055	Abu79055 Aggregati
152	27	93.1	9	2	AAE45239	Aae45239 Mutant am	225	27	93.1	15	6	ABU79056	Abu79056 Aggregati
153	27	93.1	9	4	AAU48493	Aau48493 Antifibri	226	27	93.1	15	6	ABU79062	Abu79062 Aggregati
154	27	93.1	9	5	AAU11667	Aau11667 Peptide #	227	27	93.1	15	7	ABW00190	Abw00190 Peptide #
155	27	93.1	9	6	ABP57517	Abp57517 Different	228	27	93.1	15	7	ABW00198	Abw00198 Peptide #
156	27	93.1	9	6	ABU79063	Abu79063 Aggregati	229	27	93.1	15	7	ABW00189	Abw00189 Peptide #
157	27	93.1	9	6	AAE35436	Aae35436 Abeta pep	230	27	93.1	15	7	ABW00193	Abw00193 Peptide #
158	27	93.1	9	7	ABW00197	Abw00197 Peptide #	231	27	93.1	15	7	ABW00191	Abw00191 Peptide #
159	27	93.1	9	8	ADI36003	Adi36003 Amyloid b	232	27	93.1	15	7	ABW00196	Abw00196 Peptide #
160	27	93.1	9	8	ADI35849	Adi35849 Amyloid b	233	27	93.1	15	7	ABW00194	Abw00194 Peptide #
161	27	93.1	9	8	ADI35874	Adi35874 Amyloid b	234	27	93.1	15	7	ADK82695	Adk82695 Beta-amyl
162	27	93.1	9	8	ADI35871	Adi35871 Amyloid b	235	27	93.1	15	7	ADK82697	Adk82697 Beta-amyl
163	27	93.1	9	8	ADI35903	Adi35903 Amyloid b	236	27	93.1	15	7	ADK82700	Adk82700 Beta-amyl
164	27	93.1	9	8	ADQ37260	Adq37260 Vaccine a	237	27	93.1	15	7	ADK82698	Adk82698 Beta-amyl
165	27	93.1	9	8	ADQ37332	Adq37332 Antifibri	238	27	93.1	15	7	ADK82699	Adk82699 Beta-amyl
166	27	93.1	9	9	AEA51414	Aea51414 A 16-23-C	239	27	93.1	15	8	ADJ71466	Adj71466 N-termina
167	27	93.1	9	9	AEA51417	Aea51417 C-A 16-23	240	27	93.1	15	8	ADJ71453	Adj71453 N-termina
168	27	93.1	9	9	AEA62825	Aea62825 Immunocon	241	27	93.1	15	8	ADJ71479	Adj71479 N-termina
169	27	93.1	9	9	AEA62828	Aea62828 Immunocon	242	27	93.1	15	8	ADJ71440	Adj71440 N-termina
170	27	93.1	10	3	AA79938	Aay79938 Beta-amyl	243	27	93.1	15	8	ADJ64065	Adj64065 Human bet

244	27	93.1	16	5	AAB26330	Human bet	KW	cytoprotection; amyloid deposit degradation; amyloidosis disorder;
245	27	93.1	16	8	ADJ71454	N-termina	KW	Alzheimer's disease.
246	27	93.1	16	8	ADJ71480	N-termina	XX	
247	27	93.1	16	8	ADJ71441	N-termina	OS	Homo sapiens.
248	27	93.1	16	8	ADJ71467	N-termina	XX	
249	27	93.1	16	8	ADJ71428	N-termina	PH	Location/Qualifiers
250	27	93.1	17	2	AAR54703	Beta-amyl	FT	Modified-site 6
251	27	93.1	17	2	AAB18880	Beta-amyl	PT	/note= "C-terminal amide"
252	27	93.1	17	4	AAB91774	Amyloid b	XX	WO200068263-A2.
253	27	93.1	17	4	AAB91807	Amyloid b	PN	
254	27	93.1	17	4	AAB48346	Beta-amyl	XX	16-NOV-2000.
255	27	93.1	17	5	ABO4911	Human amy	PD	
256	27	93.1	17	6	AAB35468	Beta pep	XX	
257	27	93.1	17	6	AB99611	Peptide d	XX	
258	27	93.1	17	8	ADG93165	Novel exp	PP	04-MAY-2000; 2000WO-CA000515.
259	27	93.1	17	8	ADJ65843	Amyloid B	PR	05-MAY-1999; 99US-0132592P.
260	27	93.1	17	8	ADN02827	Mammalian	XX	(NEUR-) NEUROCHEM INC.
261	27	93.1	17	8	ADQ37291	Vaccine a	XX	
262	27	93.1	17	8	AD818447	Amyloid-b	PA	Chalifour R, Gervais F, Gupta A;
263	27	93.1	18	3	AAB10963	Beta-amyl	PI	WPI; 2001-031852/04.
264	27	93.1	19	2	AAB18882	AEDANS-be	XX	
265	27	93.1	19	3	AAB18881	Tri-Beta-	DR	
266	27	93.1	19	3	AAY79935	Beta-amyl	XX	
267	27	93.1	19	4	AAB49097	Human amy	PT	Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
268	27	93.1	19	4	AAB46201	Human APP	PT	cytoprotection for treating amyloidosis disorders, comprises a peptide,
269	27	93.1	19	8	ADU24440	Novel glu	PT	its isomer or peptidomimetic.
270	27	93.1	19	8	ADU24442	Novel glu	XX	
271	27	93.1	19	8	ADU46714	Amyloid b	XX	Claim 7; Page 25; 46pp; English.
272	27	93.1	19	8	ADU46716	Gln3 amyl	CC	
273	27	93.1	19	9	ADZ71366	Human bet	XX	Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
274	27	93.1	19	9	ADZ71368	Human bet	CC	for inhibiting amyloidosis and/or for cytoprotection. The peptides of
275	27	93.1	19	9	AEA35401	Novel QC	CC	AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
276	27	93.1	19	9	AEA35399	Novel QC	CC	useful for treating amyloidosis disorders such as Alzheimer's disease.
277	27	93.1	19	9	AE92572	Glutamin	CC	Peptides AAB48474-B48496 were identified from the glycosaminoglycan
278	27	93.1	19	9	AE92574	Glutamin	CC	binding region and the prot-prot interaction region of the human amyloid
279	27	93.1	20	3	AAY79934	Beta-amyl	CC	protein
280	27	93.1	20	5	ABB06431	Beta-secr	XX	
281	27	93.1	21	2	AAY30941	Human sec	XX	Sequence 6 AA;
282	27	93.1	21	8	ADU24439	Novel glu	XX	Query Match 100.0%; Score 29; DB 4; Length 6;
283	27	93.1	21	8	ADU46713	Amyloid b	XX	Best Local Similarity 100.0%; Pred. No. 2e+06;
284	27	93.1	21	9	ADV86872	Beta-amyl	XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
285	27	93.1	21	9	ADZ71365	Human bet	XX	
286	27	93.1	21	9	AEA35398	Novel QC	XX	
287	27	93.1	21	9	AE92571	Glutamin	XX	QY 1 KIVFFFA 6
288	27	93.1	22	8	ADR83670	Amyloidog	DB	1 KIVFFFA 6
289	27	93.1	24	2	AAR52569	Alzheimer	XX	
290	27	93.1	24	9	ADW88085	T668 phos	XX	
291	27	93.1	24	9	AE909195	Human bet	XX	
292	27	93.1	24	9	AE909194	Human bet	XX	
293	27	93.1	26	2	AAW47229	Beta-amyl	XX	
294	27	93.1	26	2	AAW47229	Beta-amyl	XX	
295	27	93.1	26	6	ABU63718	Rat amylo	XX	
296	27	93.1	26	7	ADP55647	Human A b	XX	
297	27	93.1	26	9	ADY72250	N-termina	XX	
298	27	93.1	27	2	AAY33409	Human amy	XX	
299	27	93.1	28	1	AAP70594	Sequence	XX	
300	27	93.1	28	1	AAP90381	Synthetic	XX	

ALIGNMENTS

RESULT 1
 AAB48483
 ID AAB48483 standard; peptide; 6 AA.
 AC AAB48483;
 XX
 XX 02-MAR-2001 (first entry)
 XX Antifibrillogenic peptide #10.
 DE Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW

RESULT 2
 AAB48474
 ID AAB48474 standard; peptide; 6 AA.
 AC AAB48474;
 XX
 XX 02-MAR-2001 (first entry)
 XX Antifibrillogenic peptide #1.
 DE
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 OS Homo sapiens.
 XX
 XX WO200068263-A2.
 XX
 XX 16-NOV-2000.
 XX
 XX 04-MAY-2000; 2000WO-CA000515.
 XX
 XX 05-MAY-1999; 99US-0132592P.
 XX
 XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 XX cytoprotection for treating amyloidosis disorders, comprises a peptide,
 XX its isomer or peptidomimetic.
 XX
 XX Claim 7; Page 25; 46pp; English.
 XX
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 XX for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 XX AA48474-B48496 cause the breakdown of amyloid deposits and are therefore
 XX useful for treating amyloidosis disorders such as Alzheimer's disease.
 XX Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 XX binding region and the prot-prot interaction region of the human amyloid
 XX protein
 XX
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 29; DB 4; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 KIVFFA 6
 XX Db |||||
 XX 1 KIVFFA 6
 XX
 XX RESULT 3
 XX AAB82623
 XX ID AAB82623 standard; peptide; 6 AA.
 XX AC AAB82623;
 XX XX
 XX DT 02-OCT-2001 (first entry)
 XX DE All-D peptide used in Alzheimer's disease vaccine.
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 XX KW therapy; antigen.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 XX FT Misc-difference 1..6
 XX FT /note= "all D-form residues"
 XX
 XX WO200139796-A2.
 XX
 XX 07-JUN-2001.
 XX PD
 XX PP 29-NOV-2000; 2000WO-CA001413.
 XX XX
 XX PR 29-NOV-1999; 99US-0168594P.
 XX PR 28-NOV-2000; 2000US-00724842.
 XX XX
 XX PA (NEUR-) NEUROCHEM INC.
 XX XX
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX DR Preventing/treating amyloid-related disease, especially Alzheimer's
 XX PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 XX PT which elicits production of antibodies to prevent fibrillogenesis and
 XX PT associated cellular toxicity.
 XX
 XX PS Disclosure; Page 10; 31pp; English.
 XX
 XX The present sequence is that of an all-D peptide suitable for use for
 XX preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 29; DB 4; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 KIVFFA 6
 XX Db |||||
 XX 1 KIVFFA 6
 XX
 XX RESULT 4
 XX AAB82631
 XX ID AAB82631 standard; peptide; 6 AA.
 XX AC AAB82631;
 XX XX
 XX DT 02-OCT-2001 (first entry)
 XX DE All-D peptide used in Alzheimer's disease vaccine.
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 XX KW therapy; antigen.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 XX FT Misc-difference 1..6
 XX FT /note= "all D-form residues"
 XX FT Modified-site 6
 XX FT /note= "C-terminal amide"
 XX
 XX WO200139796-A2.
 XX
 XX 07-JUN-2001.
 XX PD
 XX PP 29-NOV-2000; 2000WO-CA001413.
 XX XX
 XX PR 29-NOV-1999; 99US-0168594P.
 XX PR 28-NOV-2000; 2000US-00724842.
 XX XX
 XX PA (NEUR-) NEUROCHEM INC.
 XX XX
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX DR Preventing/treating amyloid-related disease, especially Alzheimer's
 XX PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 XX PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB8622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB8623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |||||
 Db 1 KIVFFPA 6

RESULT 5

AAU96819
 ID AAU96819 standard; peptide; 6 AA.

XX AAU96819;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #9.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 1..6 /note= "Preferably D-form residue"

FT Modified-site 6 /note= "Ala is amidated"

FT WO200207781-A2.

PN 31-JAN-2002.

XX

PF 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

PA Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid

XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an

XX amyloid targeting moiety, a linker moiety and a labelling moiety. The

XX agent is of general formula A-t-(A₁n₁k)_z-A₁a₁b₁(i) where z = 0 - 1;

XX A₁t = an amyloid targeting moiety; A₁n₁k = a linker moiety; and A₁a₁b₁

XX = a labelling moiety. Also included are imaging amyloid deposition or

XX diagnosing an amyloid-related condition in a patient involving

XX administering (i) to the patient, and ultrasound imaging (i) in the

XX patient to determine the presence of amyloid or amyloid-related condition

XX ; and a kit for preparing a radiopharmaceutical preparation comprising

XX (i), a reducing agent, a buffering agent, a transchelating agent, and

XX instructions for the preparation and use of the radiopharmaceutical in

XX the imaging of amyloid or an amyloid-related condition. The agents are

XX used for imaging amyloid deposition and for diagnosing an amyloid related

XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible

XX cerebral amyloidosis (transmissible virus dementia), familial CJD,

XX scrapie, transmissible mink encephalopathy, bovine spongiform

XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,

XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible

XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,

XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral

XX amyloid angiopathy. The agents are capable of crossing the blood-brain

XX barrier and are capable of binding specifically to amyloid plaques. The

XX present sequence is a peptide forming the amyloid targeting moiety of the

XX agent of the invention

XX Sequence 6 AA;

XX Query Match 100.0%; Score 29; DB 5; Length 6;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |||||

Db 1 KIVFFPA 6

RESULT 6

AAU96811

ID AAU96811 standard; peptide; 6 AA.

XX AAU96811;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #1.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;

XX transmissible cerebral amyloidosis; transmissible virus dementia;

XX scrapie; transmissible mink encephalopathy; BSE; type II diabetes;

XX bovine spongiform encephalopathy; inflammation associated amyloid;

XX primary amyloidosis; feline spongiform encephalopathy;

XX Alzheimer's disease; prion-mediated disease; blood-brain barrier;

XX dialysis-related amyloidosis; light chain-related amyloidosis;

XX cerebral amyloid angiopathy.

XX Synthetic.

XX

XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX PT WPI; 2002-075222/10.
 XX DR
 XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX PS Disclosure; Page 10; 68pp; English.
 XX CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11659, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX CC
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 1 KIVFFPA 6
 RESULT 9
 AAE35446
 ID AAE35446 standard; peptide; 6 AA.
 XX AC AAE35446;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #17.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; bronchiectasis, decubitus
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT Modified-site 6 /note= "D-form residues"
 FT /note= "C-terminal amide"
 XX WO200296937-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX PR 29-MAY-2001; 2001US-00867847.
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX DR WPI; 2003-201269/19.
 XX PT Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX PS Claim 1; Page 59; 44pp; English.
 XX CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D-
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 1 KIVFFPA 6
 RESULT 10
 AAE35438
 ID AAE35438 standard; peptide; 6 AA.
 XX AC AAE35438;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #9.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neotropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT /note= "D-form residues"
 XX WO200296937-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX PR 29-MAY-2001; 2001US-00867847.
 XX PA (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 58; 44pp; English.
 XX
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 1 KIVFFA 6
 RESULT 11
 ADQ37322
 ID ADQ37322 standard; peptide; 6 AA.
 AC ADQ37322;
 XX
 XX 07-OCT-2004 (first entry)
 XX
 XX Antifibrillogenic amyloidosis inhibiting peptide.
 XX
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "amidated"
 XX
 XX WO2004058239-A1.

15-JUL-2004.
 24-DEC-2003; 2003WO-CA002021.
 24-DEC-2002; 2002US-0436379P.
 23-JUN-2003; 2003US-0482214P.
 (NEUR-) NEUROCHEM INT LTD.
 Gervais F, Bellini F;
 WPI; 2004-543342/52.
 Composition for treating e.g. Alzheimer's disease comprises first agent
 that prevents or treats amyloid-beta related disease and second agent
 that is either a peptide or peptidomimetic or an immune system modulator.
 Disclosure; Page 69; 143pp; English.
 The present invention describes compositions (C) comprising: (a) a first
 agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 a second agent (a2) that is: (i) a peptide or peptidomimetic that
 modulates amyloid-beta fibril formation or induces a prophylactic or
 therapeutic immune response against amyloid-beta fibril formation; or
 (ii) an immune system modulator that prevents or inhibits amyloid-beta
 fibril formation. Also described is a kit comprising (C). (C) have
 neurotropic, neuroprotective, cerebroprotective, haemostatic,
 ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 and can be used as amyloid-beta fibril formation modulators, and as
 immune system modulators. (C) can be used for preventing or treating an
 amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 mild-to-moderate cognitive impairment, vascular dementia, cerebral
 amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 Down's syndrome, inclusion body myositis, age-related macular
 degeneration, or a condition associated with Alzheimer's disease
 (including hypothyroidism, cerebrovascular disease, cardiovascular
 disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 aggression, or incontinence), a neurological condition (e.g. Huntington's
 disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 field deficits, incoordination, gait disturbance, transient ischaemic
 attack or stroke, transient alertness, attention deficit, frequent falls
 syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 damage), or a psychological condition (e.g. depression, delusions,
 illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 excessive guilt)) in a subject e.g. human having a genomic mutation in an
 amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 having amyloid-beta deposits. The present sequence represents a peptide
 that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 in the exemplification of the present invention.
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 1 KIVFFA 6
 RESULT 12
 ADQ37270
 ID ADQ37270 standard; peptide; 6 AA.

PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 69; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C) (C) have
 CC nontropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothalamic, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 |||||
 Db 1 KIVFFA 6
 RESULT 14
 ADQ37262
 ID ADQ37262 standard; peptide; 6 AA.
 XX
 AC ADQ37262;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nontropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"
 FT WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 PA Gervais F, Bellini F;
 WIPI; 2004-543342/52.
 XX
 CC Composition for treating e.g. Alzheimer's disease comprises first agent
 CC that prevents or treats amyloid-beta related disease and second agent
 CC that is either a peptide or peptidomimetic or an immune system modulator.
 PS Disclosure; Page 67; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C) (C) have
 CC nontropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothalamic, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.


```

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 1 KIVFFA 6

RESULT 15
ADY37921
ID ADY37921 standard; peptide; 6 AA.
XX AC ADY37921;
XX DT 19-MAY-2005 (first entry)
XX DE Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
XX KW transmissible spongiform encephalopathy; scrapie; BSE;
XX KW Alzheimers disease; neurological disease; amyloidosis;
XX KW non-insulin dependent diabetes; metabolic disorder.
XX OS Synthetic.
XX PN US2005048000-A1.
XX PD 03-MAR-2005.
XX PF 03-DEC-2003; 2003US-00728028.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PR 29-JAN-2003; 2003US-0443291P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais P, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX PS New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
XX PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
XX PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX PS Disclosure; SEQ ID NO 1; 34pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
XX CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
XX CC a labeling moiety via a linking moiety, and is preferably able to cross
XX CC the blood-brain barrier. The invention also relates to a kit for
XX CC preparing a radiopharmaceutical preparation from the imaging agent of the
XX CC invention, a method for imaging amyloid deposition in a patient and a
XX CC method for diagnosing an amyloid-related condition in a patient. The
XX CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
XX CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
XX CC transmissible cerebral amyloidosis (also known as transmissible virus
XX CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
XX CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
XX CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
XX CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
XX CC mediated diseases, dialysis-related amyloidosis, light chain-related
XX CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
XX CC patient. The agent does not exhibit excessive toxicity or irritation,
XX CC does not induce an allergic response, and permits an earlier diagnosis of
XX CC amyloid-related conditions, thereby allowing earlier treatment and hence
XX CC prevention of the undesirable effects of such disorders. Sequences
XX CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
XX CC the amyloid-targeting moiety in an imaging agent of the invention.

```

```

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 1 KIVFFA 6

RESULT 16
ADY37929
ID ADY37929 standard; peptide; 6 AA.
XX AC ADY37929;
XX DT 19-MAY-2005 (first entry)
XX DE Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
XX KW transmissible spongiform encephalopathy; scrapie; BSE;
XX KW Alzheimers disease; neurological disease; amyloidosis;
XX KW non-insulin dependent diabetes; metabolic disorder.
XX OS Synthetic.
XX PN US2005048000-A1.
XX PD 03-MAR-2005.
XX PF 03-DEC-2003; 2003US-00728028.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PR 29-JAN-2003; 2003US-0443291P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais P, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX PS New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
XX PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
XX PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX PS Disclosure; SEQ ID NO 9; 34pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
XX CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
XX CC a labeling moiety via a linking moiety, and is preferably able to cross
XX CC the blood-brain barrier. The invention also relates to a kit for
XX CC preparing a radiopharmaceutical preparation from the imaging agent of the
XX CC invention, a method for imaging amyloid deposition in a patient and a
XX CC method for diagnosing an amyloid-related condition in a patient. The
XX CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
XX CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
XX CC transmissible cerebral amyloidosis (also known as transmissible virus
XX CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
XX CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
XX CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
XX CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
XX CC mediated diseases, dialysis-related amyloidosis, light chain-related
XX CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
XX CC patient. The agent does not exhibit excessive toxicity or irritation,
XX CC does not induce an allergic response, and permits an earlier diagnosis of

```

CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
| | | | |
Db 1 KIVFFA 6

RESULT 17
ABG26598
ID ABG26598 standard; protein; 99 AA.

XX AC ABG26598;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #26589.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX FN WO200175067-A2.
XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS90785.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 56957; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 29; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
| | | | |
Db 63 KIVFFA 68

RESULT 18
AAB48482
ID AAB48482 standard; peptide; 6 AA.

XX AC AAB48482;
XX DT 02-MAR-2001 (first entry)
XX DE Antifibrillogenic peptide #9.
XX KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
XX KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
XX KW Alzheimer's disease.
XX OS Homo sapiens.
XX FN WO200068263-A2.
XX PD 16-NOV-2000.
XX PF 04-MAY-2000; 2000WO-CA000515.
XX PR 05-MAY-1999; 99US-0132592P.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Chalifour R, Gervais F, Gupta A;
XX DR WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
| | | | |
Db 1 KIVFFA 6

RESULT 19
AAB48490
ID AAB48490 standard; peptide; 6 AA.

XX

AC AAB48490;
 XX 02-MAR-2001 (first entry)
 XX Antifibrillogenic peptide #17.
 DE Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "C-terminal amide"
 FT
 XX WO200068263-A2.
 PN 16-NOV-2000.
 PD 04-MAY-2000; 2000WO-CA000515.
 PF 05-MAY-1999; 99US-0132592P.
 PR (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Gervais P, Gupta A;
 XX WPI; 2001-031852/04.
 DR Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 PS Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 Db 1 KVVFFFA 6
 RESULT 20
 AAB82630
 ID AAB82630 standard; peptide; 6 AA.
 AC AAB82630;
 XX 02-OCT-2001 (first entry)
 DT All-D peptide used in Alzheimer's disease vaccine.
 DE Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "all D-form residues"
 FT

XX WO200139796-A2.
 PN 07-JUN-2001.
 PD 29-NOV-2000; 2000WO-CA001413.
 PF 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Hebert L, Kong X, Gervais P;
 XX WPI; 2001-441458/47.
 DR Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 11; 31pp; English.
 PS The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 Db 1 KVVFFFA 6
 RESULT 21
 AAB82638
 ID AAB82638 standard; peptide; 6 AA.
 XX AAB82638;
 AC 02-OCT-2001 (first entry)
 DT All-D peptide used in Alzheimer's disease vaccine.
 DE Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6

FT Modified-site 6 /note= "all D-form residues"

FT Modified-site 6 /note= "C-terminal amide"

XX WO200139796-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA001413.

XX 29-NOV-1999; 99US-0168594P.

PR 28-NOV-2000; 2000US-00724842.

XX (NEUR-) NEUROCHEM INC.

PA Chalifour R, Hebert L, Kong X, Gervais F;

PI WPI; 2001-441458/47.

DR Preventing/treating amyloid-related disease, especially Alzheimer's

XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and

PT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in

CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of

CC amyloid-beta peptide (see AAB2622), and may be modified by removing or

CC inserting 1 or more amino acid residues, or by substituting 1 or more

CC amino acid residues with other amino acid residues or non-amino acid

CC fragments. Vaccines of the invention are produced using 'non-self'

CC peptides synthesised from the unnatural D-configuration amino acids to

CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be

CC aggregated to be operative or immunogenic. They preferably interact with

CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or

CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic

CC fragments, protein conjugates, immunogenic derivative peptides and

CC immunogenic peptidomimetics. Examples include all-D peptides

CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and

CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given

CC in AAB2623-64. The vaccine elicits a preferential TH-2 or TH-1 response,

CC preventing fibrillogenesis and associated cellular toxicity. The amyloid

CC related diseases may be localised amyloidosis, e.g. diabetes type II,

CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,

CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and

CC prion protein related disorders, or systemic amyloidosis associated with

CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.

CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic

CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

XX Query Match 96.6%; Score 28; DB 4; Length 6;

XX Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 1 KVVFFA 6

RESULT 22

ID AAU96818

XX AAU96818 standard; peptide; 6 AA.

AC AAU96818;

XX

DT 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #8.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;

KW transmissible cerebral amyloidosis; transmissible virus dementia;

KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;

KW bovine spongiform encephalopathy; inflammation associated amyloid;

KW primary amyloidosis; feline spongiform encephalopathy;

KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;

KW dialysis-related amyloidosis; light chain-related amyloidosis;

KW cerebral amyloid angiopathy.

XX Synthetic.

OS Key Location/Qualifiers

XX Misc-difference 1..6

FT /note= "Preferably D-form residue"

FT WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

PA Gervais F, Kong X, Chalifour R, Migneault D;

PI WPI; 2002-371447/40.

DR New amyloid-targeting imaging agents useful for in vivo imaging amyloid

PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an

CC amyloid targeting moiety, a linker moiety and a labelling moiety. The

CC agent is of general formula A_t-(A_1)_n-K-(A_1)_m-A_b (I) where z = 0 - 1;

CC A_t = an amyloid targeting moiety; A_1)_n-K = a linker moiety; and A_1)_m-

CC = a labelling moiety. Also included are imaging amyloid deposition or

CC diagnosing an amyloid-related condition in a patient involving

CC administering (I) to the patient, and ultrasound imaging (I) in the

CC patient to determine the presence of amyloid or amyloid-related condition

CC ; and a kit for preparing a radiopharmaceutical preparation comprising

CC (I), a reducing agent, a buffering agent, a transchelating agent, and

CC instructions for the preparation and use of the radiopharmaceutical in

CC the imaging of amyloid or an amyloid-related condition. The agents are

CC used for imaging amyloid deposition and for diagnosing an amyloid related

CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible

CC cerebral amyloidosis (transmissible virus dementia), familial CJD,

CC scrapie, transmissible mink encephalopathy, bovine spongiform

CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,

CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible

CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,

CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral

CC amyloid angiopathy. The agents are capable of crossing the blood-brain

CC barrier and are capable of binding specifically to amyloid plaques. The

CC present sequence is a peptide forming the amyloid targeting moiety of the

XX agent of the invention

XX Sequence 6 AA;

XX Query Match 96.6%; Score 28; DB 5; Length 6;

XX Best Local Similarity 83.3%; Pred. No. 2e+06;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 1 KVVFFA 6

RESULT 23
AAU96826
ID AAU96826 standard; peptide; 6 AA.
XX
AC AAU96826;
XX
DT 30-JUL-2002 (first entry)
XX
DE Amyloid targeting peptide #16.
XX
KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
transmissible cerebral amyloidosis; transmissible virus dementia;
scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
bovine spongiform encephalopathy; inflammation associated amyloid;
primary amyloidosis; feline spongiform encephalopathy;
Alzheimer's disease; prion-mediated disease; blood-brain barrier;
dialysis-related amyloidosis; light chain-related amyloidosis;
cerebral amyloid angiopathy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "Preferably D-form residue"
FT Modified-site 6
FT /note= "Ala is amidated"
XX
PN WO200207781-A2.
XX
PD 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
XX
XX 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX
XX WPI; 2002-371447/40.
XX
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
amyloid targeting moiety, a linker moiety and a labelling moiety. The
agent is of general formula A t-(A 1 n k) z-A 1 a b (I) where z = 0 - 1;
A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b
= a labelling moiety. Also included are imaging amyloid deposition or
diagnosing an amyloid-related condition in a patient involving
administering (I) to the patient, and ultrasound imaging (I) in the
patient to determine the presence of amyloid or amyloid-related condition
; and a kit for preparing a radiopharmaceutical preparation comprising
(I), a reducing agent, a buffering agent, a transchelating agent, and
instructions for the preparation and use of the radiopharmaceutical in
the imaging of amyloid or an amyloid-related condition. The agents are
used for imaging amyloid deposition and for diagnosing an amyloid related
condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
cerebral amyloidosis (transmissible virus dementia), familial CJD,
scrapie, transmissible mink encephalopathy, bovine spongiform
encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
primary amyloidosis, feline spongiform encephalopathy, non-transmissible
cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
amyloid angiopathy. The agents are capable of crossing the blood-brain
barrier and are capable of binding specifically to amyloid plaques. The
present sequence is a peptide forming the amyloid targeting moiety of the
agent of the invention

XX Sequence 6 AA;
SQ
Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 1 KVVFFA 6
|:||||
|:||||
RESULT 24
AAU11664
ID AAU11664 standard; peptide; 6 AA.
XX
AC AAU11664;
XX
DT 09-APR-2002 (first entry)
XX
DE Peptide #17, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
FT
XX
PN WO200185093-A2.
XX
PD 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
disease comprises contacting blood vessel wall cell with amyloid-beta 40
inhibitor.
XX
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
amyloid angiopathy. The new method of the invention involves contacting a
blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
can be used for treating disease states characterised by cerebral amyloid
angiopathy, particularly Alzheimer's disease, hereditary cerebral
haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
The present sequence represents one of a group of peptides (AAU11648-
AAU11669, AAU11910 & AAU11911) that were used in the invention as a
carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
was used in the invention to treat a disease state characterised by
cerebral amyloid angiopathy (CAA)
XX
XX Sequence 6 AA;
SQ
Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 1 KVVFFA 6
|:||||
|:||||

RESULT 25
 AAU11656
 ID AAU11656 standard; peptide; 6 AA.
 AC AAU11656;
 XX
 DT 09-APR-2002 (first entry)
 DE
 DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
 XX
 OS Synthetic.
 XX
 FN WO2000185093-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 22-DEC-2000; 2000WO-IB002078.
 XX
 PR 23-DEC-1999; 99US-0171877P.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Green AM, Gervais F;
 XX
 DR WPI; 2002-075222/10.
 XX
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX
 PS Disclosure; Page 10; 69pp; English.
 XX
 CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX
 SQ Sequence 6 AA;
 Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 1 KVVFFA 6
 |:|:|:|
 |:|:|:|
 RESULT 26
 AAU11652
 ID AAU11652 standard; peptide; 6 AA.
 AC AAU11652;
 XX
 DT 17-JUN-2003 (first entry)
 DE
 DE Abeta peptide #23.
 XX
 KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;

psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
 chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 FN WO200296937-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-CA000763.
 XX
 PR 29-MAY-2001; 2001US-00867847.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 PT Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 PS Claim 1; Page 59; 44pp; English.
 XX
 CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal, and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention

XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 1 KVVFFA 6
 |:|:|:|
 |:|:|:|
 RESULT 27
 ADQ37277
 ID ADQ37277 standard; peptide; 6 AA.
 XX
 AC ADQ37277;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment; immune system modulator;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 XX OS
 XX Key Location/Qualifiers
 FT Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "amidated"
 FT
 XX
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 XX SQ Sequence 6 AA;
 XX
 XX Query Match 96.6%; Score 28; DB 8; Length 6;
 XX Best Local Similarity 83.3%; Pred. No. 2e+06;
 XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 KIVFFA 6
 XX Db 1 KVVFFA 6
 XX
 XX
 XX RESULT 28
 XX ADQ37321
 XX ID ADQ37321 standard; peptide; 6 AA.
 XX AC ADQ37321;
 XX DT 07-OCT-2004 (first entry)
 XX DE Antifibrillogenic amyloidosis inhibiting peptide.
 XX KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 XX OS
 XX WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 69; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first

CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C): (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

Db 1 KVVFFPA 6

RESULT 29

ADQ37329

ID ADQ37329 standard; peptide; 6 AA.

XX AC ADQ37329;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;

KW vaccine antigen.
 XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 6 /note= "amidated"

XX W02004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 23-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 XX that prevents or treats amyloid-beta related disease and second agent
 XX that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 70; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C): (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;

Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 30

ADY37928
ID ADY37928 standard; peptide; 6 AA.

XX AC ADY37928;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais P, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 8; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 31

ADY37936
ID ADY37936 standard; peptide; 6 AA.

XX AC ADY37936;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais P, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 16; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|||||
 Db 1 KWVFFA 6

RESULT 32
 ADQ09761
 ID ADQ09761 standard; peptide; 22 AA.
 XX
 AC ADQ09761;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Rice 26kDa globulin signal sequence SEQ ID NO:117.
 XX
 KW prolamine; rice; plant; seed; transgenic plant; signal.
 XX
 OS Oryza sativa.
 XX
 FN WO2004056993-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 09-DEC-2003; 2003WO-JP015753.
 XX
 PR 20-DEC-2002; 2002JP-00369700.
 XX
 FA (NAAQ-) NAT AGRIC & BIO-ORIENTED RES ORG.
 XX
 PI Kuroda M;
 XX
 DR WPI; 2004-525439/50.
 DR N-PSDB; ADQ09760.
 XX
 PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding
 PT prolamine, useful for reducing expression dose of protein in seed, and
 PT for producing transgenic plant, preferably rice plant having reduced
 PT storage protein.
 XX
 PS Example 13; SEQ ID NO 117; 272pp; Japanese.
 XX
 CC The present invention describes a nucleic acid molecule (I) comprising a
 CC consecutive nucleic acid sequence (S1) of at least 15 bp in length and
 CC complementary with a nucleic acid sequence encoding a prolamine
 CC polypeptide or a nucleic acid sequence having a homology of at least
 CC about 70% to (S1). Also described: (1) a nucleic acid molecule (N1)
 CC comprising a nucleic acid sequence (A) having about 70% homology to a
 CC nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid
 CC acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable
 CC of causing RNA interference of the gene sequence encoding a prolamine
 CC polypeptide; (3) a nucleic acid cassette (III) containing (I); (4)
 CC producing (III); (5) a vector (IV) comprising (I); (6) a plant cell (V)
 CC comprising (I); (7) a plant tissue (VI) comprising (V); (8) a plant (VII)
 CC containing (I) or (V); (9) a seed (VIII) produced by (VII); (10) starch
 CC preparation produced from (VII) or (VIII); and (11) a composition
 CC containing gene product of foreign gene produced from (VII) or (VIII).
 CC (I) is useful for decreasing the expression level of a protein in the
 CC seed of a plant, for expressing a foreign gene in the seed of a plant and
 CC for decreasing the expression of a natural protein in the seed of a
 CC plant. The method of decreasing the amount of expression level of a
 CC protein in the seed of a plant involves providing (I), introducing (I)
 CC into the cell of the plant, redifferentiating the cell, producing a
 CC transgenic plant, and obtaining the seed from the transgenic plant. The
 CC method after the step of introduction, further involves selecting the
 CC cell introduced with (I), by determining resistance with respect to
 CC antibiotics. The method of expressing a foreign gene in the seed of a
 CC plant, involves providing (I) and the nucleic acid molecule encoding a

foreign gene product, introducing (I) and the nucleic acid molecule
 encoding a foreign gene product into cell of the plant, re-
 differentiating the cell, producing a transgenic plant, and obtaining the
 seed from the transgenic plant. The method further involves isolating the
 gene product of the foreign gene from the seed. (I) is useful for
 producing transgenic plants having reduced expression of storage proteins
 and for reducing the expression dose of a protein in a seed of a plant.
 The present sequence represents a rice 26kDa globulin signal sequence,
 which is used in the exemplification of the present invention.

XX
 SQ Sequence 22 AA;
 Query Match 96.6%; Score 28; DB 8; Length 22;
 Best Local Similarity 83.3%; Pred. No. 19;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|||||
 Db 4 KWVFFA 9

RESULT 33
 ADT93984
 ID ADT93984 standard; peptide; 23 AA.
 XX
 AC ADT93984;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Rice 26 kDa peptide.
 XX
 KW Storage protein; allergen specific T cell epitope;
 KW vesicle anchoring signal; transgenic plant; rice albumen;
 KW T cell epitope-attached peptide; 7crp; seed; glutelin; edible vaccine;
 KW Japanese cedar pollen antigen; CryJ1; CryJ2; allergic disease; hay fever;
 KW antiallergic; plant; 26 kDa.
 XX
 OS Oryza sativa.
 XX
 FN WO2004094637-A1.
 XX
 PD 04-NOV-2004.
 XX
 PF 23-APR-2004; 2004WO-JP005938.
 XX
 PR 24-APR-2003; 2003JP-00120639.
 XX
 FA (NORQ) NAT INST AGROBIOLOGICAL SCI.
 XX
 PI Takaiwa F, Takagi H;
 XX
 DR WPI; 2004-784905/77.
 XX
 PT Novel DNA having sequence encoding allergen specific T-cell epitope
 PT peptide, useful for accumulating T-cell epitope peptide in plants and for
 PT treating allergic diseases such as pollinosis.
 XX
 PS Disclosure; SEQ ID NO 5; 79pp; Japanese.
 XX
 CC This invention relates to a DNA (I) having a sequence under the control
 CC of a storage protein promoter, chosen from a sequence encoding storage
 CC protein signal sequence at the 5' end of a sequence encoding allergen
 CC specific T cell epitope peptide and/or a sequence encoding vesicle
 CC anchoring signal sequence at the 3' end, and a DNA sequence encoding a
 CC polypeptide having allergen specific T-cell epitope peptide inserted in
 CC the variable region of a storage protein. Also disclosed is a method of
 CC for T-cell epitope accumulated plant preparation, and a method of
 CC accumulating allergen specific T-cell epitope in a plant. The method
 CC involves introducing (I) or (II) to a plant, obtaining DNA encoding
 CC allergen specific T-cell epitope peptide, adding a DNA encoding a storage
 CC protein signal sequence to the 5' end and/or a vesicle anchoring signal
 CC sequence to the 3' end of the obtained DNA, and expressing the DNA in a
 CC plant under the control of a storage protein promoter, or obtaining DNA

CC encoding allergen specific T-cell epitope peptide, inserting a DNA into
 CC the variable region of storage protein of the plant and expressing the
 CC peptide in the transgenic plant. The invention describes the accumulation
 CC of human T cell epitope in rice albumen, a method of accumulating T cell
 CC epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp
 CC into the variable region of glutelin (the major storage protein of rice),
 CC and expressing and accumulating 7crp as part of the glutelin. The rice
 CC capable of producing the 7crp is useful as an edible vaccine against
 CC Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen
 CC is Cryj1 or Cryj2. The T-cell epitope is integrated on an edible region
 CC such as the seed of a plant. The method of the invention is useful for
 CC producing a plant accumulated with allergen specific T-cell epitope, and
 CC manufacturing a transgenic plant, preferably rice, integrated with T-cell
 CC epitope. The method is useful for preventing or treating allergic disease
 CC such as hay fever. The method enables the production of allergen specific
 CC T-cell epitope at a low cost and also reduces the amount for
 CC administration. The allergen specific T-cell epitope accumulated in a
 CC seed is stable for storage. This sequence represents rice 26 kDa peptide.
 XX
 XX Sequence 23 AA;

Query Match 96.6%; Score 28; DB 8; Length 23;
 Best Local Similarity 83.3%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 Db 4 KVVFFPA 9
 |:|||||

RESULT 34
 AAB05910
 ID AAB05910 standard; peptide; 37 AA.
 XX
 AC AAB05910;
 XX
 DT 16-OCT-2000 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase calmodulin-binding region.
 XX
 KW Mouse; inducible nitric oxide synthase; iNOS;
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
 KW AMP-activated protein kinase; AMPK; calmodulin; Cam;
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
 KW obstructive airways disease.
 XX
 OS Mus sp.
 XX
 PN WO200028076-A1.
 XX
 PD 18-MAY-2000.
 XX
 PP 05-NOV-1999; 99WO-AU000968.
 XX
 PR 06-NOV-1998; 98AU-00006976.
 XX

(SVIN-) ST VINCENTS INST MEDICAL RES.
 XX
 XX Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;
 XX
 XX WPI; 2000-376583/32.
 XX
 XX Identifying modulators of AMP-activated protein kinase-mediated
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
 PT disease, comprises testing for the increase or decrease in
 PT phosphorylation of NOS.
 XX
 XX Example 4; Fig 5; 4lpp; English.
 PS
 XX

CC The present sequence is the calmodulin (Cam)-binding region of mouse
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric

CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca²⁺-Cam. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca²⁺-Cam, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease
 XX
 XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 3; Length 37;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 Db 18 KVVFFPA 23
 |:|||||

RESULT 35
 ADK34080
 ID ADK34080 standard; peptide; 37 AA.
 XX
 AC ADK34080;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human nNOS calmodulin binding domain peptide seqid 7.
 XX
 KW vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;
 KW microvascular dysfunction; human; calmodulin binding domain;
 KW neuronal nitric oxide; nNOS.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016761-A2.
 XX
 PD 26-FEB-2004.
 XX
 PP 15-AUG-2003; 2003WO-US025626.
 XX
 PR 16-AUG-2002; 2002US-0403637P.
 XX
 XX (SCHD) SCHERING AG.
 XX
 XX Dole WP, Kauser K, Qian HS, Rubanyi G;
 XX
 XX WPI; 2004-203789/19.

PT Treating critical limb ischemia (CLI), or angiogenesis comprises
 PT administering to a patient a polynucleotide encoding a mammalian
 PT endothelial nitric oxide synthase (eNOS) polypeptide.

PS Example 1; SEQ ID NO 7; 82pp; English.

CC The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a human neuronal nitric synthase
 CC (nNOS) calmodulin binding domain peptide.
 XX

Sequence 37 AA;
 Query Match 96.6%; Score 28; DB 8; Length 37;
 Best Local Similarity 83.3%; Pred. No. 32;


```

Db      |.:|||
        38 KVVFFA 43

RESULT 38
AAO11219
ID AAO11219 standard; protein; 175 AA.
XX
AC AAO11219;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 25111.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
XX
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI; 2001-514838/56.
XX
XX N-PSDB; AA191150.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 25111; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 175 AA;
SQ
Query Match 96.6%; Score 28; DB 4; Length 175;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|.:.|
Db 128 KVVFFA 133

RESULT 39
ADC07962
ID ADC07962 standard; protein; 186 AA.
XX
XX AC ADC07962;
XX
XX 18-DEC-2003 (first entry)
XX
XX Rice protein sequence Seq ID214 related to grain filling.
DE
XX

DT 18-DEC-2003 (first entry)
XX
XX Rice protein sequence Seq ID228 related to grain filling.
XX
XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
KW gene; ds; plant.
XX
XX Oryza sativa.
XX
XX WO2003000905-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-IB002450.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX
XX 20-DEC-2001; 2001US-0342327P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
XX
XX WPI; 2003-229341/22.
XX
XX N-PSDB; ADC07961.
XX
XX New plant genes encoding polypeptides having an activity involved in or
PT associated with the synthesis, metabolism or degradation of carbohydrates
PT in the plant grain useful in generating plants having improved
PT nutritional properties.
XX
XX Claim 15; SEQ ID NO 228; 130pp; English.
XX
XX This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is the
CC amino acid sequence of a rice protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 186 AA;
SQ
Query Match 96.6%; Score 28; DB 7; Length 186;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|.:.|
Db 4 KVVFFA 9

RESULT 40
ADC07948
ID ADC07948 standard; protein; 186 AA.
XX
XX AC ADC07948;
XX
XX 18-DEC-2003 (first entry)
XX
XX Rice protein sequence Seq ID214 related to grain filling.
DE
XX

```

KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
KW gene; ds; plant.

XX Oryza sativa.

XX WO2003000905-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002WO-IB002450.

XX 22-JUN-2001; 2001US-0300112P.

PR 26-SEP-2001; 2001US-0325277P.

XX 20-DEC-2001; 2001US-0342327P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;

PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;

DR WPI; 2003-229341/22.

DR N-PSDB; ADC07947.

XX New plant genes encoding polypeptides having an activity involved in or

PT associated with the synthesis, metabolism or degradation of carbohydrates

PT in the plant grain useful in generating plants having improved

PT nutritional properties.

XX Claim 15; SEQ ID NO 214; 130pp; English.

XX This invention, in the area of plant biotechnology, relates to novel

CC polynucleotides comprising a nucleotide sequence encoding a protein which

CC is involved in or associated with the synthesis, metabolism or

CC degradation of carbohydrates in the plant grain and the expression of

CC which is up-regulated during grain filling. The plant is selected from

CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,

CC sugarbeet, wheat, and rice. The invention may be useful for the

CC improvement of protein, oil, starch, fibre and moisture content of the

CC cereal grains. In addition, carbohydrate levels may be modified to a more

CC desirable level using the present invention. The present sequence is the

CC amino acid sequence of a rice protein of the invention. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/publishedpct_sequences.

XX SQ Sequence 186 AA;

Query Match 96.6%; Score 28; DB 7; Length 186;

Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 4 KVVFFA 9

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205151P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225577P.

PR 14-AUG-2000; 2000US-0225758P.

PR 18-AUG-2000; 2000US-0225759P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 05-SEP-2000; 2000US-0229345P.

XX 05-SEP-2000; 2000US-0229509P.

XX 06-SEP-2000; 2000US-0230437P.

XX 06-SEP-2000; 2000US-0230438P.

XX 08-SEP-2000; 2000US-0231242P.

XX 08-SEP-2000; 2000US-0231243P.

XX 08-SEP-2000; 2000US-0231244P.

XX 08-SEP-2000; 2000US-0231413P.

XX 08-SEP-2000; 2000US-0231414P.

XX 08-SEP-2000; 2000US-0232080P.

XX 12-SEP-2000; 2000US-0232081P.

XX 14-SEP-2000; 2000US-0231968P.

XX 14-SEP-2000; 2000US-0232397P.

XX 14-SEP-2000; 2000US-0232398P.

XX 14-SEP-2000; 2000US-0232399P.

XX 14-SEP-2000; 2000US-0232400P.

XX 14-SEP-2000; 2000US-0232401P.

XX 14-SEP-2000; 2000US-0233063P.

XX 14-SEP-2000; 2000US-0233064P.

XX 21-SEP-2000; 2000US-0233065P.

XX 21-SEP-2000; 2000US-0234223P.

XX 25-SEP-2000; 2000US-0234274P.

XX 25-SEP-2000; 2000US-0234997P.

XX 26-SEP-2000; 2000US-0234998P.

XX 26-SEP-2000; 2000US-0235484P.

XX 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-024617P.
PR 08-NOV-2000; 2000US-024647P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 03-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 06-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
DR N-PSDB; AAK56573.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 11385; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX Sequence 190 AA;
SQ Query Match 96.6%; Score 28; DB 4; Length 190;
Best Local Similarity 83.3%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;
QY 1 KIVFFA 6
DB 14 KIVFFA 19
RESULT 42
ABB61977
ID ABB61977 standard; protein; 564 AA.
XX AC ABB61977;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 12723.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL06080.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.

XX PS Disclosure; SEQ ID NO 12723; 2lpp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent

XX CC capable of detecting 1000 or more genes from *Drosophila*. The invention is

XX CC useful in developmental biology and in elucidating cell signalling and

XX CC cell-cell interactions in higher eukaryotes for the development of

XX CC insecticides, therapeutics and pharmaceutical drugs. The invention

XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-

XX CC ABB72072). The sequence data for this patent did not form part of the

XX CC printed specification, but was obtained in electronic format directly

XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 564 AA;

Query Match 96.6%; Score 28; DB 4; Length 564;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6

Db 53 KIIFFA 58

RESULT 43

ADQ66704

ID ADQ66704 standard; protein; 854 AA.

XX AC ADQ66704;

XX DT 07-OCT-2004 (first entry)

XX DE Novel human protein sequence #1677.

XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

XX KW gene therapy; diagnostic marker; morbid state; osteoporosis;

XX KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

XX KW cancer.

XX OS Homo sapiens.

XX PN EPI440981-A2.

XX PD 28-JUL-2004.

XX PF 21-JAN-2004; 2004EP-00001196.

XX PR 21-JAN-2003; 2003JP-00102206.

XX PR 09-MAY-2003; 2003JP-00131392.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otauki T, Wakamatsu A, Sato H, Ishii S;

XX PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX WPI; 2004-535376/52.

XX N-PSDB; ADQ64516.

XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,

XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX Claim 1; SEQ ID NO 3865; 2449pp; English.

XX The invention relates to 2495 novel polynucleotides (I) and their encoded

XX polypeptides, sequences hybridizing to these nucleotides, sequences

XX encoding partial polypeptides and sequences having 70% or 90% identity to

XX the nucleotide and protein sequences. The nucleotides and polypeptides

XX are useful as diagnostic markers or therapeutic target for the diseases

XX or morbid states. They are also useful for treating osteoporosis,

XX neurological diseases, Alzheimer's diseases, Parkinson's diseases,

XX dementia and various cancers. This sequence corresponds to a protein

XX sequence of the invention.

XX SQ Sequence 854 AA;

Query Match 96.6%; Score 28; DB 8; Length 854;

Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6

Db 221 KVVFFA 226

RESULT 44

ABM83252

ID ABM83252 standard; protein; 922 AA.

XX AC ABM83252;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:3501.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

XX PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

XX PI Stevens KA, Blanchard JL, Panzer SR, Bang X, Au AP, Garstin EH;

XX PI Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;

XX PI Lagace RE, Spiro FA, Stewart EA, Wingrove J, Vitt UA, Kircon ES;

XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

XX N-PSDB; ACN41904.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX in diagnosing a condition, disease or disorder associated with human

XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

XX selected from one of the 2722 sequences defined in the specification. A

XX polynucleotide of the invention may have a use in gene therapy. The human

XX diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

XX used to diagnose a particular condition, disease or disorder associated

XX with human molecules, e.g. cell proliferative disorders,

XX autoimmune/inflammatory disorder, developmental disorder, endocrine

XX disorder, neurological disorders, gastrointestinal disorders, or

XX infections caused by virus, bacteria, fungi or parasite. The dithp

XX molecules may also be used in genetic mapping, in identifying individuals

XX from minute biological samples, in detecting single nucleotide

XX polymorphisms, as molecular weight markers, and for somatic or germline

XX gene therapy. The present sequence represents a dithp protein of the

XX invention. Note: The sequence data for this patent is not represented in

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 922 AA;
 Query Match 96.6%; Score 28; DB 8; Length 922;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 291 KVVFFA 296
 RESULT 45
 ADP76335
 ID ADF76335 standard; protein; 925 AA.
 XX AC ADP76335;
 XX DT 26-FEB-2004 (first entry)
 XX DE Novel human secreted and transmembrane protein SeqID 8.
 XX KW human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX OS Homo sapiens.
 XX KW WO2003072035-A2.
 XX PN 04-SEP-2003.
 XX PD 21-FEB-2003; 2003WO-US005241.
 XX PF 22-FEB-2002; 2002US-0359461P.
 XX PR (GETH) GENENTECH INC.
 XX PA Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 XX PI Williams PM, Wood WI, Wu TD;
 XX WPI; 2003-721702/58.
 XX DR N-PSDB; ADP76334.
 XX PT New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.
 XX PS Claim 10; SEQ ID NO 8; 918pp; English.
 XX CC This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neurotrophic factors and hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytostatic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.

XX SQ Sequence 925 AA;
 Query Match 96.6%; Score 28; DB 7; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 292 KVVFFA 297
 RESULT 46
 ADJ70225
 ID ADJ70225 standard; protein; 925 AA.
 XX AC ADJ70225;
 XX DT 06-MAY-2004 (first entry)
 XX DE Human heat mitochondrial protein as a therapeutic target SeqID2031.
 XX KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX OS Homo sapiens.
 XX KW WO2003087768-A2.
 XX PN 23-OCT-2003.
 XX PD 04-APR-2003; 2003WO-US010870.
 XX PF 12-APR-2002; 2002US-0372843P.
 XX PR 17-JUN-2002; 2002US-0389987P.
 XX PR 20-SEP-2002; 2002US-0412418P.
 XX (MITO-) MITOKOR.
 XX PA (BUCK-) BUCK INST AGE RES.
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX WPI; 2003-845369/78.
 XX PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX PS Claim 1; SEQ ID NO 2031; 180pp; English.
 XX CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nontropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

```

SQ Sequence 925 AA;
Query Match          96.6%; Score 28; DB 7; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVPFA 6
   |:||||
Db 292 KVVFFA 297

RESULT 47
ADJ75428
ID ADJ75428 standard; protein; 925 AA.
XX AC ADJ75428;
XX DT 20-MAY-2004 (first entry)
XX DE
XX KW bronchial asthma; chronic obstructive pulmonary disease;
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX KW gene therapy; marker.
XX OS Homo sapiens.
XX PN EP1394274-A2.
XX PD 03-MAR-2004.
XX PF 04-AUG-2003; 2003EP-00254857.
XX PR 06-AUG-2002; 2002JJP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX PA (GENO-) GENOX RES INC.
XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX WPI; 2004-193155/19.
XX
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
PS Example 11; SEQ ID NO 680; 241pp; English.
XX
CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a

```

```

CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 925 AA;
Query Match          96.6%; Score 28; DB 8; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVPFA 6
   |:||||
Db 292 KVVFFA 297

RESULT 48
ADJ75495
ID ADJ75495 standard; protein; 925 AA.
XX AC ADJ75495;
XX DT 20-MAY-2004 (first entry)
XX DE
XX KW bronchial asthma; chronic obstructive pulmonary disease;
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX KW gene therapy; marker.
XX OS Homo sapiens.
XX PN EP1394274-A2.
XX PD 03-MAR-2004.
XX PF 04-AUG-2003; 2003EP-00254857.
XX PR 06-AUG-2002; 2002JJP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX PA (GENO-) GENOX RES INC.
XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX WPI; 2004-193155/19.
XX
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
PS Example 11; SEQ ID NO 747; 241pp; English.
XX
CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial

```

CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. NO. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 292 KVVFFA 297
 |:|||||

RESULT 49

ID ADN04860 standard; protein; 925 AA.

XX AC ADN04860;

XX 01-JUL-2004 (first entry)

XX Antipsoriatic protein sequence #610.

DE antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX WO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;

XX WPI; 2004-305105/28.

XX N-PSDB; ADN04859.

XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

XX Claim 9; SEQ ID NO 1254; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. NO. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|||||

Db 292 KVVFFA 297

RESULT 50

ADN14233

ID ADR14233 standard; protein; 925 AA.

XX AC ADR14233;

XX 21-OCT-2004 (first entry)

XX Human NF-kappaB pathway-associated protein SeqID234.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnery; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; BAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.

XX Homo sapiens.

XX WO2004065577-A2.

XX 05-AUG-2004.

XX 13-JAN-2004; 2004WO-US000798.

XX 14-JAN-2003; 2003US-0440068P.

XX 12-MAY-2003; 2003US-0469757P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Nadler SG, Neubauer MG, Feder JN, Carman J;

XX WPI; 2004-562168/54.

XX N-PSDB; ADR14232.

XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.

XX Claim 6; SEQ ID NO 234; 237pp; English.

XX This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnery activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, BAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NP-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:||||
 Db 292 KVVFFA 297

RESULT 51
 ADP25011
 ID ADP25011 standard; protein; 925 AA.

XX AC

XX ADP25011;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:2189.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

XX antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

OS Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

XX Wu TD;

XX WPI; 2004-419628/39.

XX N-PSDB; ADP25010.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated

XX renal disease, or demyelinating diseases of the central or peripheral

XX nervous system.

XX Claim 7; SEQ ID NO 2189; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:||||
 Db 292 KVVFFA 297

RESULT 52

ADR97294
 ID ADR97294 standard; protein; 925 AA.

XX AC

XX ADR97294;

XX 02-DEC-2004 (first entry)

XX Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX human; enzyme; apoptosis; cancer; inflammation; autoimmune;

KW neurodegenerative disorder; cytostatic; antiinflammatory;

XX immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX Homo sapiens.

XX WO2004078783-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-GB000957.

XX 07-MAR-2003; 2003GB-00005267.

XX (EIRX-) EIRX THERAPEUTICS LTD.

XX Murphy FJ, Sheehan DE, Keating KE, Hayes I, Seera L;

XX WPI; 2004-662402/64.

XX N-PSDB; ADR97293.

XX Identifying an agent that modulates the function of an apoptosis-
 CC associated polypeptide, useful for diagnosing or treating e.g. cancer,
 CC comprises comparing the binding of the polypeptide to the candidate agent
 CC and to a control agent.

XX Claim 1; SEQ ID NO 2; 304pp; English.

XX This invention relates to novel agents that modulates the function of
 CC human apoptosis-associated proteins specified within the specification.
 CC Specifically, it refers to a method for the identification of target
 CC genes whose expression is correlated with an early stage in the
 CC regulation of apoptosis. The present invention describes a method of
 CC contacting either candidate agents or control agents to the target genes
 CC and assessing the difference of binding and inhibitory activity, where
 CC the candidate agent is selected from a low molecular weight organic
 CC molecule, an antibody or fragment thereof, an antisense oligonucleotide,

CC a small inhibitory dRNA, or a ribozyme. As such, the compositions and
 CC methods are useful for diagnosing and treating diseases or conditions
 CC associated with abnormal apoptosis in mammalian tissue, such as cancer,
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and
 CC neuroprotective activities. These may also be used for drug screening
 CC purposes and in gene therapy. This polypeptide sequence is a human target
 CC protein, an enzyme associated with the regulation of apoptosis whose
 CC expression is modulated by novel agents of the invention.
 XX
 SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:||||
 Db 292 KIVFFA 297

RESULT 53
 ADV17516
 ID ADV17516 standard; protein; 925 AA.

XX
 AC ADY17516;

XX 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 3322.

XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotrophic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 8; SEQ ID NO 3322; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 9; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:||||

Db 292 KIVFFA 297

RESULT 54

AEA23525

ID AEA23525 standard; protein; 925 AA.

XX AEA23525;

XX 11-AUG-2005 (first entry)

XX Human PRO polypeptide SEQ ID NO 67.

XX immune disorder; PRO; Antiinflammatory; Dermatological;

KW Musculosuppressive; Antirheumatic; Antiarthritic; Osteopathic;

KW Muscular-Gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant.

XX Homo sapiens.

XX WO2005051988-A2.

XX 09-JUN-2005.

XX 02-MAR-2004; 2004WO-US006460.

XX 03-MAR-2003; 2003US-0451884P.

XX (GETH) GENENTECH INC.

XX Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;

XX WPI; 2005-417958/42.

XX N-PSDB; AEA23524.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or
 PT psoriasis.

XX Disclosure; SEQ ID NO 67; 966pp; English.

XX The invention relates to an isolated nucleic acid. The polypeptide,
 CC compound or composition, and methods are useful for diagnosing and
 CC treating an immune related disorder, e.g. systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,
 CC spondyloarthropathies, systemic sclerosis, idiopathic inflammatory
 CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases
 CC including bullous skin diseases, erythema multiforme and contact
 CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
 CC present sequence represents the amino acid sequence of a human PRO
 CC polypeptide.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 9; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:||||
 Db 292 KIVFFA 297

RESULT 55

AAR77360

ID AAR77360 standard; protein; 1144 AA.

XX AAR77360;

XX 10-MAY-1996 (first entry)

XX

```

DE Inducible nitrogen monoxide synthase.
XX
KW nitrogen monoxide synthase; inducible; treatment; prevention;
KW vascular disease; restenosis.
XX
XX Mus musculus.
XX DE4411402-A1.
XX
XX 05-OCT-1995.
XX
XX 31-MAR-1994; 94DE-04411402.
XX
XX 31-MAR-1994; 94DE-04411402.
XX (SCHR/) SCHRADER J.
XX
XX Schrader J, Goedecke A;
XX WPI; 1995-345550/45.
XX N-PSDB; AAQ94252.
XX
XX Eukaryotic expression vector for nitrogen-monoxide synthase gene -
XX useful in the treatment and prevention of diseases of blood vessels by
XX gene therapy.
XX
XX Claim 5; Fig 1; 28pp; German.
XX
XX Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and
XX is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per
XX subunit. The activity of iNOS is independent of calmodulin and cellular
XX calcium levels. Vectors contg. the DNA are used in the treatment or
XX prevention of vascular diseases, high blood pressure, arteriosclerosis,
XX stenosis or restenosis of blood vessels, esp. coronary vessels after
XX percutane transluminal coronary angioplasty. See AAR77363 and AAR77362
XX for endothelial and brain-derived NOS
XX
XX Sequence 1144 AA;
XX
XX Query Match 96.6%; Score 28; DB 2; Length 1144;
XX Best Local Similarity 83.3%; Pred. No. 9.8e+02;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KIVFFA 6
XX |.:|||
XX 514 KWFFFA 519
XX
XX RESULT 56
XX AAW51246
XX ID AAW51246 standard; protein; 1144 AA.
XX
XX AC AAW51246;
XX
XX 25-MAR-2003 (revised)
XX 12-AUG-1998 (first entry)
XX
XX Inducible nitric oxide synthase, long isoform.
XX
XX Inducible nitric oxide synthase; iNOS; recombinant protein; cDNA library;
XX isoform.
XX
XX Mus sp.
XX
XX US5766909-A.
XX
XX 16-JUN-1998.
XX
XX 05-NOV-1993; 93US-00147812.
XX
XX 04-FEB-1992; 92US-00841641.
XX
XX (MERI ) MERCK & CO INC.
XX
XX
XX Mumford RA, Calaycay JR, Xie Q, Nathan CF;
XX WPI; 1998-361696/31.
XX N-PSDB; AAV07247.
XX
XX DNA encoding inducible nitric oxide synthase proteins - useful for
XX producing recombinant proteins.
XX
XX Claim 1; Col 25-32; 39pp; English.
XX
XX The invention relates to two DNA molecules encoding inducible nitric
XX oxide synthase (iNOS) proteins, where the DNA molecules comprise defined
XX sequences of 4041 and 4165 base pairs given in the specification and the
XX proteins have 1144 amino acids. Also claimed are expression vectors
XX containing the DNA molecules, and recombinant host cells containing the
XX vectors. The DNA molecules are useful for producing the recombinant
XX proteins. The present sequence represents inducible nitric oxide, long
XX isoform. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 1144 AA;
XX
XX Query Match 96.6%; Score 28; DB 2; Length 1144;
XX Best Local Similarity 83.3%; Pred. No. 9.8e+02;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KIVFFA 6
XX |.:|||
XX 514 KWFFFA 519
XX
XX RESULT 57
XX AAG64500
XX ID AAG64500 standard; protein; 1144 AA.
XX
XX AC AAG64500;
XX
XX 02-OCT-2001 (first entry)
XX
XX Mouse inducible nitric oxide synthase 2.
XX
XX Antisense oligonucleotide; inducible nitric oxide synthase;
XX modulate expression; immunomodulator; antidiabetic; cardiovascular;
XX cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
XX 2'-O-methoxyethyl; phosphorothioate; mouse.
XX
XX Mus sp.
XX
XX WO200152902-A1.
XX
XX 26-JUL-2001.
XX
XX 15-JAN-2001; 2001WO-US001381.
XX
XX 24-JAN-2000; 2000US-00490208.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dean NM, Cowser LM;
XX WPI; 2001-465340/50.
XX N-PSDB; AAH47974.
XX
XX New antisense oligonucleotides for modulating the expression of inducible
XX nitric oxide synthase in cells or tissues, particularly useful for
XX treating e.g. immunological, cardiovascular or neurological disorders, or
XX ischemia.
XX
XX Example 17; Page 110-114; 144pp; English.
XX
XX The invention relates to antisense compounds, especially
XX oligonucleotides, which are targeted to a nucleic acid encoding inducible
XX nitric oxide synthase and which specifically hybridise to and modulate

```

CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiac,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of
 CC mouse inducible nitric oxide synthase
 XX
 SQ Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 4; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 514 KVVFFPA 519
 |.:|||
 RESULT 58
 ABU79138
 ID ABU79138 standard; protein; 1144 AA.
 XX
 AC ABU79138;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE Inducible nitric oxide synthase protein.
 XX
 KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Unidentified.
 XX
 US2002177551-A1.
 XX
 28-NOV-2002.
 XX
 30-MAY-2001; 2001US-00870759.
 XX
 31-MAY-2000; 2000US-0208128P.
 XX
 (TERM/) TERMAN D S.
 XX
 Terman DS;
 XX
 WPI; 2003-361759/34.
 XX
 N-PSDB; ACA64740.
 XX
 A mammalian cell receptor, useful in the treatment of cancer by binding
 FT to tumor associated lipids where the binding induces anergy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 Example 2; Page; 167pp; English.
 XX
 The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a

CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 6; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 514 KVVFFPA 519
 |.:|||
 RESULT 59
 ADP43404
 ID ADP43404 standard; protein; 1144 AA.
 XX
 AC ADP43404;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE INOS polypeptide seqid 124.
 XX
 KW receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; INOS.
 XX
 OS Unidentified.
 XX
 US2003157113-A1.
 XX
 21-AUG-2003.
 XX
 28-DEC-2000; 2000US-00751708.
 XX
 28-DEC-1999; 99US-0173371P.
 XX

PA (TERM/) Terman D S.
XX Terman DS;
PI
XX WPI; 2003-787326/74.
DR N-PSDB; ADF43403.
XX
PT New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.
XX
XX Example 3; SEQ ID NO 124; 151pp; English.
XX
XX The invention describes a receptor in a mammalian cell that inhibits
XX regular activation by receptors specific for lipid-based tumour
XX associated antigen. The receptor has cytostatic and antimicrobial
XX properties and is suitable for use in gene therapy. The receptors,
XX methods and compositions are useful for treating a neoplastic disease or
XX tumour (cancer), and infectious diseases. This sequence represents INOS
XX polypeptide, a cell surface moiety, the DNA of which can be transfected
XX into a cell with superantigen DNA to generate antitumour immunity.
XX
SQ Sequence 1144 AA;
Query Match 96.6%; Score 28; DB 7; Length 1144;
Best Local Similarity 83.3%; Pred. NO. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVRFA 6
DB 514 KVVFFA 519
|:|||||
|:|||||
RESULT 60
ADF77432
ID ADF77432 standard; protein; 1144 AA.
XX
AC ADF77432;
XX
DT 26-FEB-2004 (first entry)
XX
DE Mouse inducible nitric oxide synthase, INOS.
XX
KW Mouse; inducible nitric oxide synthase; INOS; cardiac; vasodilator;
KW cytostatic; gynaecological; restenotic response; angioplasty;
KW vasodilation; angina; cancer; cell death; premature labour; tumour;
KW nervous system; brain; erectile dysfunction; uterus; lung; vascular tone;
KW regional blood flow.
XX
OS Mus musculus.
XX
XX US6620616-B1.
XX
XX 16-SEP-2003.
XX
XX 13-SEP-2000; 2000US-00661259.
XX
XX 13-SEP-2000; 2000US-00661259.
XX
XX (CLEV-) CLEVELAND CLINIC FOUND.
XX
XX Stuehr DJ, Adak S;
PI
XX WPI; 2003-895427/82.
XX
XX New isolated polynucleotide encoding a variant of a corresponding wild-
XX type nitric oxide synthase, useful for reducing the restenotic response
XX after angioplasty, or for inhibiting the development or onset of
XX premature labor.
XX
XX Disclosure; SEQ ID NO 5; 35pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a variant of
XX
PA a corresponding wild-type nitric oxide synthase (NOS). The variant has
XX the tryptophan in the alpha 3 helix substituted by tyrosine or
XX phenylalanine. Also included are a nucleic acid construct comprising the
XX nucleotide sequence that encodes a variant of a corresponding wild-type
XX nitric oxide synthase and a promoter operably linked to the encoding
XX sequence of the variant and a transformed cell comprising the construct,
XX where the cell expresses the nitric oxide synthase variant. The variant
XX has an in vitro enzymatic activity that is greater than the in vitro
XX enzymatic activity of the corresponding wild-type nitric oxide synthase.
XX The variant can preferably be of a corresponding wild-type endothelial
XX nitric oxide synthase (eNOS), neuronal nitric oxide synthase (nNOS), or
XX inducible nitric oxide synthase (iNOS). The polynucleotides are useful
XX for reducing the restenotic response after angioplasty, or related
XX interventional procedures, or to enhance the vasodilation response in
XX treating angina, for anticancer therapy to promote cell death, and for
XX inhibiting the development or onset of premature labour. The
XX polynucleotides are useful to achieve or augment expression of NOS
XX variant proteins or polypeptides in vivo to increase NOS production in
XX target tissue, tumour tissue, tissue of the nervous system, including
XX brain, penis (e.g. in erectile dysfunction) and uterine tissue, and lung
XX tissue. NOS is useful for maintaining vascular tone and regulating
XX regional blood flow. The present sequence is wild-type mouse INOS.
XX
SQ Sequence 1144 AA;
Query Match 96.6%; Score 28; DB 7; Length 1144;
Best Local Similarity 83.3%; Pred. NO. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVRFA 6
DB 514 KVVFFA 519
|:|||||
|:|||||
RESULT 61
ADF76212
ID ADJ76212 standard; protein; 1144 AA.
XX
AC ADJ76212;
XX
XX 20-MAY-2004 (first entry)
XX
XX Marker gene related amino acid sequence SEQ ID NO:1464.
XX
DE bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.
XX
XX Mus musculus.
OS
XX
XX EPI394274-A2.
XX
XX 03-MAR-2004.
XX
XX 04-AUG-2003; 2003EP-00254857.
XX
XX 06-AUG-2002; 2002JP-00229312.
XX
XX 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
PI
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX
XX Claim 16; SEQ ID NO 1464; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
XX

or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;

Best Local Similarity 83.3%; Pred. No. 9.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 514 KVVFFA 519

RESULT 62

ID ADJ76136 standard; protein; 1144 AA.

AC ADJ76136;

XX 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.

XX Mus musculus.

XX EP1394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample

PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.

XX Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
or chronic obstructive pulmonary disease. The method comprises
determining the expression level of a marker gene in a biological sample
from a subject, comparing the expression level determined with the
expression level of the marker gene in a biological sample from a healthy
subject, and judging whether the subject has bronchial asthma or chronic
obstructive pulmonary disease. The marker gene comprises: (a) a group of
genes (S1) whose expression levels increase when respiratory epithelial
cells are stimulated with interleukin-13; or (b) a group of genes (S2)
whose expression levels decrease when respiratory epithelial cells are
stimulated with interleukin-13. Also described: (1) a reagent (I) for
testing for bronchial asthma or chronic obstructive pulmonary disease;
(2) a kit for screening for a candidate compound for a therapeutic agent
to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
an animal model for bronchial asthma or chronic obstructive pulmonary
disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
method for producing an animal model for bronchial asthma or chronic
obstructive pulmonary disease; (6) a therapeutic agent for bronchial
asthma or chronic obstructive pulmonary disease, comprising the compound,
a marker gene or an antisense nucleic acid corresponding to a portion of
the marker gene, a ribozyme, a polynucleotide that suppresses the
expression of the gene through an RNAi effect or an antibody recognising
a protein encoded by a marker gene; and (7) a DNA chip for testing for
bronchial asthma or a chronic obstructive pulmonary disease, on which a
probe has been immobilised to assay a marker gene. (I) has respiratory
and antiasthmatic activities, and can be used in gene therapy. The method
is useful for testing for or screening for a therapeutic agent for
bronchial asthma or chronic obstructive pulmonary disease. The present
sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;

Best Local Similarity 83.3%; Pred. No. 9.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 514 KVVFFA 519

RESULT 63

ID AEA03075 standard; protein; 1144 AA.

XX AEA03075;

XX 28-JUL-2005 (first entry)

XX VEGF amino acid sequence SEQ ID NO:101.

XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
KW vascular endothelial cell growth factor.

XX Unidentified.

XX US2005112141-A1.

XX 26-MAY-2005.

XX 08-SEP-2004; 2004US-00937758.

XX 30-AUG-2000; 2000US-00650884.

XX (TERM/) Terman D S.

XX Terman DS;

DR WPI; 2005-394926/40.
 DR N-PSDB; AEA03074.
 XX
 PT New composition for treating a tumor or neoplastic disease in a subject
 PT comprises conjugates comprising superantigen polypeptides or nucleic
 PT acids with other molecules that produce a tumoricidal response.
 XX
 PS Example 3; SEQ ID NO 101; 125pp; English.
 XX
 CC The invention relates to a composition for treating a tumor or neoplastic
 CC disease in a subject. Also described: (1) a mammalian cell comprising an
 CC exogenous nucleic acid encoding a superantigen expressed in the cell,
 CC which cell also produces or expresses all alpha-anomers of
 CC monoglycosylceramide or diglycosylceramide, where expression of the
 CC superantigen and the mono- or diglycosylceramide is capable of eliciting
 CC an antitumor immune response in a mammal into which the cell is
 CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
 CC preparing a population of immunotherapeutic T or natural killer T (NKT)
 CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
 CC apoptotic cell preparation or lysate useful for treating a tumor or
 CC neoplastic disease in a subject, comprising a cell population that has
 CC been transfected with naked DNA encoding a superantigen, and treated to
 CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
 CC transfected with the above apoptotic preparation or lysate, thus,
 CC rendering the cell effective in presenting material expressed from
 CC transfecting nucleic acid or material ingested to the immune system of a
 CC mammal to elicit an anti-tumor immune response. The composition and
 CC methods are useful for treating tumors or neoplastic diseases. The
 CC present sequence represents a VEGF protein sequence, which is used in an
 CC example from the present invention. Note - The sequence data for this
 CC patent is not represented in the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site.
 XX
 SQ Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 9; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 KIVFFFA 6
 Db 514 KVVFFA 519
 ||:||||
 RESULT 64
 ABB68472
 ID ABB68472 standard; protein; 1443 AA.
 XX
 AC ABB68472;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 32208.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US009231.
 XX
 XX 23-MAR-2000; 2000US-0191637P.
 XX
 XX 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI; 2001-656860/75.
 XX
 PS

DR N-PSDB; ABL12575.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 32208; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1443 AA;
 Query Match 96.6%; Score 28; DB 4; Length 1443;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 KIVFFFA 6
 Db 1204 KIIFFA 1209
 ||:||||
 RESULT 65
 AAW02314
 ID AAW02314 standard; peptide; 6 AA.
 XX
 AC AAW02314;
 XX
 DT 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #5.
 XX
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 XX WO9628471-A1.
 XX
 XX 19-SEP-1996.
 XX
 XX 14-MAR-1996; 96WO-US003492.
 XX
 XX 14-MAR-1995; 95US-00404831.
 XX
 XX 07-JUN-1995; 95US-00475579.
 XX
 XX 27-OCT-1995; 95US-00548998.
 XX
 XX (PHAR-) PHARM PEPTIDES INC.
 XX
 XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
 XX Kaaman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;
 XX Kubasek W, Chin J, Lee J, Kelley M;
 XX
 XX WPI; 1996-433762/43.
 XX
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 XX protein coupled (in)directly to at least 1 modifying gp., useful in
 XX treatment of Alzheimer's disease.
 XX
 XX Claim 16; Page 91; 106pp; English.

XX AAW02310-W02332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kadalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients. The
 CC amyloid modulators of the invention comprise an amyloidogenic protein or
 CC peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as declain, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease
 XX
 SQ Sequence 6 AA;
 Query Match 93.1%; Score 27; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 |:||||
 Db 1 KLVFFPA 6
 RESULT 66
 AAW89378
 ID AAW89378 standard; peptide; 6 AA.
 XX
 AC AAW89378;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Beta-amyloid peptide derivative A-beta-16-21.
 XX
 KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; BAP.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US5854204-A.
 XX
 PD 29-DEC-1998.
 XX
 PP 14-MAR-1996; 96US-00612785.
 XX
 PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Hundal A, Geffer ML, Kaaman L, Musso G, Molineaux S, Benjamin H;
 PI Findels MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
 PI Garnick MB, Kubasek W, Signer BR;
 XX
 DR WPI; 1999-094964/08.
 XX
 PT New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
 PT aggregation - and neurotoxicity, specifically for treatment and

PT prevention of Alzheimer's disease.
 XX
 PS Example 12; Col 64; 52pp; English.
 XX
 CC The present invention describes beta-amyloid peptide (BAP) derivatives.
 CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically BAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of BAP to
 CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation
 CC even when BAP is present in molar excess. The present sequence represents
 CC a BAP derivative
 XX
 SQ Sequence 6 AA;
 Query Match 93.1%; Score 27; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 |:||||
 Db 1 KLVFFPA 6
 RESULT 67
 AAB48484
 ID AAB48484 standard; peptide; 6 AA.
 XX
 AC AAB48484;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #11.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 FT WO200068263-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX
 PP 04-MAY-2000; 2000WO-CA000515.
 XX
 PR 05-MAY-1999; 99US-0132592P.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalifour R, Gervais F, Gupta A;
 XX
 DR WPI; 2001-031852/04.
 XX
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX
 PS Claim 7; Page 25; 46pp; English.
 XX
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid

Db 1 KLVFFA 6

RESULT 70
ABG71009
ID ABG71009 standard; peptide; 6 AA.
XX AC ABG71009;
XX DT 05-DEC-2002 (first entry)
XX DE Long form beta-amyloid protein fragment #6.
XX KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis; familial amyloid polyneuropathy; familial amyloid cardiomyopathy; isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma; bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease; adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome; insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis; macroglobulinaemia-associated amyloidosis; reactive amyloidosis; primary localised cutaneous nodular amyloidosis; Sjogren's syndrome; hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome; hereditary non-neuropathic systemic amyloidosis; familial Mediterranean Fever.
XX OS Homo sapiens.
XX PN US2002098173-A1.
XX PD 25-JUL-2002.
XX PF 04-OCT-2001; 2001US-00972475.
XX PR 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX PR 14-MAR-1996; 96US-00617267.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PI Pindis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX WPI; 2002-697709/75.
XX PT Amyloid modulator useful for treating a disorder associated with amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment coupled to a modifying group.
XX PS Example 12; Page 35; 41pp; English.
XX CC The invention describes an amyloid modulator comprising an amyloidogenic protein and/or peptide fragment coupled to a modifying group so that the compound modulates the aggregation of natural amyloid proteins or peptides. The modulator is used for treating a disorder associated with amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese and Swedish types), familial amyloid cardiomyopathy (Danish type), isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or macroglobulinaemia-associated amyloidosis, primary localised cutaneous nodular amyloidosis associated with Sjogren's syndrome, reactive (secondary) amyloidosis, familial Mediterranean Fever and familial amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome), hereditary cerebral haemorrhage with amyloidosis of Icelandic type, amyloidosis associated with long term haemodialysis, hereditary non-neuropathic systemic amyloidosis (familial amyloid polyneuropathy III), familial amyloidosis of Finnish type, amyloidosis associated with medullary carcinoma of the thyroid, fibrinogen-associated hereditary renal amyloidosis and lysosome-associated hereditary systemic amyloidosis. The compound is capable of altering and inhibiting beta-

CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins or peptides when contacted with a molar excess amount of natural beta-APs relative to the modulator. This sequence represents a fragment of the long form of beta-amyloid used in the creation of an amyloid modulator

XX SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KLVFFA 6
DB 1 KLVFFA 6

RESULT 71
ABB05157
ID ABB05157 standard; peptide; 6 AA.
XX AC ABB05157;
XX DT 02-APR-2002 (first entry)
XX DE Beta amyloid peptide (16-21) SEQ ID NO:9.
XX KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta; APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease; neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory; antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic; amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome; amyloidogenic disease; beta amyloid deposition; amyloidosis; hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US6319498-B1.
XX PD 20-NOV-2001.
XX PR 14-MAR-1996; 96US-00617267.
XX PR 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PI Pindis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX WPI; 2002-146668/19.
XX PT Amyloid modulator compound useful for treatment of an amyloidogenic disease such as Alzheimer's disease comprises an aggregation core domain and a modifying group attached to it.
XX PS Disclosure; Col 18; 54pp; English.
XX CC The present invention describes an amyloid modulator compound (I) comprising an aggregation core domain and a modifying group attached to it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial, antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic and auditory activities, and can be used as a natural amyloid aggregation inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide (beta-AP). (I) are used in the manufacture of a medicament for the diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's disease and other clinical occurrences of beta amyloid deposition such as Down's syndrome individuals and in patients with hereditary cerebral haemorrhage with amyloidosis, and for treating a disorder associated with amyloidosis such as familial amyloid polyneuropathy. (I) reduces the toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)

CC not only reduces the formation of neurotoxic aggregates but also have the
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
 CC present sequence represents a beta-AP peptide, which is used in the
 CC exemplification of the present invention

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 72

AAU96820
 ID AAU96820 standard; peptide; 6 AA.

AC AAU96820;

DT 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #10.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

Key Location/Qualifiers

FT Misc-difference 1..6

FT /note= "Preferably D-form residue"

FT Modified-site 6 /note= "Ala is amidated"

XX WO200207781-A2.

PN 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

PI WPI; 2002-371447/40.

DR New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A_t-[A₁-n₁]-A₂ where n₁ = 0 - 1;
 CC A_t = an amyloid targeting moiety; A₁-n₁ = a linker moiety; and A₂ =
 CC a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and

CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 73

ABB83305
 ID ABB83305 standard; peptide; 6 AA.

XX ABB83305;

XX 29-AUG-2002 (first entry)

XX Amyloid-beta (Abeta) peptide fragment.

XX Human; islet amyloid polypeptide; IAPP; antifibrillogenic; amylin;
 KW fibrillar accumulation; amyloidosis; diabetes; cytoprotection; neurotropic;
 KW chronic infection; tuberculosis; inflammation; rheumatoid arthritis;
 KW fever; neurodegenerative disease; scrapie; neuroprotective; antipyretic;
 KW bovine spongiform encephalitis; Creutzfeldt-Jacob disease; amyloid-beta;
 KW Alzheimer's disease; cerebral amyloid angiopathy; anti-diabetic;
 KW tuberculostatic; antiarthritic; antirheumatic; cerebroprotective.

XX Unidentified.

XX WO200224727-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-CA001333.

XX 19-SEP-2000; 2000US-0233482P.

XX (UTOR) UNIV TORONTO.

XX Fraser P;

XX WPI; 2002-519078/55.

XX New antifibrillogenic peptide useful for inhibiting amyloidosis and/or
 PT for cytoprotection in the treatment of amyloidosis disorders e.g. type I
 PT or type II.

XX Disclosure; Page 5; 77pp; English.

XX The present invention relates to antifibrillogenic agents (ABB83281-
 CC ABB83298), derived from human islet amyloid polypeptide (IAPP, ABB83307).
 CC The present sequence is a peptide fragment of the amyloid-beta (Abeta).
 CC peptide. Aggregation of IAPP also known as amylin, or Abeta results in
 CC fibrillar accumulations, leading to amyloidosis. The antifibrillogenic
 CC peptides prevent fibril formation and amyloidosis and hence control
 CC folding or deposition of amyloid proteins. The antifibrillogenic peptides

CC of the invention are useful in the manufacture of a medicament for
 CC inhibiting or treating amyloidosis or amyloid deposits e.g. Type I and
 CC Type II diabetes and/or for cytoprotection. They are also useful for
 CC treating secondary amyloidosis associated with chronic infection e.g.
 CC tuberculosis and chronic inflammation e.g. rheumatoid arthritis, and
 CC familial inflammation, fever, neurodegenerative diseases e.g. scrapie,
 CC bovine spongy form encephalitis, Creutzfeldt-Jacob disease, Alzheimer's
 CC disease, cerebral amyloid angiopathy

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 1 KLVFFA 6

RESULT 74

AAU11658
 ID AAU11658 standard; peptide; 6 AA.

XX

AC AAU11658;

XX 09-APR-2002 (first entry)

XX Peptide #11, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 1 KLVFFA 6

RESULT 75

AAU11650
 ID AAU11650 standard; peptide; 6 AA.

XX

AC AAU11650;

XX 09-APR-2002 (first entry)

XX Peptide #3, used as a carrier for amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:33:10
 Job time : 90.7742 secs

THIS PAGE BLANK (USPTO)

TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-63

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 74
US-08-766-596A-65
; Sequence 65, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-65

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 75
US-09-264-709A-2
; Sequence 2, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; TITLE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-2

Query Match 93.1%; Score 27; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

Search completed: December 29, 2005, 17:52:31
Job time : 22.1323 secs

STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-60

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 5 KLVFFA 10
|:|||||

RESULT 72
US-08-766-596A-61
Sequence 61, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 5 KLVFFA 10
|:|||||

RESULT 73
US-08-766-596A-63
Sequence 63, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

US-08-766-596A-56

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 69

US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 70

US-08-766-596A-58

; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 71

US-08-766-596A-60
; Sequence 60, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLY APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 6 KLVFFA 11

RESULT 67
US-08-617-267C-14
Sequence 14, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KLVFFA 6

RESULT 68
US-08-766-596A-56
Sequence 56, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 63

US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 64

US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 65

US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:

APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-14

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 66

US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:

APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 60
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 61
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: OF AMYLOID FORMATION

; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 62
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10220-14

Query Match 93.1%; Score 27; DB 4; Length 11;

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 57
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 58
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-630-645-14

Query Match          93.1%; Score 27; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 59
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
```

```
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-20

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
       |:||||
Db       5 KLVFFA 10

RESULT 54
US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-0047500C
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-21

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
       |:||||
Db       4 KLVFFA 9

RESULT 55
US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686
```

```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-0047500C
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
       |:||||
Db       3 KLVFFA 8

RESULT 56
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-0047500C
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
```


; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 50

US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 51

US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 52

US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 53

US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
US-09-724-940-20

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 46

US-09-580-018-23
; Sequence 23, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-23

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 47

US-09-580-018-24
; Sequence 24, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)

US-09-580-018-24

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 48

US-09-724-551-20
; Sequence 20, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-20

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 49

US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 2 KLVFFA 7

RESULT 42

US-09-724-961-24
 ; Sequence 24, Application US/09724961
 ; Patent No. 6743427
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Vasquez, Nickl
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004750UC
 ; CURRENT APPLICATION NUMBER: US/09/724,961
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/580,015
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: US 09/201,430
 ; PRIOR FILING DATE: 1998-11-30
 ; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
 ; PRIOR FILING DATE: 1998-11-30
 ; PRIOR APPLICATION NUMBER: US 60/080,970
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US 60/067,740
 ; PRIOR FILING DATE: 1997-12-02
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
 ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
 ; OTHER INFORMATION: peptide)
 US-09-724-961-24

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 43

US-09-580-018-20
 ; Sequence 20, Application US/09580018
 ; Patent No. 6761888
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004760US
 ; CURRENT APPLICATION NUMBER: US/09/580,018
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 10

; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
 ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
 ; OTHER INFORMATION: peptide)
 US-09-580-018-20

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 5 KLVFFA 10

RESULT 44

US-09-580-018-21
 ; Sequence 21, Application US/09580018
 ; Patent No. 6761888
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004760US
 ; CURRENT APPLICATION NUMBER: US/09/580,018
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
 ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
 ; OTHER INFORMATION: peptide)
 US-09-580-018-21

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 4 KLVFFA 9

RESULT 45

US-09-580-018-22
 ; Sequence 22, Application US/09580018
 ; Patent No. 6761888
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004760US
 ; CURRENT APPLICATION NUMBER: US/09/580,018
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

```
;
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5,6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
Db 5 KLVFFA 10

RESULT 39
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5,6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
Db 4 KLVFFA 9

RESULT 40
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
;
;
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5,6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
Db 3 KLVFFA 8

RESULT 41
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-23
```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 64:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-766-596A-64

Query Match 93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

RESULT 36

US-09-747-408-20

; Sequence 20, Application US/09747408

; Patent No. 6670399

; GENERAL INFORMATION:

; APPLICANT: Green, Allan M.

; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: Compounds And Methods For Modulating

; TITLE OF INVENTION: Cerebral Amyloid Angiopathy

; FILE REFERENCE: NBI-088

; CURRENT APPLICATION NUMBER: US/09/747,408

; CURRENT FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/171,877

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-747-408-20

Query Match 93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 4 KLVFFA 9

RESULT 37

US-08-970-833-3

; Sequence 3, Application US/08970833

; Patent No. 602859

; GENERAL INFORMATION:

; APPLICANT: Kiessling, Laura L.

; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Quarles & Brady

; STREET: 411 East Wisconsin Avenue

; CITY: Milwaukee

; STATE: Wisconsin

; COUNTRY: U.S.A.

; ZIP: 53202-4497

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/970,833

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Baker, Jean C.

; REGISTRATION NUMBER: 35,433

; REFERENCE/DOCKET NUMBER: 960296.94291

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (414) 277-5709

; TELEFAX: (414) 271-3552

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-970-833-3

Query Match 93.1%; Score 27; DB 2; Length 10;

Best Local Similarity 83.3%; Pred. No. 5.6;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 1 KLVFFA 6

RESULT 38

US-09-724-961-20

; Sequence 20, Application US/09724961

; Patent No. 6743427

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vasquez, Nicki

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 152703-004750UC

; CURRENT APPLICATION NUMBER: US/09/724,961

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 10

ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-1

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 33

US-09-668-314C-73
Sequence 73, Application US/09668314C
Patent No. 6844148
GENERAL INFORMATION:
APPLICANT: Gurney, et al

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/5280NCP
CURRENT APPLICATION NUMBER: US/09/668,314C
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/169,232
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-668-314C-73

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 34

PCT-US96-10220-1
Sequence 1, Application PC/TUS9610220
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10220
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-10220-1

Query Match 93.1%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 35

US-08-766-596A-64
Sequence 64, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio

APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-28

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 30
US-08-617-267C-5
Sequence 5, Application US/08617267C
Patent No. 6319498

GENERAL INFORMATION:
APPLICANT: Findexis, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||

Db 3 KLVFFA 8

RESULT 31

US-09-095-106A-44
Sequence 44, Application US/09095106A
Patent No. 6331440
GENERAL INFORMATION:
APPLICANT: NORDSTEDT, Christer
APPLICANT: NASLUND, Jan
APPLICANT: THYBERG, Johan
APPLICANT: TJERNBERG, Lars O.
APPLICANT: TERNIUS, Lars

TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
FILE REFERENCE: 000500-124
CURRENT APPLICATION NUMBER: US/09/095,106A
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/009,386
PRIOR FILING DATE: 1995-12-29
PRIOR APPLICATION NUMBER: PCT/SE96/01621
PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 8
TYPE: PRT
ORGANISM: Amyloidosis
US-09-095-106A-44

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 32

US-08-766-596A-1
Sequence 1, Application US/08766596A
Patent No. 6462171

GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995

```
;/ NUMBER OF SEQUENCES: 40
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: LAHIVE & COCKFIELD
;/ STREET: 28 State Street, Suite 510
;/ CITY: Boston
;/ STATE: Massachusetts
;/ COUNTRY: USA
;/ ZIP: 02109-1875
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/612,785B
;/ FILING DATE: Herewith
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/404,831
;/ FILING DATE: 14-MAR-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/475,579
;/ FILING DATE: 07-JUN-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/548,998
;/ FILING DATE: 27-OCT-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: DeConti, Giulio A.
;/ REGISTRATION NUMBER: 31,503
;/ REFERENCE/DOCKET NUMBER: PPI-002CP3
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617)227-7400
;/ TELEFAX: (617)742-4214
;/ INFORMATION FOR SEQ ID NO: 5:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-612-785B-5

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 3 KLVFFA 8

RESULT 28
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Bias
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/630,645
;/ FILING DATE:
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/478,326
;/ FILING DATE: 06-JUN-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: YUN, Allen C.
;/ REGISTRATION NUMBER: 37,971
;/ REFERENCE/DOCKET NUMBER: SOTO-JARA-1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-628-5197
;/ TELEFAX: 202-737-3528
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-630-645-1

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 1 KLVFFA 6

RESULT 29
US-08-703-675C-28
; Sequence 28, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
```


; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 24

US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NEI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 25

US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Francine
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NEI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 26

PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564 or 783-6030
; TELEFAX: (202) 783-6031
; TELEX: None
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
PCT-US94-10475-14

Query Match 93.1%; Score 27; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 27

US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation

<hr/>					
; ZIP: 02109-1875					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; OPERATING SYSTEM: IBM PC compatible					
; SOFTWARE: PatentIn Release #1.0, Version #1.25					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/703.675C					
; FILING DATE: 27-AUG-1996					
; CLASSIFICATION: 514					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/404,831					
; FILING DATE: 14-MAR-1995					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/475,579					
; FILING DATE: 07-JUN-1995					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/548,998					
; FILING DATE: 27-OCT-1995					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/616,081					
; FILING DATE: 14-MAR-1996					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Kara, Catherine J.					
; REGISTRATION NUMBER: 41,106					
; REFERENCE/DOCKET NUMBER: PPI-016CP2					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (617)227-7400					
; TELEFAX: (617)742-4214					
; INFORMATION FOR SEQ ID NO: 30:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 7 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; MOLECULE TYPE: peptide					
US-08-703-675C-30					
Query Match 93.1%; Score 27; DB 2; Length 7;					
Best Local Similarity 83.3%; Pred. No. 4.6e+05;					
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 KLVFFA 6				
	:				
Db	2 KLVFFA 7				
RESULT 21					
US-08-617-267C-7					
; Sequence 7, Application US/08617267C					
; Patent No. 6319498					
; GENERAL INFORMATION:					
; APPLICANT: Findeis, Mark A. et al.					
; TITLE OF INVENTION: Modulators of Amyloid Aggregation					
; NUMBER OF SEQUENCES: 45					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: LAHIVE & COCKFIELD, LLP					
; STREET: 28 State Street					
; CITY: Boston					
; STATE: Massachusetts					
; COUNTRY: USA					
; ZIP: 02109-1875					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/617,267C					
; FILING DATE: 14-MAR-1996					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/404,831					
; FILING DATE: 14-MAR-1995					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/475,579					
; FILING DATE: 07-JUN-1995					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/548,998					
; FILING DATE: 27-OCT-1995					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: USSN 08/616,081					
; FILING DATE: 14-MAR-1996					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Kara, Catherine J.					
; REGISTRATION NUMBER: 41,106					
; REFERENCE/DOCKET NUMBER: PPI-016CP2					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (617)227-7400					
; TELEFAX: (617)742-4214					
; INFORMATION FOR SEQ ID NO: 30:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 7 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; MOLECULE TYPE: peptide					
US-08-703-675C-30					
Query Match 93.1%; Score 27; DB 2; Length 7;					
Best Local Similarity 83.3%; Pred. No. 4.6e+05;					
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 KLVFFA 6				
	:				
Db	2 KLVFFA 7				
RESULT 23					
US-09-747-408-2					
; Sequence 2, Application US/09747408					
; Patent No. 6670399					
; GENERAL INFORMATION:					
; APPLICANT: Green, Allan M.					
; APPLICANT: Gervais, Francine					
; TITLE OF INVENTION: Compounds And Methods For Modulating					
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy					
; FILE REFERENCE: NBI-088					
; CURRENT APPLICATION NUMBER: US/09/747,408					
; CURRENT FILING DATE: 2000-12-22					
; PRIOR APPLICATION NUMBER: 60/171,877					
; PRIOR FILING DATE: 1999-12-23					
Query Match 93.1%; Score 27; DB 2; Length 7;					
Best Local Similarity 83.3%; Pred. No. 4.6e+05;					
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 KIVFFA 6				
	:				
Db	1 KLVFFA 6				
RESULT 23					
US-09-747-408-2					
; Sequence 2, Application US/09747408					
; Patent No. 6670399					
; GENERAL INFORMATION:					
; APPLICANT: Green, Allan M.					
; APPLICANT: Gervais, Francine					
; TITLE OF INVENTION: Compounds And Methods For Modulating					
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy					
; FILE REFERENCE: NBI-088					
; CURRENT APPLICATION NUMBER: US/09/747,408					
; CURRENT FILING DATE: 2000-12-22					
; PRIOR APPLICATION NUMBER: 60/171,877					
; PRIOR FILING DATE: 1999-12-23					

; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 18
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amesic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-14

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 19
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-7

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 20
US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

Aggregation Comprising D-

```
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/703,675C
/ FILING DATE: 27-AUG-1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/404,831
/ FILING DATE: 14-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/475,579
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/548,998
/ FILING DATE: 27-OCT-1995
/ APPLICATION NUMBER: USSN 08/616,081
/ FILING DATE: 14-MAR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kara, Catherine J.
/ REGISTRATION NUMBER: 41,106
/ REFERENCE/DOCKET NUMBER: PPI-016CP2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-703-675C-32

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 15
US-08-617-267C-9
/ Sequence 9, Application US/08617267C
/ Patent No. 6319498
/ GENERAL INFORMATION:
/ APPLICANT: Findels, Mark A. et al.
/ TITLE OF INVENTION: Modulators of Amyloid Aggregation
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD, LLP
/ STREET: 28 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/617,267C
/ FILING DATE: 14-MAR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/404,831

/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/703,675C
/ FILING DATE: 27-AUG-1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/404,831
/ FILING DATE: 14-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/475,579
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/548,998
/ FILING DATE: 27-OCT-1995
/ APPLICATION NUMBER: USSN 08/616,081
/ FILING DATE: 14-MAR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kara, Catherine J.
/ REGISTRATION NUMBER: 41,106
/ REFERENCE/DOCKET NUMBER: PPI-016CP2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-703-675C-32

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 16
US-09-747-408-3
/ Sequence 3, Application US/09747408
/ Patent No. 6670399
/ GENERAL INFORMATION:
/ APPLICANT: Green, Allan M.
/ TITLE OF INVENTION: Compounds And Methods For Modulating
/ TITLE OF INVENTION: Cerebral Amyloid Angiopathy
/ FILE REFERENCE: NBI-088
/ CURRENT APPLICATION NUMBER: US/09/747,408
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/171,877
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-747-408-3

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 17
US-09-747-408-11
/ Sequence 11, Application US/09747408
/ Patent No. 6670399
/ GENERAL INFORMATION:
/ APPLICANT: Green, Allan M.
/ APPLICANT: Gervais, Francine
/ TITLE OF INVENTION: Compounds And Methods For Modulating
/ TITLE OF INVENTION: Cerebral Amyloid Angiopathy
/ FILE REFERENCE: NBI-088
/ CURRENT APPLICATION NUMBER: US/09/747,408
```

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/809,917
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION NUMBER: PCT/US95/13198
;; FILING DATE:
;; APPLICATION NUMBER: US 08/361,063
;; FILING DATE: 21-DEC-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/319,866
;; FILING DATE: 07-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1144 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-809-917-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:|||||
Db 514 KLVFFA 519

RESULT 12
US-09-419-371-12
;; Sequence 12, Application US/09419371
;; Patent No. 6890516
;; GENERAL INFORMATION:
;; APPLICANT: Tully, Timothy P.
;; APPLICANT: Yin, Jerry Chi-Ping
;; TITLE OF INVENTION: Cloning and Characterizing of Genes
;; TITLE OF INVENTION: Associated With Long-Term Memory
;; FILE REFERENCE: CSHL94-03A3Z
;; CURRENT APPLICATION NUMBER: US/09/419,371
;; CURRENT FILING DATE: 1999-10-14
;; PRIOR APPLICATION NUMBER: 08/809,917
;; PRIOR FILING DATE: 1997-07-07
;; PRIOR APPLICATION NUMBER: PCT/US95/13198
;; PRIOR FILING DATE: 1995-10-06
;; PRIOR APPLICATION NUMBER: 08/361,063
;; PRIOR FILING DATE: 1994-12-21
;; PRIOR APPLICATION NUMBER: 08/319,866
;; PRIOR FILING DATE: 1994-10-07
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 12
;; LENGTH: 1144
;; TYPE: PRT
;; ORGANISM: mouse
US-09-419-371-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:|||||

Db 514 KLVFFA 519
RESULT 13
US-08-612-785B-9
;; Sequence 9, Application US/08612785B
;; Patent No. 5854204
;; GENERAL INFORMATION:
;; APPLICANT: Findeis, Mark A. et al.
;; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 28 State Street, Suite 510
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/612,785B
;; FILING DATE: Herewith
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/404,831
;; FILING DATE: 14-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/475,579
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/548,998
;; FILING DATE: 27-OCT-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeConti, Giulio A.
;; REGISTRATION NUMBER: 31,503
;; REFERENCE/DOCKET NUMBER: PPI-002CP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 93.1%; Score 27; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:|||||
Db 1 KLVFFA 6

RESULT 14
US-08-703-675C-32
;; Sequence 32, Application US/08703675C
;; Patent No. 6303567
;; GENERAL INFORMATION:
;; APPLICANT: Findeis, Mark A. et al.
;; TITLE OF INVENTION: Modulators of -Amyloid Peptide
;; NUMBER OF SEQUENCES: 46
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,866
; FILING DATE: 7-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-319-866-12

Query Match          96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 8
US-09-123-708-2
; Sequence 2, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GOEDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-09-123-708-2

Query Match          96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 9
US-09-123-624-2
; Sequence 2, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Jurgen
; APPLICANT: GOEDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-123-624-2

Query Match          96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 10
US-09-661-258-5
; Sequence 5, Application US/09661258
; Patent No. 6620616
; GENERAL INFORMATION:
; APPLICANT: Stuehr, Dennis J.
; APPLICANT: Adak, Subrata
; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
; FILE REFERENCE: 26473/04028
; CURRENT APPLICATION NUMBER: US/09/661,258
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-661-258-5

Query Match          96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 11
US-08-809-917-12
; Sequence 12, Application US/08809917
; Patent No. 6689557
; GENERAL INFORMATION:
; APPLICANT: APPLICANT
; APPLICANT: APPLICANT
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
```

Qy 1 KIVFFA 6
|:||||
Db 1 KWVFFA 6

RESULT 4

US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399

GENERAL INFORMATION:

; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KWVFFA 6

RESULT 5

US-09-513-999C-6921
; Sequence 6921, Application US/09513999C
; Patent No. 6783961

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6921

Query Match 96.6%; Score 28; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 38 KWVFFA 43

RESULT 6

US-08-147-812-5
; Sequence 5, Application US/08147812
; Patent No. 5766909

GENERAL INFORMATION:

; APPLICANT: Xie, Qiao-wen
; APPLICANT: Nathan, Carl F.
; APPLICANT: Mumford, Richard A.
; APPLICANT: Calaycay, Jimmy Ramos
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 East Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh Centris650
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,812
; FILING DATE: No. 5766909 Available
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/841,641
; FILING DATE: 02-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 186581A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-147-812-5

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 514 KWVFFA 519

RESULT 7

US-08-319-866-12
; Sequence 12, Application US/08319866
; Patent No. 5929223

GENERAL INFORMATION:

; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry C.
; APPLICANT: Regulski, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
247 27 93.1 42 2 US-09-005-215-20
248 27 93.1 42 2 US-09-242-724-23
249 27 93.1 42 2 US-08-922-930-2
250 27 93.1 42 2 US-09-660-954-1
251 27 93.1 42 2 US-08-923-055-2
252 27 93.1 42 2 US-08-922-885-2
253 27 93.1 42 2 US-09-731-460-1
254 27 93.1 42 2 US-09-133-866-2
255 27 93.1 42 2 US-09-723-384-1
256 27 93.1 42 2 US-09-724-961-42
257 27 93.1 42 2 US-09-724-552-1
258 27 93.1 42 2 US-09-580-018-42
259 27 93.1 42 2 US-10-455-218-2
260 27 93.1 42 2 US-09-723-927-1
261 27 93.1 42 2 US-09-724-489-1
262 27 93.1 42 2 US-09-724-477-1
263 27 93.1 42 2 US-09-723-762-1
264 27 93.1 42 2 US-09-201-430-1
265 27 93.1 42 2 US-09-724-551-42
266 27 93.1 42 2 US-10-815-353-1
267 27 93.1 42 2 US-10-278-181-1
268 27 93.1 42 2 US-10-816-529-1
269 27 93.1 42 2 US-09-623-548A-955
270 27 93.1 42 2 US-09-623-548A-961
271 27 93.1 42 2 US-09-623-548A-967
272 27 93.1 42 2 US-09-623-548A-988
273 27 93.1 42 2 US-09-623-548A-994
274 27 93.1 42 2 US-10-815-391-1
275 27 93.1 42 2 US-10-816-022-1
276 27 93.1 42 2 US-09-724-953-34
277 27 93.1 42 2 US-09-657-276-955
278 27 93.1 42 2 US-09-657-276-961
279 27 93.1 42 2 US-09-657-276-967
280 27 93.1 42 2 US-09-657-276-988
281 27 93.1 42 2 US-09-657-276-994
282 27 93.1 42 2 US-09-724-567-34
283 27 93.1 42 2 US-09-724-940-42
284 27 93.1 42 2 US-09-865-294A-65
285 27 93.1 42 2 US-09-979-952-34
286 27 93.1 42 2 US-09-585-817-34
287 27 93.1 42 2 US-09-962-955D-37
288 27 93.1 42 2 US-09-706-574A-20
289 27 93.1 42 2 US-10-934-609-1
290 27 93.1 42 2 US-10-884-892-1
291 27 93.1 42 4 PCT-US92-06700-2
292 27 93.1 42 4 PCT-US93-00325-1
293 27 93.1 42 4 PCT-US95-08302-5
294 27 93.1 42 6 5220013-12
295 27 93.1 42 6 5220013-14
296 27 93.1 42 6 5223482-12
297 27 93.1 43 1 US-08-235-400-1
298 27 93.1 43 1 US-08-437-067-1
299 27 93.1 43 1 US-08-302-808-6
300 27 93.1 43 1 US-08-079-511-1

ALIGNMENTS

RESULT 1
US-09-747-408-1
; Sequence 1, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; QUERY Match 96.6%; Score 28; DB 2; Length 6;
; Best Local Similarity 83.3%; Pred. No. 4.6e+05;
; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2
US-09-747-408-10
; Sequence 10, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,877
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,877
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```


101	27	93.1	20	2	US-09-724-953-33	Sequence 33, Appl	174	27	93.1	38	2	US-09-657-276-1002	Sequence 1002, Ap
102	27	93.1	20	2	US-09-724-567-33	Sequence 33, Appl	175	27	93.1	39	1	US-08-304-585-5	Sequence 5, Appl
103	27	93.1	20	2	US-09-979-952-33	Sequence 33, Appl	176	27	93.1	39	1	US-08-302-808-2	Sequence 2, Appl
104	27	93.1	20	2	US-09-585-817-33	Sequence 33, Appl	177	27	93.1	39	1	US-08-609-090-7	Sequence 7, Appl
105	27	93.1	26	1	US-08-304-585-7	Sequence 4, Appl	178	27	93.1	39	1	US-08-682-245A-1	Sequence 1, Appl
106	27	93.1	28	1	US-08-346-849-4	Sequence 4, Appl	179	27	93.1	39	1	US-08-986-948-2	Sequence 2, Appl
107	27	93.1	28	1	US-08-302-808-7	Sequence 7, Appl	180	27	93.1	40	1	US-07-744-767A-1	Sequence 1, Appl
108	27	93.1	28	1	US-08-609-090-2	Sequence 2, Appl	181	27	93.1	40	1	US-08-235-400-2	Sequence 2, Appl
109	27	93.1	28	1	US-08-986-948-7	Sequence 7, Appl	182	27	93.1	40	1	US-08-476-464A-2	Sequence 2, Appl
110	27	93.1	28	1	US-08-293-284A-4	Sequence 4, Appl	183	27	93.1	40	1	US-08-304-585-1	Sequence 1, Appl
111	27	93.1	28	1	US-08-461-216-2	Sequence 2, Appl	184	27	93.1	40	1	US-08-304-585-8	Sequence 8, Appl
112	27	93.1	28	2	US-09-388-890-3	Sequence 2, Appl	185	27	93.1	40	1	US-08-302-808-3	Sequence 3, Appl
113	27	93.1	28	2	US-09-388-890-2	Sequence 2, Appl	186	27	93.1	40	1	US-08-433-734-1	Sequence 1, Appl
114	27	93.1	28	2	US-09-388-890-4	Sequence 4, Appl	187	27	93.1	40	1	US-08-609-090-8	Sequence 8, Appl
115	27	93.1	28	2	US-09-388-890-5	Sequence 5, Appl	188	27	93.1	40	1	US-07-737-371B-69	Sequence 69, Appl
116	27	93.1	28	2	US-09-388-890-6	Sequence 6, Appl	189	27	93.1	40	1	US-08-682-245A-2	Sequence 2, Appl
117	27	93.1	28	2	US-09-388-890-7	Sequence 7, Appl	190	27	93.1	40	1	US-08-986-948-3	Sequence 3, Appl
118	27	93.1	28	2	US-09-388-890-8	Sequence 8, Appl	191	27	93.1	40	1	US-08-461-216-1	Sequence 1, Appl
119	27	93.1	28	2	US-09-388-890-9	Sequence 9, Appl	192	27	93.1	40	2	US-08-959-148-1	Sequence 1, Appl
120	27	93.1	28	2	US-09-388-890-10	Sequence 10, Appl	193	27	93.1	40	2	US-09-242-724-22	Sequence 22, Appl
121	27	93.1	28	2	US-09-388-890-12	Sequence 12, Appl	194	27	93.1	40	2	US-08-723-661B-1	Sequence 1, Appl
122	27	93.1	28	2	US-09-388-890-13	Sequence 13, Appl	195	27	93.1	40	2	US-09-062-365-3	Sequence 3, Appl
123	27	93.1	28	2	US-09-388-890-14	Sequence 14, Appl	196	27	93.1	40	2	US-09-133-866-1	Sequence 1, Appl
124	27	93.1	28	2	US-09-264-709A-1	Sequence 1, Appl	197	27	93.1	40	2	US-09-861-847A-7	Sequence 7, Appl
125	27	93.1	28	2	US-08-723-661B-2	Sequence 2, Appl	198	27	93.1	40	2	US-09-861-847A-8	Sequence 8, Appl
126	27	93.1	28	2	US-09-660-954-2	Sequence 2, Appl	199	27	93.1	40	2	US-09-988-842-3	Sequence 3, Appl
127	27	93.1	28	2	US-09-660-954-3	Sequence 3, Appl	200	27	93.1	40	2	US-10-455-218-1	Sequence 1, Appl
128	27	93.1	28	2	US-09-660-954-4	Sequence 4, Appl	201	27	93.1	40	2	US-10-151-614-1	Sequence 1, Appl
129	27	93.1	28	2	US-09-660-954-5	Sequence 5, Appl	202	27	93.1	40	2	US-09-623-548A-956	Sequence 956, App
130	27	93.1	28	2	US-09-660-954-6	Sequence 6, Appl	203	27	93.1	40	2	US-09-623-548A-962	Sequence 962, App
131	27	93.1	28	2	US-09-660-954-7	Sequence 7, Appl	204	27	93.1	40	2	US-09-623-548A-968	Sequence 968, App
132	27	93.1	28	2	US-09-660-954-8	Sequence 8, Appl	205	27	93.1	40	2	US-09-623-548A-978	Sequence 978, App
133	27	93.1	28	2	US-09-660-954-9	Sequence 9, Appl	206	27	93.1	40	2	US-09-623-548A-988	Sequence 988, App
134	27	93.1	28	2	US-09-660-954-10	Sequence 10, Appl	207	27	93.1	40	2	US-09-623-548A-995	Sequence 995, App
135	27	93.1	28	2	US-09-660-954-12	Sequence 12, Appl	208	27	93.1	40	2	US-09-623-548A-1005	Sequence 1005, Ap
136	27	93.1	28	2	US-09-660-954-13	Sequence 13, Appl	209	27	93.1	40	2	US-09-657-276-956	Sequence 956, App
137	27	93.1	28	2	US-09-660-954-14	Sequence 14, Appl	210	27	93.1	40	2	US-09-657-276-962	Sequence 962, App
138	27	93.1	28	2	US-08-898-300-4	Sequence 4, Appl	211	27	93.1	40	2	US-09-657-276-968	Sequence 968, App
139	27	93.1	28	2	US-08-824-513-4	Sequence 4, Appl	212	27	93.1	40	2	US-09-657-276-978	Sequence 978, App
140	27	93.1	28	2	US-09-623-548A-959	Sequence 959, App	213	27	93.1	40	2	US-09-657-276-989	Sequence 989, App
141	27	93.1	28	2	US-09-623-548A-965	Sequence 965, App	214	27	93.1	40	2	US-09-657-276-995	Sequence 995, App
142	27	93.1	28	2	US-09-623-548A-976	Sequence 976, App	215	27	93.1	40	2	US-09-657-276-1005	Sequence 1005, Ap
143	27	93.1	28	2	US-09-623-548A-992	Sequence 992, App	216	27	93.1	40	2	US-09-962-955D-36	Sequence 36, Appl
144	27	93.1	28	2	US-09-623-548A-1003	Sequence 1003, Ap	217	27	93.1	40	4	FCT-US92-06700-1	Sequence 1, Appl
145	27	93.1	28	2	US-09-657-276-959	Sequence 959, App	218	27	93.1	41	1	US-07-819-361-1	Sequence 1, Appl
146	27	93.1	28	2	US-09-657-276-965	Sequence 965, App	219	27	93.1	41	1	US-08-302-808-4	Sequence 4, Appl
147	27	93.1	28	2	US-09-657-276-976	Sequence 976, App	220	27	93.1	41	1	US-08-682-245A-3	Sequence 3, Appl
148	27	93.1	28	2	US-09-657-276-992	Sequence 992, App	221	27	93.1	41	1	US-08-986-948-4	Sequence 4, Appl
149	27	93.1	28	2	US-09-657-276-1003	Sequence 1003, Ap	222	27	93.1	42	1	US-07-744-767A-2	Sequence 2, Appl
150	27	93.1	28	2	US-09-865-294A-66	Sequence 66, Appl	223	27	93.1	42	1	US-08-179-574-1	Sequence 1, Appl
151	27	93.1	30	1	US-08-609-090-3	Sequence 3, Appl	224	27	93.1	42	1	US-08-271-162-5	Sequence 5, Appl
152	27	93.1	30	2	US-09-861-847A-1	Sequence 1, Appl	225	27	93.1	42	1	US-08-347-144-1	Sequence 1, Appl
153	27	93.1	33	1	US-08-609-090-4	Sequence 4, Appl	226	27	93.1	42	1	US-08-462-859A-19	Sequence 19, Appl
154	27	93.1	34	1	US-08-475-579A-4	Sequence 4, Appl	227	27	93.1	42	1	US-08-123-659A-19	Sequence 19, Appl
155	27	93.1	35	1	US-08-304-585-6	Sequence 6, Appl	228	27	93.1	42	1	US-08-464-247A-19	Sequence 19, Appl
156	27	93.1	35	1	US-08-612-785B-16	Sequence 16, Appl	229	27	93.1	42	1	US-08-464-248A-19	Sequence 19, Appl
157	27	93.1	35	1	US-08-612-785B-36	Sequence 36, Appl	230	27	93.1	42	1	US-08-476-464A-1	Sequence 1, Appl
158	27	93.1	35	1	US-08-612-785B-38	Sequence 38, Appl	231	27	93.1	42	1	US-08-302-808-5	Sequence 5, Appl
159	27	93.1	35	1	US-08-612-785B-40	Sequence 40, Appl	232	27	93.1	42	1	US-08-302-808-2	Sequence 2, Appl
160	27	93.1	35	2	US-08-617-267C-16	Sequence 16, Appl	233	27	93.1	42	1	US-08-268-348A-1	Sequence 1, Appl
161	27	93.1	35	2	US-09-623-548A-979	Sequence 979, App	234	27	93.1	42	1	US-08-268-348A-2	Sequence 2, Appl
162	27	93.1	35	2	US-09-623-548A-1006	Sequence 1006, Ap	235	27	93.1	42	1	US-08-268-348A-3	Sequence 3, Appl
163	27	93.1	35	2	US-09-657-276-979	Sequence 979, App	236	27	93.1	42	1	US-08-268-348A-4	Sequence 4, Appl
164	27	93.1	35	2	US-09-657-276-1006	Sequence 1006, Ap	237	27	93.1	42	1	US-08-268-348A-5	Sequence 5, Appl
165	27	93.1	36	1	US-08-609-090-6	Sequence 6, Appl	238	27	93.1	42	1	US-08-268-348A-6	Sequence 6, Appl
166	27	93.1	36	2	US-09-861-847A-6	Sequence 6, Appl	239	27	93.1	42	1	US-08-433-734-2	Sequence 2, Appl
167	27	93.1	36	2	US-09-861-847A-11	Sequence 11, Appl	240	27	93.1	42	1	US-08-609-090-9	Sequence 9, Appl
168	27	93.1	38	1	US-08-302-808-1	Sequence 1, Appl	241	27	93.1	42	1	US-07-737-371B-72	Sequence 72, Appl
169	27	93.1	38	1	US-08-737-371E-68	Sequence 68, Appl	242	27	93.1	42	1	US-08-422-333-4	Sequence 4, Appl
170	27	93.1	38	1	US-08-986-948-1	Sequence 1, Appl	243	27	93.1	42	1	US-08-682-245A-4	Sequence 4, Appl
171	27	93.1	38	2	US-09-623-548A-975	Sequence 975, App	244	27	93.1	42	1	US-08-986-948-5	Sequence 5, Appl
172	27	93.1	38	2	US-09-623-548A-1002	Sequence 1002, Ap	245	27	93.1	42	2	US-08-717-551A-2	Sequence 2, Appl
173	27	93.1	38	2	US-09-657-276-975	Sequence 975, App	246	27	93.1	42	2	US-09-388-890-1	Sequence 1, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
 - 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
 - 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
 - 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
 - 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
 - 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-1
2	29	100.0	6	2	US-09-747-408-10
3	28	96.6	6	2	US-09-747-408-9
4	28	96.6	6	2	US-09-747-408-17
5	28	96.6	77	2	US-09-513-999C-6921
6	28	96.6	1144	1	US-08-147-812-5
7	28	96.6	1144	1	US-08-319-866-12
8	28	96.6	1144	2	US-09-123-708-2
9	28	96.6	1144	2	US-09-123-624-2
10	28	96.6	1144	2	US-09-661-258-5
11	28	96.6	1144	2	US-08-809-917-12
12	28	96.6	1144	2	US-09-419-371-12
13	27	93.1	6	1	US-08-612-785B-9
14	27	93.1	6	2	US-08-703-675C-32
15	27	93.1	6	2	US-08-617-267C-9
16	27	93.1	6	2	US-09-747-408-3
17	27	93.1	6	2	US-09-747-408-11
18	27	93.1	7	1	US-08-127-904-14
19	27	93.1	7	1	US-08-612-785B-7
20	27	93.1	7	2	US-08-703-675C-30
21	27	93.1	7	2	US-08-617-267C-7
22	27	93.1	7	2	US-09-264-709A-13
23	27	93.1	7	2	US-09-747-408-2
24	27	93.1	7	2	US-09-747-408-18
25	27	93.1	7	2	US-09-747-408-19
26	27	93.1	7	4	PCT-US94-10475-14
27	27	93.1	8	1	US-08-612-785B-5

28	27	93.1	8	1	US-08-630-645-1	Sequence 1, Appli
29	27	93.1	8	2	US-08-703-675C-28	Sequence 28, Appl
30	27	93.1	8	2	US-08-617-267C-5	Sequence 5, Appli
31	27	93.1	8	2	US-09-095-106A-44	Sequence 44, Appl
32	27	93.1	8	2	US-08-766-596A-1	Sequence 1, Appli
33	27	93.1	8	2	US-09-668-314C-73	Sequence 73, Appl
34	27	93.1	8	4	PCT-US96-10220-1	Sequence 1, Appli
35	27	93.1	9	2	US-08-766-596A-64	Sequence 64, Appl
36	27	93.1	9	2	US-09-747-408-20	Sequence 20, Appl
37	27	93.1	10	2	US-08-970-833-3	Sequence 3, Appli
38	27	93.1	10	2	US-09-724-961-20	Sequence 20, Appl
39	27	93.1	10	2	US-09-724-961-21	Sequence 21, Appl
40	27	93.1	10	2	US-09-724-961-22	Sequence 22, Appl
41	27	93.1	10	2	US-09-724-961-23	Sequence 23, Appl
42	27	93.1	10	2	US-09-724-961-24	Sequence 24, Appl
43	27	93.1	10	2	US-09-580-018-20	Sequence 20, Appl
44	27	93.1	10	2	US-09-580-018-21	Sequence 21, Appl
45	27	93.1	10	2	US-09-580-018-22	Sequence 22, Appl
46	27	93.1	10	2	US-09-580-018-23	Sequence 23, Appl
47	27	93.1	10	2	US-09-580-018-24	Sequence 24, Appl
48	27	93.1	10	2	US-09-724-551-20	Sequence 20, Appl
49	27	93.1	10	2	US-09-724-551-21	Sequence 21, Appl
50	27	93.1	10	2	US-09-724-551-22	Sequence 22, Appl
51	27	93.1	10	2	US-09-724-551-23	Sequence 23, Appl
52	27	93.1	10	2	US-09-724-551-24	Sequence 24, Appl
53	27	93.1	10	2	US-09-724-940-20	Sequence 20, Appl
54	27	93.1	10	2	US-09-724-940-21	Sequence 21, Appl
55	27	93.1	10	2	US-09-724-940-22	Sequence 22, Appl
56	27	93.1	10	2	US-09-724-940-23	Sequence 23, Appl
57	27	93.1	10	2	US-09-724-940-24	Sequence 24, Appl
58	27	93.1	11	1	US-08-630-645-14	Sequence 14, Appl
59	27	93.1	11	2	US-08-766-596A-14	Sequence 14, Appl
60	27	93.1	11	2	US-09-988-842-9	Sequence 9, Appli
61	27	93.1	11	2	US-09-988-842-25	Sequence 25, Appl
62	27	93.1	11	4	PCT-US96-10220-14	Sequence 14, Appl
63	27	93.1	14	2	US-09-594-366-5	Sequence 5, Appli
64	27	93.1	14	2	US-09-592-800-5	Sequence 5, Appli
65	27	93.1	15	1	US-08-612-785B-14	Sequence 14, Appl
66	27	93.1	15	1	US-08-612-785B-37	Sequence 37, Appl
67	27	93.1	15	2	US-08-617-267C-14	Sequence 14, Appl
68	27	93.1	15	2	US-08-766-596A-56	Sequence 56, Appl
69	27	93.1	15	2	US-08-766-596A-57	Sequence 57, Appl
70	27	93.1	15	2	US-08-766-596A-58	Sequence 58, Appl
71	27	93.1	15	2	US-08-766-596A-60	Sequence 60, Appl
72	27	93.1	15	2	US-08-766-596A-61	Sequence 61, Appl
73	27	93.1	15	2	US-08-766-596A-63	Sequence 63, Appl
74	27	93.1	15	2	US-08-766-596A-65	Sequence 65, Appl
75	27	93.1	17	2	US-09-264-709A-2	Sequence 2, Appli
76	27	93.1	17	2	US-09-594-366-3	Sequence 3, Appli
77	27	93.1	17	2	US-09-623-548A-950	Sequence 950, App
78	27	93.1	17	2	US-09-623-548A-983	Sequence 983, App
79	27	93.1	17	2	US-09-992-800-3	Sequence 3, Appli
80	27	93.1	17	2	US-09-657-276-950	Sequence 950, App
81	27	93.1	17	2	US-09-657-276-983	Sequence 983, App
82	27	93.1	19	2	US-08-970-833-11	Sequence 11, Appl
83	27	93.1	19	2	US-09-723-384-5	Sequence 5, Appli
84	27	93.1	19	2	US-09-724-961-75	Sequence 75, Appl
85	27	93.1	19	2	US-09-724-552-5	Sequence 5, Appli
86	27	93.1	19	2	US-09-580-018-75	Sequence 75, Appl
87	27	93.1	19	2	US-09-723-927-5	Sequence 5, Appli
88	27	93.1	19	2	US-09-724-489-5	Sequence 5, Appli
89	27	93.1	19	2	US-09-724-477-5	Sequence 5, Appli
90	27	93.1	19	2	US-09-723-762-5	Sequence 5, Appli
91	27	93.1	19	2	US-09-201-430-5	Sequence 5, Appli
92	27	93.1	19	2	US-09-724-551-75	Sequence 75, Appl
93	27	93.1	19	2	US-10-815-353-5	Sequence 5, Appli
94	27	93.1	19	2	US-10-816-529-5	Sequence 5, Appli
95	27	93.1	19	2	US-10-815-391-5	Sequence 5, Appli
96	27	93.1	19	2	US-10-816-022-5	Sequence 5, Appli
97	27	93.1	19	2	US-09-724-940-75	Sequence 75, Appl
98	27	93.1	19	2	US-09-724-940-5	Sequence 5, Appli
99	27	93.1	19	2	US-10-884-892-5	Sequence 5, Appli
100	27	93.1	20	2	US-08-970-833-10	Sequence 10, Appl

```
; TITLE OF INVENTION:  US THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; PRIOR FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-17
```

```
Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6
```

```
RESULT 75
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT:  Gervais, Francine
; APPLICANT:  Kong, Xianqi
; APPLICANT:  Chalifour, Robert
; APPLICANT:  Migneault, David
; TITLE OF INVENTION:  ANYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-18
```

```
Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6
```

Search completed: December 29, 2005, 18:49:33
Job time : 70.2903 secs

```
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 71
US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 72
US-09-972-475-7
; Sequence 7, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 73
US-09-915-092-2
; Sequence 2, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-2

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 74
US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
```

```
RESULT 67
US-10-825-958-18
; Sequence 18, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR FILING DATE: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-18

Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 68
US-10-666-095-3
; Sequence 3, Application US/10666095
; Publication No. US20050119187A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Robert P.
; APPLICANT: Fu, Yanwen
; APPLICANT: Aucoin, Jed P.
; APPLICANT: Miller, Tod J.
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: McCarley, Robin L.
; TITLE OF INVENTION: Anti-fibril Peptides
; FILE REFERENCE: 0212.1 Hammer
; CURRENT APPLICATION NUMBER: US/10/666,095
; CURRENT FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,081
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-095-3

Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match          93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match          93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 2 KLVFFA 7
```

```
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-10
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```

```
RESULT 64
US-10-728-028-27
; Sequence 27, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-27
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```

```
RESULT 65
US-10-728-028-28
; Sequence 28, Application US/10728028
```

```
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-28
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```

```
RESULT 66
US-10-825-958-7
; Sequence 7, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-7
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
```

```
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 56
US-09-972-475-9
; Sequence 9, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-972-475-9
Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 57
US-09-915-092-10
; Sequence 10, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139

US-09-915-092-10
Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 58
US-09-915-092-28
; Sequence 28, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: D-amino acids

US-09-915-092-28
Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 59
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
```



```
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-10-097-143-32208

Query Match          96.6%; Score 28; DB 6; Length 1443;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1204 KIIFFA 1209

RESULT 53
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Audrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match          96.6%; Score 28; DB 4; Length 1640;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1596 KIVFFA 1601
```

```
RESULT 54
US-09-867-847-7
; Sequence 7, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KLVFFA 6

RESULT 55
US-09-867-847-20
; Sequence 20, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)_
; OTHER INFORMATION: AMIDATION
US-09-867-847-20

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Db 514 KVVFFA 519

RESULT 48

US-10-428-817A-120
; Sequence 120, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-428-817A-120

Query Match 96.6%; Score 28; DB 4; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 49

US-10-937-758A-101
; Sequence 101, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-758A-101

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 50

US-10-631-467-1388
; Sequence 1388, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1388
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1388

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 51

US-10-631-467-1464
; Sequence 1464, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 52

US-11-097-143-32208
; Sequence 32208, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match 96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 44

US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1

; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match 96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 45

US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1

; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312

; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match 96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 46

US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match 96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 47

US-09-751-708A-124
; Sequence 124, Application US/09751708A
; Publication No. US20030157113A1

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-124

Query Match 96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||

US-10-408-765A-2031
; Sequence 2031, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2031
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2031

Query Match 96.6%; Score 28; DB 6; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 40
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match 96.6%; Score 28; DB 6; Length 564;
Best Local Similarity 83.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KIVFFA 6
|:||||
Db 53 KIIFFA 58

RESULT 41

US-10-408-765A-2031
; Sequence 2031, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2031
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2031

Query Match 96.6%; Score 28; DB 4; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 42
US-10-755-889-234
; Sequence 234, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-234

Query Match 96.6%; Score 28; DB 4; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 43
US-10-370-715B-8
; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patent Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pep
US-10-437-963-172452

Query Match 96.6%; Score 28; DB 4; Length 198;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 36
US-10-055-475-14
; Sequence 14, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-055-475-14

Query Match 96.6%; Score 28; DB 4; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 37
US-11-042-922-14
; Sequence 14, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul

; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-042-922-14

Query Match 96.6%; Score 28; DB 6; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 38
US-10-055-475-13
; Sequence 13, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-055-475-13

Query Match 96.6%; Score 28; DB 4; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 39
US-11-042-922-13
; Sequence 13, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT

Best Local Similarity 83.3%; Pred. No. 3.3e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 32

US-10-481-032A-214
; Sequence 214, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 214
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 5; Length 186;
Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 33

US-10-481-032A-228
; Sequence 228, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228

Query Match 96.6%; Score 28; DB 5; Length 186;
Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 34

US-10-437-963-172476
; Sequence 172476, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pep
US-10-437-963-172476

Query Match 96.6%; Score 28; DB 4; Length 188;
Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 35

US-10-437-963-172452
; Sequence 172452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 28

US-10-437-963-133986
; Sequence 133986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pap
US-10-437-963-133986

Query Match 96.6%; Score 28; DB 4; Length 87;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 6 KVVFFA 11

RESULT 29

US-10-437-963-105773
; Sequence 105773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pap
US-10-437-963-105773

Query Match 96.6%; Score 28; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 30

US-10-437-963-141578
; Sequence 141578, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141578
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pap
US-10-437-963-141578

Query Match 96.6%; Score 28; DB 4; Length 135;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 31

US-10-437-963-122124
; Sequence 122124, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122124
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(175)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pap
US-10-437-963-122124

Query Match 96.6%; Score 28; DB 4; Length 175;

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 24
US-10-825-958-24
; Sequence 24, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangl
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 25
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 5303AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 18 KVVFFA 23

RESULT 26
US-10-642-255-7
; Sequence 7, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubany1, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: eNOS
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 18 KVVFFA 23

RESULT 27
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pep
US-10-437-963-173619

Query Match 96.6%; Score 28; DB 4; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 20
US-09-747-408-17

; Sequence 17, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 21

US-10-728-028-8
; Sequence 8, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 22

US-10-728-028-16
; Sequence 16, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 23

US-10-825-958-16
; Sequence 16, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-16

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 1 KVVFFA 6

RESULT 16
US-09-867-847-26
; Sequence 26, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Hebert, Robert
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-26

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 1 KVVFFA 6

RESULT 17
US-09-915-092-8
; Sequence 8, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
```

```
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 1 KVVFFA 6

RESULT 18
US-09-915-092-16
; Sequence 16, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 1 KVVFFA 6

RESULT 19
US-09-747-408-9
; Sequence 9, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9
```

; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
US-10-425-115-280164

Query Match 100.0%; Score 29; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 28 KIVFFA 33

RESULT 12
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
US-10-424-599-165325

Query Match 100.0%; Score 29; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 21 KIVFFA 26

RESULT 13
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
US-10-424-599-240310

Query Match 100.0%; Score 29; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 34 KIVFFA 39

RESULT 14
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56957

Query Match 100.0%; Score 29; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 63 KIVFFA 68

RESULT 15
US-09-867-847-18
; Sequence 18, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Robet
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 8
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 9
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-10-825-958-9

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 11
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```

```

; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 4
US-09-915-092-9
; Sequence 9, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 5
US-09-747-408-1
; Sequence 1, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 6
US-09-747-408-10
; Sequence 10, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 7
US-10-728-028-1
; Sequence 1, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
247 93.1 20 3 US-09-908-943A-25 Sequence 25, Appl
248 93.1 20 5 US-10-801-487-25 Sequence 25, Appl
249 93.1 20 5 US-10-801-938-25 Sequence 25, Appl
250 93.1 20 5 US-10-801-509-25 Sequence 25, Appl
251 93.1 20 5 US-10-801-486-25 Sequence 25, Appl
252 93.1 20 5 US-10-801-493-25 Sequence 25, Appl
253 93.1 24 5 US-10-728-246-5 Sequence 6, Appl
254 93.1 24 5 US-10-728-246-6 Sequence 11, Appl
255 93.1 26 3 US-09-792-079-11 Sequence 11, Appl
256 93.1 26 4 US-10-159-279-11 Sequence 4, Appl
257 93.1 28 3 US-09-867-847-4 Sequence 66, Appl
258 93.1 28 3 US-09-865-294-66 Sequence 5, Appl
259 93.1 28 3 US-09-792-079-5 Sequence 2, Appl
260 93.1 28 4 US-10-159-279-5 Sequence 7, Appl
261 93.1 28 4 US-10-363-082-2 Sequence 4, Appl
262 93.1 28 4 US-10-433-385-7 Sequence 4, Appl
263 93.1 28 4 US-10-390-472-4 Sequence 36, Appl
264 93.1 28 4 US-10-741-205-36 Sequence 7, Appl
265 93.1 28 4 US-10-416-262B-7 Sequence 4, Appl
266 93.1 28 4 US-10-478-308-4 Sequence 4, Appl
267 93.1 28 4 US-10-478-307-4 Sequence 66, Appl
268 93.1 28 5 US-10-861-614-66 Sequence 4, Appl
269 93.1 28 5 US-10-825-958-4 Sequence 3, Appl
270 93.1 28 6 US-11-091-309-3 Sequence 959, App
271 93.1 28 6 US-11-066-697-959 Sequence 965, App
272 93.1 28 6 US-11-066-697-965 Sequence 976, App
273 93.1 28 6 US-11-066-697-976 Sequence 992, App
274 93.1 28 6 US-11-066-697-992 Sequence 1003, App
275 93.1 28 6 US-11-066-697-1003 Sequence 1, Appl
276 93.1 30 4 US-09-861-847-1 Sequence 1, Appl
277 93.1 30 4 US-10-301-488A-1 Sequence 9, Appl
278 93.1 30 4 US-10-666-423-1 Sequence 24, Appl
279 93.1 30 4 US-10-617-876-9 Sequence 1, Appl
280 93.1 30 4 US-10-619-454-24 Sequence 5, Appl
281 93.1 30 4 US-10-301-448-1 Sequence 99, Appl
282 93.1 30 5 US-10-775-562-5 Sequence 295, App
283 93.1 32 4 US-10-732-862A-99 Sequence 84, Appl
284 93.1 32 3 US-09-930-915A-295 Sequence 85, Appl
285 93.1 33 4 US-10-082-014-84 Sequence 85, Appl
286 93.1 33 4 US-10-372-076-85 Sequence 98, Appl
287 93.1 33 4 US-10-732-862A-98 Sequence 295, App
288 93.1 33 4 US-10-806-006-295 Sequence 85, Appl
289 93.1 33 4 US-10-677-074-85 Sequence 295, App
290 93.1 35 3 US-10-805-913-295 Sequence 3, Appl
291 93.1 35 3 US-09-867-847-3 Sequence 16, Appl
292 93.1 35 3 US-09-972-475-16 Sequence 16, Appl
293 93.1 35 4 US-10-463-729-16 Sequence 3, Appl
294 93.1 35 5 US-10-825-958-3 Sequence 979, App
295 93.1 35 6 US-11-066-697-979 Sequence 1006, App
296 93.1 35 6 US-11-066-697-1006 Sequence 6, Appl
297 93.1 36 3 US-09-861-847-6 Sequence 11, Appl
298 93.1 36 3 US-09-861-847-11 Sequence 6, Appl
299 93.1 36 4 US-09-301-488A-6 Sequence 11, Appl
300 93.1 36 4 US-10-301-488A-11

ALIGNMENTS

RESULT 1
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2
US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)_
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
```

101	27	93.1	9	4	US-10-619-454-25	Sequence 25, Appl	174	27	93.1	13	4	US-10-281-458-1	Sequence 1, Appl
102	27	93.1	9	4	US-10-619-454-28	Sequence 28, Appl	175	27	93.1	13	5	US-10-625-854-127	Sequence 127, App
103	27	93.1	9	4	US-10-619-454-57	Sequence 57, Appl	176	27	93.1	13	5	US-10-625-854-140	Sequence 140, App
104	27	93.1	9	4	US-10-619-454-157	Sequence 157, Appl	177	27	93.1	14	3	US-09-992-800-5	Sequence 5, Appl
105	27	93.1	10	3	US-09-867-847-29	Sequence 29, Appl	178	27	93.1	14	3	US-09-992-994-5	Sequence 5, Appl
106	27	93.1	10	3	US-09-915-092-19	Sequence 19, Appl	179	27	93.1	14	4	US-10-385-065-5	Sequence 5, Appl
107	27	93.1	10	5	US-10-889-999-20	Sequence 20, Appl	180	27	93.1	14	5	US-10-810-881A-114	Sequence 114, App
108	27	93.1	10	5	US-10-889-999-21	Sequence 21, Appl	181	27	93.1	14	5	US-10-505-313-2	Sequence 2, Appl
109	27	93.1	10	5	US-10-889-999-22	Sequence 22, Appl	182	27	93.1	14	5	US-10-625-854-115	Sequence 115, App
110	27	93.1	10	5	US-10-889-999-23	Sequence 23, Appl	183	27	93.1	14	5	US-10-625-854-128	Sequence 128, App
111	27	93.1	10	5	US-10-889-999-24	Sequence 24, Appl	184	27	93.1	14	5	US-10-625-854-141	Sequence 141, App
112	27	93.1	10	5	US-10-890-070-20	Sequence 20, Appl	185	27	93.1	14	6	US-11-063-350-5	Sequence 5, Appl
113	27	93.1	10	5	US-10-890-070-21	Sequence 21, Appl	186	27	93.1	15	3	US-09-972-475-14	Sequence 14, Appl
114	27	93.1	10	5	US-10-890-070-22	Sequence 22, Appl	187	27	93.1	15	3	US-09-996-357-9	Sequence 9, Appl
115	27	93.1	10	5	US-10-890-070-23	Sequence 23, Appl	188	27	93.1	15	4	US-10-235-483-56	Sequence 56, Appl
116	27	93.1	10	5	US-10-890-070-24	Sequence 24, Appl	189	27	93.1	15	4	US-10-235-483-57	Sequence 57, Appl
117	27	93.1	10	5	US-10-890-000-20	Sequence 20, Appl	190	27	93.1	15	4	US-10-235-483-58	Sequence 58, Appl
118	27	93.1	10	5	US-10-890-000-21	Sequence 21, Appl	191	27	93.1	15	4	US-10-235-483-60	Sequence 60, Appl
119	27	93.1	10	5	US-10-890-000-22	Sequence 22, Appl	192	27	93.1	15	4	US-10-235-483-61	Sequence 61, Appl
120	27	93.1	10	5	US-10-890-000-23	Sequence 23, Appl	193	27	93.1	15	4	US-10-235-483-63	Sequence 63, Appl
121	27	93.1	10	5	US-10-890-000-24	Sequence 24, Appl	194	27	93.1	15	4	US-10-235-483-65	Sequence 65, Appl
122	27	93.1	10	5	US-10-823-463-20	Sequence 20, Appl	195	27	93.1	15	4	US-10-463-729-14	Sequence 14, Appl
123	27	93.1	10	5	US-10-823-463-21	Sequence 21, Appl	196	27	93.1	15	5	US-10-625-854-103	Sequence 103, App
124	27	93.1	10	5	US-10-823-463-22	Sequence 22, Appl	197	27	93.1	15	5	US-10-625-854-116	Sequence 116, App
125	27	93.1	10	5	US-10-823-463-23	Sequence 23, Appl	198	27	93.1	15	5	US-10-625-854-129	Sequence 129, App
126	27	93.1	10	5	US-10-823-463-24	Sequence 24, Appl	199	27	93.1	15	5	US-10-625-854-142	Sequence 142, App
127	27	93.1	10	5	US-10-777-792-19	Sequence 19, Appl	200	27	93.1	16	5	US-10-625-854-91	Sequence 91, Appl
128	27	93.1	10	5	US-10-822-968-20	Sequence 20, Appl	201	27	93.1	16	5	US-10-625-854-104	Sequence 104, App
129	27	93.1	10	5	US-10-822-968-21	Sequence 21, Appl	202	27	93.1	16	5	US-10-625-854-117	Sequence 117, App
130	27	93.1	10	5	US-10-822-968-22	Sequence 22, Appl	203	27	93.1	16	5	US-10-625-854-130	Sequence 130, App
131	27	93.1	10	5	US-10-822-968-23	Sequence 23, Appl	204	27	93.1	16	5	US-10-625-854-143	Sequence 143, App
132	27	93.1	10	5	US-10-822-968-24	Sequence 24, Appl	205	27	93.1	17	3	US-09-992-800-3	Sequence 3, Appl
133	27	93.1	10	5	US-10-777-792-20	Sequence 20, Appl	206	27	93.1	17	3	US-09-992-994-3	Sequence 3, Appl
134	27	93.1	10	5	US-10-777-792-21	Sequence 21, Appl	207	27	93.1	17	3	US-09-998-491-8	Sequence 8, Appl
135	27	93.1	10	5	US-10-777-792-22	Sequence 22, Appl	208	27	93.1	17	4	US-10-385-065-3	Sequence 3, Appl
136	27	93.1	10	5	US-10-777-792-23	Sequence 23, Appl	209	27	93.1	17	4	US-10-451-367-26	Sequence 26, Appl
137	27	93.1	10	5	US-10-777-792-24	Sequence 24, Appl	210	27	93.1	17	4	US-10-475-281-8	Sequence 8, Appl
138	27	93.1	10	5	US-10-825-958-27	Sequence 27, Appl	211	27	93.1	17	4	US-10-810-919-3	Sequence 3, Appl
139	27	93.1	10	5	US-10-890-071-20	Sequence 20, Appl	212	27	93.1	17	5	US-10-684-346-24	Sequence 24, Appl
140	27	93.1	10	5	US-10-890-071-21	Sequence 21, Appl	213	27	93.1	17	5	US-10-997-078-46	Sequence 46, Appl
141	27	93.1	10	5	US-10-890-071-22	Sequence 22, Appl	214	27	93.1	17	5	US-10-997-700-19	Sequence 19, Appl
142	27	93.1	10	5	US-10-890-071-23	Sequence 23, Appl	215	27	93.1	17	6	US-11-063-350-3	Sequence 3, Appl
143	27	93.1	10	5	US-10-890-071-24	Sequence 24, Appl	216	27	93.1	17	6	US-11-066-697-950	Sequence 950, App
144	27	93.1	10	5	US-10-890-024-20	Sequence 20, Appl	217	27	93.1	17	6	US-11-066-697-983	Sequence 983, App
145	27	93.1	10	5	US-10-890-024-21	Sequence 21, Appl	218	27	93.1	19	3	US-09-825-242-5	Sequence 5, Appl
146	27	93.1	10	5	US-10-890-024-22	Sequence 22, Appl	219	27	93.1	19	4	US-10-429-216-5	Sequence 5, Appl
147	27	93.1	10	5	US-10-890-024-23	Sequence 23, Appl	220	27	93.1	19	4	US-10-816-022-5	Sequence 5, Appl
148	27	93.1	10	5	US-10-890-024-24	Sequence 24, Appl	221	27	93.1	19	4	US-10-816-529-5	Sequence 5, Appl
149	27	93.1	10	5	US-10-928-926-20	Sequence 20, Appl	222	27	93.1	19	4	US-10-815-353-5	Sequence 5, Appl
150	27	93.1	10	5	US-10-928-926-21	Sequence 21, Appl	223	27	93.1	19	4	US-10-815-391-5	Sequence 5, Appl
151	27	93.1	10	5	US-10-928-926-22	Sequence 22, Appl	224	27	93.1	19	5	US-10-828-548-5	Sequence 5, Appl
152	27	93.1	10	5	US-10-928-926-23	Sequence 23, Appl	225	27	93.1	19	5	US-10-816-380-5	Sequence 5, Appl
153	27	93.1	10	5	US-10-928-926-24	Sequence 24, Appl	226	27	93.1	19	5	US-10-889-999-75	Sequence 75, Appl
154	27	93.1	10	6	US-11-058-757-20	Sequence 20, Appl	227	27	93.1	19	5	US-10-890-070-75	Sequence 75, Appl
155	27	93.1	10	6	US-11-058-757-21	Sequence 21, Appl	228	27	93.1	19	5	US-10-890-000-75	Sequence 75, Appl
156	27	93.1	10	6	US-11-058-757-22	Sequence 22, Appl	229	27	93.1	19	5	US-10-788-666-5	Sequence 5, Appl
157	27	93.1	10	6	US-11-058-757-23	Sequence 23, Appl	230	27	93.1	19	5	US-10-923-471-5	Sequence 5, Appl
158	27	93.1	10	6	US-11-058-757-24	Sequence 24, Appl	231	27	93.1	19	5	US-10-823-463-75	Sequence 75, Appl
159	27	93.1	11	3	US-09-988-842-9	Sequence 9, Appl	232	27	93.1	19	5	US-10-923-469-5	Sequence 5, Appl
160	27	93.1	11	3	US-09-988-842-25	Sequence 25, Appl	233	27	93.1	19	5	US-10-933-559-5	Sequence 5, Appl
161	27	93.1	11	4	US-10-235-483-14	Sequence 14, Appl	234	27	93.1	19	5	US-10-815-404-5	Sequence 5, Appl
162	27	93.1	11	4	US-10-050-200-33	Sequence 33, Appl	235	27	93.1	19	5	US-10-934-609-5	Sequence 5, Appl
163	27	93.1	11	4	US-10-237-673-20	Sequence 20, Appl	236	27	93.1	19	5	US-10-923-474-5	Sequence 5, Appl
164	27	93.1	11	5	US-10-464-117-13	Sequence 13, Appl	237	27	93.1	19	5	US-10-884-892-5	Sequence 5, Appl
165	27	93.1	11	5	US-10-772-230-9	Sequence 9, Appl	238	27	93.1	19	5	US-10-822-968-75	Sequence 75, Appl
166	27	93.1	11	5	US-10-772-230-25	Sequence 25, Appl	239	27	93.1	19	5	US-10-777-792-75	Sequence 75, Appl
167	27	93.1	12	3	US-09-867-847-8	Sequence 8, Appl	240	27	93.1	19	5	US-10-890-071-75	Sequence 75, Appl
168	27	93.1	12	5	US-10-810-881A-115	Sequence 115, App	241	27	93.1	19	5	US-10-930-024-75	Sequence 75, Appl
169	27	93.1	12	5	US-10-810-881A-117	Sequence 117, App	242	27	93.1	19	5	US-10-934-819-5	Sequence 5, Appl
170	27	93.1	12	5	US-10-508-586-2	Sequence 2, Appl	243	27	93.1	19	5	US-10-923-267-5	Sequence 5, Appl
171	27	93.1	12	5	US-10-508-586-3	Sequence 3, Appl	244	27	93.1	19	5	US-10-928-926-75	Sequence 75, Appl
172	27	93.1	12	5	US-10-625-854-139	Sequence 139, App	245	27	93.1	19	6	US-11-058-757-75	Sequence 75, Appl
173	27	93.1	12	6	US-11-012-979A-33	Sequence 33, Appl	246	27	93.1	19	6	US-11-108-102-5	Sequence 5, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVFPA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications_AA_Main:*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	3	US-09-867-847-11
2	29	100.0	6	3	US-09-867-847-19
3	29	100.0	6	3	US-09-915-092-1
4	29	100.0	6	3	US-09-915-092-9
5	29	100.0	6	3	US-09-747-408-1
6	29	100.0	6	3	US-09-747-408-10
7	29	100.0	6	5	US-10-728-028-1
8	29	100.0	6	5	US-10-728-028-9
9	29	100.0	6	5	US-10-825-958-9
10	29	100.0	6	5	US-10-825-958-17
11	29	100.0	58	4	US-10-425-115-280164
12	29	100.0	90	4	US-10-424-599-165325
13	29	100.0	93	4	US-10-424-599-240310
14	29	100.0	99	5	US-10-450-763-56957
15	28	96.6	6	3	US-09-867-847-18
16	28	96.6	6	3	US-09-867-847-26
17	28	96.6	6	3	US-09-915-092-8
18	28	96.6	6	3	US-09-915-092-16
19	28	96.6	6	3	US-09-747-408-9
20	28	96.6	6	3	US-09-747-408-17
21	28	96.6	6	5	US-10-728-028-8
22	28	96.6	6	5	US-10-728-028-16
23	28	96.6	6	5	US-10-825-958-16
24	28	96.6	6	5	US-10-825-958-24
25	28	96.6	37	4	US-10-641-924-7
26	28	96.6	37	4	US-10-642-255-7
27	28	96.6	60	4	US-10-437-963-173619

28	96.6	87	4	US-10-437-963-133986	Sequence 133986,
28	96.6	109	4	US-10-437-963-105773	Sequence 105773,
28	96.6	135	4	US-10-437-963-141578	Sequence 141578,
28	96.6	175	4	US-10-437-963-122124	Sequence 122124,
28	96.6	186	5	US-10-481-032A-214	Sequence 214, App
28	96.6	186	5	US-10-481-032A-228	Sequence 228, App
28	96.6	188	4	US-10-437-963-172476	Sequence 172476,
28	96.6	198	4	US-10-437-963-172452	Sequence 172452,
28	96.6	416	6	US-10-055-475-14	Sequence 14, Appl
28	96.6	416	6	US-11-042-922-14	Sequence 14, Appl
28	96.6	514	4	US-10-055-475-13	Sequence 13, Appl
28	96.6	514	6	US-11-042-922-13	Sequence 13, Appl
28	96.6	564	6	US-11-097-143-12723	Sequence 12723, A
28	96.6	925	4	US-10-408-765A-2031	Sequence 2031, Ap
28	96.6	925	5	US-10-755-889-234	Sequence 234, App
28	96.6	925	5	US-10-370-715B-8	Sequence 8, Appli
28	96.6	925	5	US-10-631-467-680	Sequence 680, App
28	96.6	925	5	US-10-631-467-747	Sequence 747, App
28	96.6	1144	3	US-09-870-759-124	Sequence 124, App
28	96.6	1144	3	US-09-751-708A-124	Sequence 124, App
28	96.6	1144	4	US-10-428-817A-120	Sequence 120, App
28	96.6	1144	5	US-10-937-758A-101	Sequence 101, App
28	96.6	1144	5	US-10-631-467-1388	Sequence 1388, Ap
28	96.6	1144	5	US-10-631-467-1464	Sequence 1464, Ap
28	96.6	1443	6	US-11-097-143-32208	Sequence 32208, A
28	96.6	1640	4	US-10-437-963-109646	Sequence 109646,
27	93.1	6	3	US-09-867-847-7	Sequence 7, Appli
27	93.1	6	3	US-09-867-847-20	Sequence 20, Appl
27	93.1	6	3	US-09-972-475-9	Sequence 9, Appli
27	93.1	6	3	US-09-915-092-10	Sequence 10, Appl
27	93.1	6	3	US-09-915-092-28	Sequence 28, Appl
27	93.1	6	3	US-09-956-625-25	Sequence 25, Appl
27	93.1	6	3	US-09-747-408-3	Sequence 3, Appli
27	93.1	6	3	US-09-747-408-11	Sequence 11, Appl
27	93.1	6	4	US-10-463-729-9	Sequence 9, Appli
27	93.1	6	5	US-10-728-028-10	Sequence 10, Appl
27	93.1	6	5	US-10-728-028-27	Sequence 27, Appl
27	93.1	6	5	US-10-728-028-28	Sequence 28, Appl
27	93.1	6	5	US-10-825-958-7	Sequence 7, Appli
27	93.1	6	5	US-10-825-958-18	Sequence 18, Appl
27	93.1	6	5	US-10-666-095-3	Sequence 3, Appli
27	93.1	7	3	US-09-867-847-12	Sequence 12, Appl
27	93.1	7	3	US-09-867-847-27	Sequence 27, Appl
27	93.1	7	3	US-09-867-847-28	Sequence 28, Appl
27	93.1	7	3	US-09-972-475-7	Sequence 7, Appli
27	93.1	7	3	US-09-915-092-2	Sequence 2, Appli
27	93.1	7	3	US-09-915-092-17	Sequence 17, Appl
27	93.1	7	3	US-09-915-092-18	Sequence 18, Appl
27	93.1	7	3	US-09-915-092-2	Sequence 2, Appli
27	93.1	7	3	US-09-747-408-2	Sequence 2, Appli
27	93.1	7	3	US-09-747-408-18	Sequence 18, Appl
27	93.1	7	3	US-09-747-408-19	Sequence 19, Appl
27	93.1	7	4	US-10-463-729-7	Sequence 7, Appli
27	93.1	7	5	US-10-728-028-2	Sequence 2, Appli
27	93.1	7	5	US-10-728-028-17	Sequence 17, Appl
27	93.1	7	5	US-10-728-028-18	Sequence 18, Appl
27	93.1	7	5	US-10-825-958-10	Sequence 10, Appl
27	93.1	7	5	US-10-825-958-25	Sequence 25, Appl
27	93.1	7	5	US-10-825-958-26	Sequence 26, Appl
27	93.1	7	5	US-10-810-881A-128	Sequence 128, App
27	93.1	7	5	US-10-505-313-269	Sequence 269, App
27	93.1	8	3	US-09-850-061A-44	Sequence 44, Appl
27	93.1	8	3	US-09-972-475-5	Sequence 5, Appli
27	93.1	8	4	US-10-235-483-1	Sequence 1, Appli
27	93.1	8	4	US-10-463-729-5	Sequence 5, Appli
27	93.1	8	4	US-10-281-092-42	Sequence 42, Appl
27	93.1	8	4	US-10-721-774-44	Sequence 44, Appl
27	93.1	8	5	US-10-810-881A-125	Sequence 125, App
27	93.1	8	5	US-10-817-979-73	Sequence 73, Appl
27	93.1	9	3	US-09-867-847-9	Sequence 9, Appli
27	93.1	9	3	US-09-899-815-2	Sequence 2, Appli
27	93.1	9	3	US-09-747-408-20	Sequence 20, Appl
27	93.1	9	4	US-10-235-483-64	Sequence 64, Appl
27	93.1	9	4	US-10-619-454-3	Sequence 3, Appli

; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-46

Query Match 72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVEFA 6
|::||
Db 211 KLMYFA 216

RESULT 75
US-11-073-460-46
; Sequence 46, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-46

Query Match 72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVEFA 6
|::||
Db 211 KLMYFA 216

Search completed: December 29, 2005, 18:50:13
Job time : 6.29032 secs

```
RESULT 70
US-10-467-657-290
; Sequence 290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 290
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-290

Query Match 72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 41 LIFFA 45

RESULT 71
US-10-467-657-5750
; Sequence 5750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5750
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5750

Query Match 72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 41 LIFFA 45

RESULT 72
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: PAGANO, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF-
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
```

```
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match 72.4%; Score 21; DB 6; Length 254;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 159 ILFFA 163

RESULT 73
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match 72.4%; Score 21; DB 6; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 211 KLMYFA 216

RESULT 74
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF-
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
```

```

; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2836

Query Match          72.4%; Score 21; DB 6; Length 182;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |::|
Db 14 KVTFFS 19

RESULT 66
US-10-467-657-3510
; Sequence 3510, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3510
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3510

Query Match          72.4%; Score 21; DB 6; Length 182;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
   |::|
Db 17 ILFFA 21

RESULT 67
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436

```

```

Query Match          72.4%; Score 21; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |::|
Db 46 KTVFYA 51

RESULT 68
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PLS_SEQ_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372

Query Match          72.4%; Score 21; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |::|
Db 33 KTVIFA 38

RESULT 69
US-10-467-657-8102
; Sequence 8102, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8102
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8102

Query Match          72.4%; Score 21; DB 6; Length 216;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
   |::|
Db 18 LIFFA 22

```

US-10-467-657-5166
; Sequence 5166, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5166
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5166

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 29 ILFFA 33

RESULT 62
US-10-793-626-2374
; Sequence 2374, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2374
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2374

Query Match 72.4%; Score 21; DB 6; Length 134;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 7 KIIVF 11

RESULT 63
US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420

Query Match 72.4%; Score 21; DB 6; Length 155;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 18 MVFFA 22

RESULT 64
US-10-965-694-23
; Sequence 23, Application US/10965694
; Publication No. US20050271644A1
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Johannes
; APPLICANT: Muller-Reible, Clemens
; APPLICANT: Fregin, Andreas
; APPLICANT: Rost, Simone
; APPLICANT: Strom, Tim
; TITLE OF INVENTION: VITAMIN K EPOXID RECYCLING POLYPEPTIDE VKORC1, A THERAPEUTIC TARGET
; TITLE OF INVENTION: OF COUMARIN AND THEIR DERIVATIVES
; FILE REFERENCE: MBP-025XX
; CURRENT APPLICATION NUMBER: US/10/965,694
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 60/511,041
; PRIOR FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-965-694-23

Query Match 72.4%; Score 21; DB 6; Length 175;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 91 IVFYA 95

RESULT 65
US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2836

; SEQ ID NO 7886
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7886

Query Match 72.4%; Score 21; DB 6; Length 43;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 14 KRVFFA 19

RESULT 57

US-10-467-657-2216
; Sequence 2216, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2216
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2216

Query Match 72.4%; Score 21; DB 6; Length 52;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 42 RIVWFA 47

RESULT 58

US-10-467-657-5690
; Sequence 5690, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5690
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5690

Query Match 72.4%; Score 21; DB 6; Length 76;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:|||||
Db 23 QIVFF 27

RESULT 59

US-10-821-234-1703
; Sequence 1703, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt_SEQ_genes Version 1.0
; SEQ ID NO 1703
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1703

Query Match 72.4%; Score 21; DB 6; Length 91;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:|||||
Db 22 EIVFF 26

RESULT 60

US-10-793-626-430
; Sequence 430, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 430
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-430

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:|||||
Db 78 IVFFS 82

RESULT 61

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7120
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7120

Query Match 75.9%; Score 22; DB 6; Length 601;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
:||||
Db 251 RIVFF 255

RESULT 53

US-10-821-234-1673
; Sequence 1673, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821a
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1673
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1673

Query Match 75.9%; Score 22; DB 6; Length 635;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
:||||
Db 259 KIVFF 263

RESULT 54

US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347

; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-6

Query Match 75.9%; Score 22; DB 6; Length 858;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
:||||
Db 348 LVFFA 352

RESULT 55

US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hanabro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2233
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 75.9%; Score 22; DB 6; Length 2233;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
:||||
Db 1895 KVQFFA 1900

RESULT 56

US-10-467-657-7886
; Sequence 7886, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

```

; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-678

Query Match      75.9%; Score 22; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 428 KIMFF 432

RESULT 49
US-11-082-389-198
; Sequence 198, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 198
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-198

Query Match      75.9%; Score 22; DB 7; Length 453;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 401 LVFFA 405

RESULT 50
US-11-210-316-22
; Sequence 22, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.

```

```

; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (102)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-22

Query Match      75.9%; Score 22; DB 7; Length 510;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 96 VIFFA 100

RESULT 51
US-11-210-316-26
; Sequence 26, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-210-316-26

Query Match      75.9%; Score 22; DB 7; Length 539;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 121 VIFFA 125

RESULT 52
US-10-467-657-7120
; Sequence 7120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta

```

```
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-572

Query Match          75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      ||| ||
Db      61 KIVVFA 66

RESULT 46
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
```

```
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-836

Query Match          75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      ||| ||
Db      61 KIVVFA 66

RESULT 47
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MEI
; FILE REFERENCE: 00592.US1 (MAR 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match          75.9%; Score 22; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVVFF 5
      ||| ||
Db      4 KILFF 8

RESULT 48
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 678
; LENGTH: 449
```


Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFF 5
Db 3 KIMFF 7

RESULT 42
US-10-793-626-2734
; Sequence 2734, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793.626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2734
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2734

Query Match 75.9%; Score 22; DB 6; Length 330;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 3 KIMFF 7
RESULT 43
US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878.556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match 75.9%; Score 22; DB 6; Length 338;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 76 KLIFF 80

RESULT 44
US-10-131-826A-376
; Sequence 376, Application US/10131826A

; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match 75.9%; Score 22; DB 6; Length 344;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 279 KLIFF 283

RESULT 45
US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838
```

```
Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 IVFFA 6
:|||||
Db 156 LVFFA 160
```

```
RESULT 38
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322
```

```
Query Match 75.9%; Score 22; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 IVFFA 6
:|||||
Db 166 LVFFA 170
```

```
RESULT 39
US-10-467-657-432
; Sequence 432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 432
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-432
```

```
Query Match 75.9%; Score 22; DB 6; Length 239;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
:|||||
Db 128 KVIFA 133
```

```
RESULT 40
US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500
```

```
Query Match 75.9%; Score 22; DB 6; Length 265;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
:|||||
Db 230 KVFFMA 235
```

```
RESULT 41
US-10-793-626-2476
; Sequence 2476, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2476
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2476
```

```
Query Match 75.9%; Score 22; DB 6; Length 330;
```

Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 105 VIFFA 109

RESULT 34

US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 19 LVFFA 23

RESULT 35

US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: DeNoviers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR APPLICATION NUMBER: 2002-04-24
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match 75.9%; Score 22; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 166 LVFFA 170

RESULT 36

US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 156 LVFFA 160

RESULT 37

US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

QY 2 IVFFA 6
|:|:|
Db 371 IIVFA 375

RESULT 30

US-10-995-561-593
; Sequence 593, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 593
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-593

Query Match 79.3%; Score 23; DB 6; Length 3623;
Best Local Similarity 60.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0;

QY 1 KIVFF 5
|:|:|
Db 2544 KIVFF 2548

RESULT 31

US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match 75.9%; Score 22; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 36 KIVFF 40

RESULT 32

US-10-467-657-4746
; Sequence 4746, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4746
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746

Query Match 75.9%; Score 22; DB 6; Length 98;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 62 KIVFF 66

RESULT 33

US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (98)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18

Query Match 75.9%; Score 22; DB 7; Length 167;

```
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2450

Query Match          79.3%; Score 23; DB 6; Length 311;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      296 VVFFA 300

RESULT 26
US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-959

Query Match          79.3%; Score 23; DB 6; Length 481;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      275 KMVFFA 280

RESULT 27
US-11-080-991-104
; Sequence 104, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
```

```
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-104

Query Match          79.3%; Score 23; DB 7; Length 522;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      260 IIVFA 264

RESULT 28
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match          79.3%; Score 23; DB 6; Length 528;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFF 5
Db      477 KLVFF 481

RESULT 29
US-10-467-657-2868
; Sequence 2868, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2868
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2868

Query Match          79.3%; Score 23; DB 6; Length 533;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

US-10-131-826A-230

Query Match 82.8%; Score 24; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 557 IVFFA 561

RESULT 22

US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Lebat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match 82.8%; Score 24; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|:|
Db 579 KAVFFA 584

RESULT 23

US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match 79.3%; Score 23; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.3e+04; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5

Db |:|:|
1 KLVFF 5

RESULT 24

US-10-131-826A-410
; Sequence 410, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-410

Query Match 79.3%; Score 23; DB 6; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 118 KVIFF 122

RESULT 25

US-10-793-626-2450
; Sequence 2450, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

```
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2120

Query Match      82.8%; Score 24; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      414 IVFFA 418

RESULT 19
US-10-689-742-13
; Sequence 13, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M
; APPLICANT: Jacobs, Kenneth
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racine, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-13

Query Match      82.8%; Score 24; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      404 IVFFA 408

RESULT 20
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978

; TYPE: PRT
; ORGANISM: Homo sapiens

; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match      82.8%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      531 KAVFFA 536

RESULT 21
US-10-131-826A-230
; Sequence 230, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
```

```
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056
```

```
Query Match      86.2%; Score 25; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFF 5
        |||||
Db       7 KIVFF 11
```

```
RESULT 15
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892
```

```
Query Match      82.8%; Score 24; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFF 5
        ||:|
Db      33 KIVFF 37
```

```
RESULT 16
US-10-467-657-2014
; Sequence 2014, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
```

```
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2014
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2014
```

```
Query Match      82.8%; Score 24; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 IVFFA 6
        |||||
Db      73 IVFFA 77
```

```
RESULT 17
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070
```

```
Query Match      82.8%; Score 24; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 IVFFA 6
        |||||
Db      264 IVFFA 268
```

```
RESULT 18
US-10-467-657-2120
; Sequence 2120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2120
; LENGTH: 426
```


OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
OTHER INFORMATION: Alzheimer's disease amyloid protein

FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(17)
OTHER INFORMATION: signal peptide

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(40)

OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (18)..(687)

OTHER INFORMATION: soluble APP-alpha

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (18)..(671)

OTHER INFORMATION: soluble APP-beta

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)..(770)

OTHER INFORMATION: C99

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)..(713)

OTHER INFORMATION: beta-amyloid protein 42

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)..(711)

OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(770)

OTHER INFORMATION: C83

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(713)

OTHER INFORMATION: P3(42)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(711)

OTHER INFORMATION: P3(40)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (712)..(770)

OTHER INFORMATION: gamma-CTF(59)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (714)..(770)

OTHER INFORMATION: gamma-CTF(57)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (721)..(770)

OTHER INFORMATION: gamma-CTF(50)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (740)..(770)

OTHER INFORMATION: C31

US-10-982-545-15

Query Match 93.1%; Score 27; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 687 KLVFFA 692

RESULT 12

US-10-789-273-38

; Sequence 38, Application US/10789273
; Publication No. US20050249725A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurik
; APPLICANT: Saldanha, Jose
; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

; FILE REFERENCE: ELN-002CP

; CURRENT APPLICATION NUMBER: US/10789,273

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US/10/388,389

; PRIOR FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 10/010,942

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: US 60/251,892

; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 38

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-789-273-38

Query Match 93.1%; Score 27; DB 6; Length 770;

Best Local Similarity 83.3%; Pred. No. 56;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

|:|||||

Db 687 KLVFFA 692

RESULT 13

US-10-467-657-330

; Sequence 330, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 330

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-330

Query Match 86.2%; Score 25; DB 6; Length 269;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5

|||||

Db 11 KIVFF 15

RESULT 14

US-10-793-626-1056

; Sequence 1056, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-016-706-37

Query Match 93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 8

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/667,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 9

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 10

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 11

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 4
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; FILE REFERENCE: PTO-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 5
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 6
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 7
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

```
245 20 69.0 692 7 US-11-103-957-29 Sequence 29, Appl
246 20 69.0 708 7 US-11-174-150-25 Sequence 25, Appl
247 20 69.0 710 7 US-11-078-189-18 Sequence 18, Appl
248 20 69.0 721 6 US-10-467-962B-49 Sequence 49, Appl
249 20 69.0 736 7 US-11-174-150-26 Sequence 26, Appl
250 20 69.0 736 7 US-11-078-189-9 Sequence 9, Appl
251 20 69.0 739 7 US-11-082-389-94 Sequence 94, Appl
252 20 69.0 739 7 US-11-078-189-12 Sequence 12, Appl
253 20 69.0 739 7 US-11-107-028-6 Sequence 6, Appl
254 20 69.0 741 6 US-10-467-657-6266 Sequence 6266, Ap
255 20 69.0 745 6 US-11-147-109-2 Sequence 2, Appl
256 20 69.0 748 6 US-10-821-234-1479 Sequence 1479, Ap
257 20 69.0 817 6 US-10-793-626-2948 Sequence 2948, Ap
258 20 69.0 852 6 US-10-467-657-5004 Sequence 5004, Ap
259 20 69.0 856 6 US-10-467-657-8534 Sequence 8534, Ap
260 20 69.0 874 6 US-10-510-386-28 Sequence 28, Appl
261 20 69.0 896 7 US-11-192-219-3 Sequence 3, Appl
262 20 69.0 898 7 US-11-166-730-3 Sequence 3, Appl
263 20 69.0 902 7 US-11-057-058-64 Sequence 64, Appl
264 20 69.0 916 6 US-10-467-657-4242 Sequence 4242, Ap
265 20 69.0 923 7 US-11-192-219-4 Sequence 4, Appl
266 20 69.0 989 7 US-10-821-234-975 Sequence 975, App
267 20 69.0 1013 7 US-11-103-957-9 Sequence 9, Appl
268 20 69.0 1047 6 US-10-510-386-200 Sequence 200, App
269 20 69.0 1165 7 US-11-192-219-2 Sequence 2, Appl
270 20 69.0 1167 6 US-10-601-368-18 Sequence 18, Appl
271 20 69.0 1217 7 US-11-074-176-252 Sequence 252, App
272 20 69.0 1730 7 US-11-192-967-4 Sequence 4, Appl
273 20 69.0 1730 7 US-11-193-715-4 Sequence 4, Appl
274 20 69.0 2844 6 US-10-770-726-45 Sequence 45, Appl
275 20 69.0 7968 7 US-11-186-731-5 Sequence 5, Appl
276 19 65.5 13 7 US-11-016-706-29 Sequence 29, Appl
277 19 65.5 27 7 US-11-157-930-14 Sequence 14, Appl
278 19 65.5 35 6 US-10-821-234-1704 Sequence 1704, Ap
279 19 65.5 43 7 US-11-075-400-28 Sequence 28, Appl
280 19 65.5 44 7 US-11-000-463-372 Sequence 372, App
281 19 65.5 46 6 US-10-467-657-9119 Sequence 9119, Ap
282 19 65.5 47 6 US-10-467-657-9186 Sequence 9186, Ap
283 19 65.5 57 6 US-10-467-657-5448 Sequence 5448, Ap
284 19 65.5 71 7 US-11-000-463-772 Sequence 772, App
285 19 65.5 80 6 US-10-986-501-200 Sequence 200, App
286 19 65.5 83 6 US-10-467-657-5366 Sequence 5366, Ap
287 19 65.5 86 6 US-10-467-657-3962 Sequence 3962, Ap
288 19 65.5 98 6 US-10-467-657-3376 Sequence 3376, Ap
289 19 65.5 100 7 US-11-123-896-137 Sequence 137, App
290 19 65.5 103 6 US-10-793-626-1708 Sequence 1708, Ap
291 19 65.5 103 6 US-10-793-626-2074 Sequence 2074, Ap
292 19 65.5 104 6 US-10-793-626-2512 Sequence 2512, Ap
293 19 65.5 106 7 US-11-064-174-50 Sequence 50, Appl
294 19 65.5 107 6 US-10-793-626-1586 Sequence 1586, Ap
295 19 65.5 107 6 US-10-467-657-1018 Sequence 1018, Ap
296 19 65.5 107 6 US-10-467-657-2102 Sequence 2102, Ap
297 19 65.5 107 7 US-11-000-463-300 Sequence 300, App
298 19 65.5 115 6 US-10-432-483-10 Sequence 10, Appl
299 19 65.5 117 6 US-10-467-657-2282 Sequence 2282, Ap
300 19 65.5 122 6 US-10-467-657-606 Sequence 606, App
```

ALIGNMENTS

```
RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US2005024972A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
```

```
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5
```

```
Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9
```

RESULT 2

```
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5
```

```
Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9
```

RESULT 3

```
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
```

99	20	69.0	19	6	US-10-467-657-8712	Sequence 8712, Ap	172	20	69.0	325	6	US-10-454-437-142	Sequence 142, App
100	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	173	20	69.0	329	6	US-10-793-626-1942	Sequence 1942, Ap
101	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	174	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
102	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	337	6	US-10-485-517-234	Sequence 234, App
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	342	6	US-11-082-389-214	Sequence 214, App
104	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	177	20	69.0	343	6	US-10-467-657-4824	Sequence 4824, Ap
105	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	178	20	69.0	343	6	US-10-467-657-7256	Sequence 7256, Ap
106	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	179	20	69.0	348	6	US-10-467-657-7256	Sequence 7256, Ap
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	348	6	US-10-467-657-7256	Sequence 7256, Ap
108	20	69.0	42	6	US-10-250-581-18	Sequence 18, Appl	181	20	69.0	355	6	US-10-467-657-7996	Sequence 7996, Ap
109	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	182	20	69.0	355	6	US-10-995-561-636	Sequence 636, App
110	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	183	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
111	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	184	20	69.0	357	6	US-10-467-657-2500	Sequence 2500, Ap
112	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	185	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
113	20	69.0	54	6	US-10-467-657-4978	Sequence 4978, Ap	186	20	69.0	362	6	US-10-995-561-637	Sequence 637, App
114	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	187	20	69.0	389	7	US-11-018-018-2	Sequence 2, Appl
115	20	69.0	95	6	US-10-510-386-114	Sequence 114, App	188	20	69.0	389	7	US-11-047-757-2	Sequence 2, Appl
116	20	69.0	95	6	US-10-467-657-2518	Sequence 2518, Ap	189	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
117	20	69.0	102	6	US-10-793-626-2592	Sequence 2592, Ap	190	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
118	20	69.0	105	6	US-10-467-657-2209	Sequence 2209, Ap	191	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
119	20	69.0	108	6	US-10-467-657-4266	Sequence 4266, Ap	192	20	69.0	399	7	US-11-018-018-3	Sequence 3, Appl
120	20	69.0	114	6	US-10-821-234-1140	Sequence 1140, Ap	193	20	69.0	406	6	US-10-467-657-7420	Sequence 7420, Ap
121	20	69.0	114	6	US-10-467-657-124	Sequence 124, App	194	20	69.0	409	6	US-10-821-234-1425	Sequence 1425, Ap
122	20	69.0	114	6	US-10-467-657-1414	Sequence 1414, Ap	195	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
123	20	69.0	114	6	US-10-467-657-3162	Sequence 3162, Ap	196	20	69.0	414	6	US-10-878-556A-1	Sequence 1, Appl
124	20	69.0	114	6	US-10-467-657-3754	Sequence 3754, Ap	197	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
125	20	69.0	114	6	US-10-467-657-8674	Sequence 8674, Ap	198	20	69.0	432	7	US-11-113-424-186	Sequence 186, App
126	20	69.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	199	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
127	20	69.0	116	6	US-10-467-657-5514	Sequence 5514, Ap	200	20	69.0	436	6	US-11-082-389-256	Sequence 256, App
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	201	20	69.0	443	6	US-10-793-626-1860	Sequence 1860, Ap
129	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	202	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
130	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appl	203	20	69.0	445	6	US-10-873-528-30	Sequence 30, Appl
131	20	69.0	131	6	US-10-467-657-5308	Sequence 5308, Ap	204	20	69.0	448	6	US-10-763-712A-69	Sequence 69, Appl
132	20	69.0	137	6	US-10-821-234-1701	Sequence 1701, Ap	205	20	69.0	448	6	US-10-763-712A-112	Sequence 112, App
133	20	69.0	140	6	US-10-467-657-2486	Sequence 2486, Ap	206	20	69.0	449	6	US-10-821-234-1075	Sequence 1075, Ap
134	20	69.0	144	6	US-10-793-626-1640	Sequence 1640, Ap	207	20	69.0	450	6	US-10-467-657-7094	Sequence 7094, Ap
135	20	69.0	144	6	US-10-793-626-1958	Sequence 1958, Ap	208	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
136	20	69.0	156	6	US-10-467-657-1280	Sequence 1280, Ap	209	20	69.0	450	6	US-10-763-712A-76	Sequence 76, Appl
137	20	69.0	179	6	US-10-467-657-2232	Sequence 2232, Ap	210	20	69.0	451	6	US-10-467-657-7104	Sequence 7104, Ap
138	20	69.0	182	6	US-10-980-388-89	Sequence 89, Appl	211	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
139	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	212	20	69.0	466	7	US-11-102-240-104	Sequence 104, App
140	20	69.0	186	6	US-10-467-657-3918	Sequence 3918, Ap	213	20	69.0	467	7	US-11-186-284-123	Sequence 123, App
141	20	69.0	195	7	US-11-019-955-24	Sequence 24, Appl	214	20	69.0	471	6	US-10-995-561-901	Sequence 901, App
142	20	69.0	197	6	US-10-793-626-2856	Sequence 2856, Ap	215	20	69.0	477	6	US-10-131-826A-452	Sequence 452, App
143	20	69.0	200	6	US-10-793-626-394	Sequence 394, App	216	20	69.0	481	6	US-10-467-657-3124	Sequence 3124, Ap
144	20	69.0	200	6	US-10-793-626-1242	Sequence 1242, Ap	217	20	69.0	481	7	US-11-090-439-16	Sequence 16, Appl
145	20	69.0	204	6	US-10-980-388-102	Sequence 102, App	218	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appl
146	20	69.0	210	6	US-10-467-657-6318	Sequence 6318, Ap	219	20	69.0	488	6	US-10-821-234-1654	Sequence 1654, Ap
147	20	69.0	214	6	US-10-508-263-108	Sequence 108, App	220	20	69.0	488	7	US-11-186-284-121	Sequence 121, App
148	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	221	20	69.0	489	6	US-10-467-657-7846	Sequence 7846, Ap
149	20	69.0	239	6	US-10-467-657-8743	Sequence 8743, Ap	222	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
150	20	69.0	241	7	US-11-019-955-27	Sequence 27, Appl	223	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
151	20	69.0	250	7	US-11-082-389-216	Sequence 216, App	224	20	69.0	508	7	US-11-082-389-178	Sequence 178, App
152	20	69.0	257	7	US-11-102-240-94	Sequence 94, Appl	225	20	69.0	514	6	US-10-793-626-12	Sequence 12, Appl
153	20	69.0	266	6	US-10-995-561-544	Sequence 544, App	226	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
154	20	69.0	267	6	US-10-995-561-943	Sequence 543, App	227	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
155	20	69.0	268	7	US-11-019-955-28	Sequence 28, Appl	228	20	69.0	558	7	US-11-078-189-19	Sequence 19, Appl
156	20	69.0	271	6	US-10-793-626-1156	Sequence 1156, Ap	229	20	69.0	560	6	US-10-623-155-225	Sequence 225, App
157	20	69.0	272	6	US-10-467-657-2520	Sequence 2520, Ap	230	20	69.0	563	6	US-10-821-234-1067	Sequence 1067, Ap
158	20	69.0	276	6	US-10-873-528-134	Sequence 134, App	231	20	69.0	578	6	US-10-858-720-103	Sequence 103, App
159	20	69.0	280	6	US-10-858-720-200	Sequence 200, App	232	20	69.0	585	6	US-10-967-457-18	Sequence 18, Appl
160	20	69.0	280	6	US-10-467-657-2130	Sequence 2130, Ap	233	20	69.0	585	6	US-10-939-890-500	Sequence 500, App
161	20	69.0	288	7	US-11-082-389-324	Sequence 324, App	234	20	69.0	585	7	US-11-078-663-18	Sequence 18, Appl
162	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	235	20	69.0	585	7	US-11-078-914-18	Sequence 18, Appl
163	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	236	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
164	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	237	20	69.0	626	6	US-10-467-657-6426	Sequence 6426, Ap
165	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	238	20	69.0	637	6	US-10-873-528-53	Sequence 53, Appl
166	20	69.0	299	6	US-10-467-657-2190	Sequence 2190, Ap	239	20	69.0	647	7	US-11-080-991-32	Sequence 32, Appl
167	20	69.0	312	7	US-11-055-822-16	Sequence 16, Appl	240	20	69.0	657	7	US-11-080-991-48	Sequence 48, Appl
168	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appl	241	20	69.0	659	7	US-11-119-683-2	Sequence 2, Appl
169	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	242	20	69.0	675	6	US-10-467-657-4004	Sequence 4004, Ap
170	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	243	20	69.0	690	6	US-10-939-890-501	Sequence 501, App
171	20	69.0	324	6	US-10-467-657-8440	Sequence 8440, Ap	244	20	69.0	690	6		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-1
Perfect score: 29
Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- Published Applications AA_New.*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	93.1	19	6	US-10-923-605-5
2	27	93.1	19	6	US-10-934-818-5
3	27	93.1	40	7	US-11-016-706-36
4	27	93.1	40	7	US-11-098-674-12
5	27	93.1	42	6	US-10-923-605-1
6	27	93.1	42	6	US-10-934-818-1
7	27	93.1	42	7	US-11-016-706-37
8	27	93.1	43	6	US-10-934-818-6
9	27	93.1	43	6	US-10-250-581-1
10	27	93.1	43	6	US-10-250-581-1
11	27	93.1	770	6	US-10-982-545-15
12	27	93.1	770	6	US-10-789-273-38
13	25	86.2	269	6	US-10-467-657-330
14	25	86.2	400	6	US-10-793-626-1056
15	24	82.8	50	6	US-10-467-657-7892
16	24	82.8	347	6	US-10-467-657-2014
17	24	82.8	402	6	US-10-467-657-9070
18	24	82.8	426	6	US-10-467-657-2120
19	24	82.8	524	6	US-10-689-742-13
20	24	82.8	660	7	US-11-186-284-125
21	24	82.8	677	6	US-10-131-826A-230
22	24	82.8	708	6	US-10-821-234-917
23	23	79.3	5	7	US-11-098-674-1
24	23	79.3	229	6	US-10-131-826A-410
25	23	79.3	311	6	US-10-793-626-2450

26	23	79.3	481	6	US-10-995-561-959	Sequence 959, App
27	23	79.3	522	7	US-11-080-991-104	Sequence 104, App
28	23	79.3	528	6	US-10-793-626-1930	Sequence 1930, Ap
29	23	79.3	533	6	US-10-467-657-2868	Sequence 2868, Ap
30	23	79.3	3623	6	US-10-995-561-593	Sequence 593, App
31	22	75.9	47	6	US-10-467-657-5436	Sequence 5436, Ap
32	22	75.9	98	6	US-10-467-657-4746	Sequence 4746, Ap
33	22	75.9	167	7	US-11-210-316-18	Sequence 18, Appl
34	22	75.9	211	6	US-10-467-657-6932	Sequence 6932, Ap
35	22	75.9	215	6	US-10-131-826A-4	Sequence 4, Appli
36	22	75.9	228	6	US-10-467-657-568	Sequence 568, App
37	22	75.9	228	6	US-10-467-657-4838	Sequence 4838, Ap
38	22	75.9	233	6	US-10-821-234-1322	Sequence 1322, Ap
39	22	75.9	239	6	US-10-467-657-432	Sequence 432, App
40	22	75.9	265	6	US-10-793-626-2500	Sequence 2500, Ap
41	22	75.9	330	6	US-10-793-626-2476	Sequence 2476, Ap
42	22	75.9	330	6	US-10-793-626-2734	Sequence 2734, Ap
43	22	75.9	338	6	US-10-878-556A-19	Sequence 19, Appl
44	22	75.9	344	6	US-10-131-826A-376	Sequence 376, App
45	22	75.9	358	7	US-11-055-822-572	Sequence 572, App
46	22	75.9	358	7	US-11-055-822-836	Sequence 836, App
47	22	75.9	432	7	US-11-194-246-308	Sequence 308, App
48	22	75.9	449	6	US-10-467-657-678	Sequence 678, App
49	22	75.9	453	7	US-11-082-389-198	Sequence 198, App
50	22	75.9	510	7	US-11-210-316-22	Sequence 22, Appl
51	22	75.9	539	7	US-11-210-316-26	Sequence 26, Appl
52	22	75.9	601	6	US-10-467-657-7120	Sequence 7120, Ap
53	22	75.9	635	6	US-10-821-234-1673	Sequence 1673, Ap
54	22	75.9	858	6	US-10-613-744-6	Sequence 6, Appli
55	22	75.9	2233	6	US-10-873-528-2	Sequence 2, Appli
56	21	72.4	43	6	US-10-467-657-7886	Sequence 7886, Ap
57	21	72.4	52	6	US-10-467-657-2216	Sequence 2216, Ap
58	21	72.4	76	6	US-10-467-657-5690	Sequence 5690, Ap
59	21	72.4	91	6	US-10-821-234-1703	Sequence 1703, Ap
60	21	72.4	123	6	US-10-793-626-430	Sequence 430, App
61	21	72.4	123	6	US-10-467-657-5166	Sequence 5166, Ap
62	21	72.4	134	6	US-10-793-626-2374	Sequence 2374, Ap
63	21	72.4	155	6	US-10-467-657-2420	Sequence 2420, Ap
64	21	72.4	175	6	US-10-965-694-23	Sequence 23, Appl
65	21	72.4	182	6	US-10-793-626-2836	Sequence 2836, Ap
66	21	72.4	182	6	US-10-467-657-3510	Sequence 3510, Ap
67	21	72.4	190	6	US-10-467-657-3436	Sequence 3436, Ap
68	21	72.4	211	6	US-10-821-234-1372	Sequence 1372, Ap
69	21	72.4	216	6	US-10-467-657-8102	Sequence 8102, Ap
70	21	72.4	221	6	US-10-467-657-230	Sequence 290, App
71	21	72.4	221	6	US-10-467-657-5750	Sequence 5750, Ap
72	21	72.4	254	6	US-10-467-657-6144	Sequence 6144, Ap
73	21	72.4	272	6	US-10-632-150-46	Sequence 46, Appl
74	21	72.4	272	7	US-11-073-457-46	Sequence 46, Appl
75	21	72.4	272	7	US-11-073-460-46	Sequence 46, Appl
76	21	72.4	278	6	US-10-957-569-45	Sequence 45, Appl
77	21	72.4	370	6	US-10-821-234-1105	Sequence 1105, Ap
78	21	72.4	440	7	US-11-082-389-106	Sequence 106, App
79	21	72.4	463	6	US-10-467-657-6352	Sequence 6352, Ap
80	21	72.4	463	6	US-10-467-657-7604	Sequence 7604, Ap
81	21	72.4	482	6	US-10-793-626-24	Sequence 24, Appl
82	21	72.4	496	7	US-11-067-121-12	Sequence 12, Appl
83	21	72.4	522	6	US-10-995-561-1030	Sequence 1030, Ap
84	21	72.4	525	7	US-11-082-389-350	Sequence 350, App
85	21	72.4	569	7	US-11-082-389-104	Sequence 104, App
86	21	72.4	582	7	US-11-090-439-58	Sequence 58, App
87	21	72.4	592	6	US-10-467-657-4888	Sequence 4888, Ap
88	21	72.4	615	6	US-10-995-561-940	Sequence 940, App
89	21	72.4	662	6	US-10-995-561-943	Sequence 943, App
90	21	72.4	702	6	US-10-995-561-942	Sequence 942, App
91	21	72.4	737	7	US-11-147-047-48	Sequence 48, Appl
92	21	72.4	747	7	US-11-018-018-1	Sequence 1, Appli
93	21	72.4	747	7	US-11-047-757-1	Sequence 1, Appli
94	21	72.4	754	6	US-10-995-561-941	Sequence 941, App
95	21	72.4	1061	7	US-11-000-463-347	Sequence 347, App
96	21	72.4	1070	7	US-11-147-047-49	Sequence 49, Appl
97	21	72.4	1091	7	US-11-000-463-348	Sequence 348, App
98	21	72.4	3507	7	US-11-075-185-7	Sequence 7, Appli

```

OX  NCBI_TaxID=7200;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Salivary gland;
RX  PubMed=15371479; DOI=10.1242/jeb.01185;
RA  Valenzuela J.G., Garfield M., Rowton B.D., Pham V.M.;
RT  "Identification of the most abundant secreted proteins from the
RT  salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT  Leishmania chagasi.";
RL  J. Exp. Biol. 207:3717-3729(2004).
DR  EMBL; AY445935; AAS05318.1; -; mRNA.
DR  InterPro: IPR003534; Royaljelly.
DR  Pfam: PF03022; MRJP; 1.
SQ  SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match      93.1%; Score 27; DB 2; Length 399;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches  4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 KIVFFA 6
    |::|||
Db  305 KVIFFA 310

Search completed: December 29, 2005, 17:46:50
Job time : 92.1936 secs

```

THIS PAGE BLANK (USPTO)

RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuiki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK076506; BAC36369.1; -; mRNA.
 DR HSSP; P08592; 1NMJ.
 DR SMR; OSBPC7; 74-183.
 DR MGI; MGI:88059; App.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0030198; F:extracellular matrix organization and bioge. .; IGI.
 DR InterPro; IPR008155; A4 APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOID.
 DR PROSITE; PS00304; BETAAMYLOID.
 FT NON TER 1
 SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE693173 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 384;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
 Db 301 KLVFFA 306
 |:|||||
 13-SEP-2005 (TrEMBLrel. 31, Created)
 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=rp02_0195;
 OS Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OX NCBI_TaxID=5875;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
 RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
 RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
 RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
 RA Venter J.C., Fraser C.M., Nene V.;
 RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
 RT lymphocytes.";
 RL Science 309:134-137(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;
 RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
 RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
 RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAGK01000002; EAK32476.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 391 AA; 44445 MW; 129227F0ABAP933C CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLVFFA 6
 Db 130 KLVFFA 135
 |:|||||
 25-OCT-2004 (TrEMBLrel. 28, Created)
 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE 43.2 kDa salivary protein.
 GN ORFNames=LJM11_Clu9;
 OS Lutzomyia longipalpis (Sand fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
 OC Psychodidae; Lutzomyia; Lutzomyia.

RESULT 75

QSWPU9_LUTLO
 ID QSWPU9_LUTLO PRELIMINARY; PRT; 399 AA.
 AC QSWPU9;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE 43.2 kDa salivary protein.

GN ORFNames=LJM11_Clu9;
 OS Lutzomyia longipalpis (Sand fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
 OC Psychodidae; Lutzomyia; Lutzomyia.

DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00320; AA_INTRA; 1.
 FT NON_TER 1_1
 SQ SEQUENCE 357 AA; 40962 MW; 07D9BEFF6C5B2D8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 357;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 274 KLVFFA 279

RESULT 71

QBPL1 XANAC
 ID QBPL1 XANAC PRELIMINARY; PRT; 366 AA.

AC QBPL1
 DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DE Hypothetical protein XAC0675.

GN OrderedLocusNames=XAC0675;

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

RA Almeida N.F., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,

RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergro F.,

RA Ciapina L.P., Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

RA El-Borhy H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spicola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RL Nature 417:459-463(2002).

DR EMBL; AE011696; AM35564.1; -; Genomic_DNA.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 366 AA; 40845 MW; 6EF65B2BEC8844 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 366;

Best Local Similarity 83.3%; Pred. No. 6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 340 KLVFFA 345

RESULT 72

O67225 AQAAE

ID O67225 AQAAE PRELIMINARY; PRT; 380 AA.

AC O67225

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DE Hypothetical protein XAC0675.

DE Hydrogenase expression/formation protein HypD.

GN Name=hypD; OrderedLocusNames=AQ_1157;
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

OX NCBI_TaxID=63363;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Overbeek R., Snead M.A., Keller M., Auja M., Huber R.,

RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex

RT aeolicus."

RL Nature 392:353-358(1998).

DR EMBL; AB000726; AAC07185.1; -; Genomic_DNA.

DR PIR; F70399; F70399.

DR InterPro; IPR002780; HypD.

DR Pfam; PF01924; HypD; 1.

DR PIRSF; PIRSF005622; Hydrn_mat_hypD; 1.

DR TIGRFAMs; TIGR00075; hypD; 1.

KW Complete proteome.

SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 380;

Best Local Similarity 66.7%; Pred. No. 6.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 141 KVIFFA 146

RESULT 73

QBPC7 MOUSE

ID QBPC7 MOUSE PRELIMINARY; PRT; 384 AA.

AC QBPC7;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched

DE library, clone:483432I09 product:amyloid beta (A4) protein, full

DE insert sequence. (Fragment).

DE Name=App;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning."

RT Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Glaszi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Bevan M., Robben J., Grymonprez B., Volckaert G., Bancroft I.,
 RA Mewes H.W., Rudd S., Schoof H., Mayer K.F.X.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RA Robben J., Grymonprez B., Volckaert G., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL079349; CAB53090.1; -; Genomic DNA.
 DR EMBL; AL161535; CAB78332.1; -; Genomic DNA.
 DR PIR; H85138; H85138. GILT.
 DR InterPro; IPR004911; GILT.
 DR InterPro; IPR000834; Peptidase_M14.
 DR Pfam; PF03227; GILT; 1.
 DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 231 AA; 26025 MW; 734109A78E942295 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 231;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 12 KLVFFA 17

RESULT 68
 Q9XGY6 SIMCH PRELIMINARY; PRT; 352 AA.
 AC Q9XGY6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Wax synthase
 OS Simmondsia chinensis (Jojoba).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Simmondsiaceae; Simmondsia.
 OX NCBI_TaxID=3999;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20177844; PubMed=10712527; DOI=10.1104/pp.122.3.645;
 RX Lardizabal K.D., Metz J.G., Sakamoto T., Hutton W.C., Pollard M.R.,
 RA Lasser M.W.;
 RT "Purification of a jojoba embryo wax synthase, cloning of its cDNA and
 RT production of high levels of wax in seeds of transgenic Arabidopsis.";
 RL Plant Physiol. 122:645-655 (2000).
 DR EMBL; AF149919; AAD38041.1; -; mRNA.
 DR PIR; T48903; T48903.
 DR InterPro; IPR004299; MBOAT_fam.
 DR Pfam; PF03062; MBOAT; 1.
 SQ SEQUENCE 352 AA; 40156 MW; F91D6BD896003629 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 135 KLVFFA 140

RESULT 69
 Q8U460 PYRFU
 ID Q8U460 PYRFU PRELIMINARY; PRT; 357 AA.
 AC Q8U460;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein PF0234.
 GN OrderedLocustNames=PF0234;
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE010148; AAL80358.1; -; Genomic DNA.
 DR InterPro; IPR008553; DUF835.
 DR Pfam; PF05763; DUF835; 1.
 DR Complete proteome; Hypothetical protein.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 357 AA; 39940 MW; 9EEFE2540CFC8D65 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 357;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 197 KLVFFA 202

RESULT 70
 Q8UUI8 BRARE
 ID Q8UUI8 BRARE PRELIMINARY; PRT; 357 AA.
 AC Q8UUI8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative membrane protein (Fragment).
 GN Nameaappa;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole embryo;
 RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
 RA Musa A., Leirach H., Russo V.E.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human
 RT APP gene during embryonic development.";
 RL Dev. Genes Evol. 211:563-567 (2001).
 DR EMBL; AJ315637; CAC85734.1; -; mRNA.
 DR HSP; Q16019; IHZ3.
 DR SMR; Q8UUI8; 62-170.
 DR ZFIN; ZDB-GENE-000616-13; appa.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR008155; A4_APP.

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehama J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK052448; BAC34997.1; -; mRNA.
DR HSSP; P08592; INM3.
DR MGI; MGI:88059; App.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0016020; C-membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030198; P:extracellular matrix organization and bioge. .; IGI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0203; AMTLOIDA4.
DR PRINTS; PRO0204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 218;
Best Local Similarity 83.3%; Pred. NO. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 135 KLVFFA 140
|:|||||
|:|||||
RESULT 66
Q8VY56 ARATH
ID Q8VY56_ARATH PRELIMINARY; PRT; 229 AA.
AC Q8VY56;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12870.
GN Name=At4g12870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072432; AAL62424.1; -; mRNA.
DR EMBL; AY128863; RAM91263.1; -; mRNA.
DR InterPro; IPR004911; GILT.
DR Pfam; PF03227; GILT; 1.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25707 MW; BF3DD2587EAA82D6 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. NO. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 9 KLVFFA 14
|:|||||
|:|||||
RESULT 67
Q9SV79 ARATH
ID Q9SV79_ARATH PRELIMINARY; PRT; 231 AA.
AC Q9SV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12900.
GN Name=At4g12900; Synonyms=AT4g12900;

DE Hypothetical protein.
GN OrderedLocusNames=RS6777;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=1117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294144; CAD75000.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 15530 MW; 5DCC133B06CC5FC0 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 85 KLVFFA 90

RESULT 63
Q5ST29 ARATH PRELIMINARY; PRT; 152 AA.
AC Q5ST29;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein T20K18.220 (Hypothetical protein AT4g12870).
GN Name=T20K18.220; Synonyms=AT4g12870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049640; CAB41004.1; -; Genomic DNA.
DR EMBL; AL161535; CAB78329.1; -; Genomic DNA.
DR PIR; T06645; T06645.
DR InterPro; IPR004911; GILT.
DR Pfam; PF03227; GILT; 1.
KW Hypothetical protein.
SQ SEQUENCE 152 AA; 17095 MW; ED47CEAE7607B131 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 9 KLVFFA 14

RESULT 64
Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.
AC Q6AKE9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Related to Mcbg protein.
GN OrderedLocusNames=DP2447;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902 (2004).
DR EMBL; CR522870; CAG37176.1; -; Genomic DNA.
DR InterPro; IPR001646; 5peptide_repeat.
DR Pfam; PF00805; Pentapeptide; 3.
KW Complete proteome.
SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;

Query Match 93.1%; Score 27; DB 2; Length 203;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 52 KLVFFA 57

RESULT 65
Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.
AC Q8BPV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone:D430025B14 product:amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaashizaki Y.,
RA Carninci P., Hayaashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90089-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; X56124; CAA39589.1; -; mRNA.
DR EMBL; X56126; CAA39591.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 59
FT CHAIN 7 >59
FT CHAIN 7 48
FT CHAIN 7 46
FT CHAIN 47 >59
FT CHAIN 49 >59
FT CHAIN 49 >59
FT TOPO_DOM <1 34
FT TRANSMEM 35 58
FT TOPO_DOM 59 >59
FT NON_TER 1 1
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 59;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 22 KLVFFA 27

RESULT 60
O35463 CRIGR PRELIMINARY; PRT; 79 AA.
AC O35463
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN Name-beta APP;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;

[1]
NUCLEOTIDE SEQUENCE.
RP Sanbamurti K., Pinnix I., Gandhi S.;
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030413; AAB86608.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1 79
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 36 KLVFFA 41

RESULT 61
Q8JH58 CHESE PRELIMINARY; PRT; 113 AA.
AC Q8JH58
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
protein family in the hypothalamus of the snapping turtle, Chelydra
serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275 (2002).
DR EMBL; AF541917; AAN04908.1; -; mRNA.
DR HSSP; Q16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 113;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 30 KLVFFA 35

RESULT 62
Q7UPR1 RHOB PRELIMINARY; PRT; 137 AA.
ID Q7UPR1 RHOB
AC Q7UPR1
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).

GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RN NCBI_TaxID=9986;

RP [1]
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the APP family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; X56129; CAA39594.1; -; mRNA.
DR HSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Amyloid; Transmembrane.

FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 21 KLVFFA 26

RESULT 58

A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal

fragment 57)] (Fragment).

GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the APP family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; X56130; CAA39595.1; -; mRNA.
DR HSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.

DR PROSITE; PS00319; A4 EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Amyloid; Transmembrane.

FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 21 KLVFFA 26

RESULT 59

A4_BOVIN
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE C-terminal fragment 59]; Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
 DE fragment 57)] (Fragment).
 GN Name=APP;
 OS Ursus maritimus (Polar bear) (Thalassidroma maritimus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Ursidae;
 OC Ursus.
 OX NCBI_TaxID=29073;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=92017079; PubMed=156157; DOI=10.1016/0169-328X(91)90088-F;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RA "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; X56128; CAA39593.1; -; mRNA.
 CC PIR; B60045; B60045.
 CC HSP; P08592; INMW.
 CC InterPro; IPR008155; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PRINTS; PR00204; BETAAMYLOID.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 5 Soluble APP-beta (By similarity).
 FT CHAIN 6 >57 CTF-alpha (By similarity).
 FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
 FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 33 Extracellular (Potential).
 FT TRANSMEM 34 57 Potential.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 57;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 |:|:|:|
 DB 21 KLVFFA 26
 RESULT 56
 A4 CANFA
 ID A4 CANFA STANDARD; PRT; 58 AA.
 AC Q28280;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE C-terminal fragment 59]; Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
 DE fragment 57)] (Fragment).
 GN Name=APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Canidae;
 OC Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=156157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; X56125; CAA39590.1; -; mRNA.
 CC HSP; P08592; INMW.
 CC Ensembl; ENSCAFG00000008557; Canis familiaris.
 CC InterPro; IPR008155; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PRINTS; PR00204; BETAAMYLOID.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 6 Soluble APP-beta (By similarity).
 FT CHAIN 7 >58 CTF-alpha (By similarity).
 FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
 FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 34 Extracellular (Potential).
 FT TRANSMEM 35 58 Potential.
 FT NON_TER 1 1
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 58;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 |:|:|:|
 DB 22 KLVFFA 27
 RESULT 57
 A4 RABIT
 ID A4 RABIT STANDARD; PRT; 58 AA.
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);


```
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -, mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 52
Q56J7 TURTR
ID Q56J7 TURTR PRELIMINARY; PRT; 42 AA.
AC Q56J7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottlenose dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -, mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 53
Q7M088 CAVPO
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
```

```
RP PROTEIN SEQUENCE.
RX MEDLINE=3290653; PubMed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance P receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR PIR; P0512; P0512.
DR HSP; Q16019; ILYT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 54
Q8WZ99 HUMAN
ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.
AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15203367; DOI=10.1136/jnnp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
RA Ninomiya H., Saido TC., Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
RT probable familial Alzheimer's disease.";
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
DR EMBL; AB066441; BAB71958.2; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5597 MW; 3F0E8B9EC18011AD CRC64;

Query Match 93.1%; Score 27; DB 2; Length 52;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 55
A4 URSWA
ID A4 URSWA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
```

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEO03589; AAS64635.1; -; Genomic_DNA.
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR001680; WD40.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1503 AA; 167957 MW; A0DDDF3532590486 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1503;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 1264 KIIFFA 1269
RESULT 49
ID Q8A6R7_BACTN PRELIMINARY; PRT; 1676 AA.
AC Q8A6R7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein, with weak HamHI domain.
GN OrderedLocusNames=Bt1809;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
RL EMBL: AB016933; AAO76916.1; -; Genomic_DNA.
DR InterPro: IPR002048; EF-hand.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1676;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 1656 KIIFFA 1661
RESULT 50
Q9UC33 HUMAN
ID Q9UC33 HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSSP: Q16019; 1BA4.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00204; BETAAMYLOID.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFE2F4167ABD0 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 16 KLVFFA 21
RESULT 51
ID Q56JU6_GRAGR PRELIMINARY; PRT; 42 AA.
AC Q56JU6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)

```

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hopkins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003589; AAF51483.1; -; Genomic_DNA.
DR FlyBase; FBGN0031262; Ose3.
DR GO; GO:0005488; F-binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1443 AA; 161316 MW; A8C5997678040B88 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1443;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1204 KIIFFA 1209

RESULT 47
ID Q5BI64_DROME PRELIMINARY; PRT; 1458 AA.
AC Q5BI64;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LP14662p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BT021360; AAX33508.1; -; mRNA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1458 AA; 163133 MW; 2D704C8970E541EC CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1458;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1219 KIIFFA 1224

RESULT 48
ID Q7KTZ4_DROME PRELIMINARY; PRT; 1503 AA.
AC Q7KTZ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG11838-PB, isoform B
GN Name=Ose3; ORFNames=CG11838;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gdycayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foerster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Neshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Sridharling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

```

```

RESULT 44
Q68K27 CHLRE
ID Q68K27_CHLRE PRELIMINARY; PRT; 1384 AA.
AC Q68K27;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Intraflagellar transport particle protein 140.
GN Name=IFT140;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;
RT "Intraflagellar transport protein IFT140."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY686103; AAT95430.1; -; mRNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 5.
DR TIGRPfam; TIGR00756; PPR; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Flagellum.
SQ SEQUENCE 1384 AA; 154603 MW; 5D3E70C9440DABCD CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1384;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 1154 KIIFPA 1159

RESULT 45
Q7QEF0 ANOQA
ID Q7QEF0_ANOQA PRELIMINARY; PRT; 1408 AA.
AC Q7QEF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001545 (Fragment).
OS Anopheles gambiae str. PEST.
GN Anopheles gambiae.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG "Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; ARA0100847; EAA06955.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

```

```

FT NON_TER 1408 1408
SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1408;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 1212 KIIFPA 1217

RESULT 46
Q9VPR0 DROME
ID Q9VPR0_DROME PRELIMINARY; PRT; 1443 AA.
AC Q9VPR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG11838-PA; isoform A.
GN Name=Oseg3; ORFNames=CG11838;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

```

```

RESULT 42
QBR410_MOUSE
ID QBR410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC QBR410;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ICR;
RA Hagiwara K., Endo Y., Xin H., Takahashi M., Huguin, Nukiwa T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090567; AAM11887.1; -; mRNA.
DR HSSP; P29477; 1DWV.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. . .; ISS.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO_synthase.
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PROSITE; PS00371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130685 MW; DAD5AAPF53680B005 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 515 KIVFFA 520

RESULT 43
Q6P6A0_MOUSE
ID Q6P6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q6P6A0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Nos2 protein.

```

```

GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=2477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altshuler R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausch S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062378; AAH62378.1; -; mRNA.
DR HSSP; P29477; 1JWK.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042803; F:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; IMP.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; IMP.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO_synthase.
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PROSITE; PS00371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130671 MW; C36E09F536923295 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 515 KIVFFA 520

```

perins.";

RT Biochemistry 39:4608-4621(2000).

RL [12]

RT X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF TRP-457 MUTANTS.

RL MEDLINE=21526413; PubMed=11669619; DOI=10.1021/bi011183k;

RX RA Aoyagi M., Arvai A.S., Ghosh S., Stuehr D.J., Tainer J.A.,

RA Getzoff E.D.;

RA "Structures of tetrahydrobiopterin binding-site mutants of inducible nitric oxide synthase oxygenase dimer and implicated roles of Trp457.";

RT Biochemistry 40:12826-12832(2001).

RL [13]

RT X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.

RL MEDLINE=22335496; PubMed=12437348; DOI=10.1021/bi026313j;

RX RA Rosenfeld R.J., Garcin E.D., Panda K., Andersson G., Abernethy A.,

RA Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,

RA Getzoff E.D.;

RA "Conformational changes in nitric oxide synthases induced by chlorzoxazone and nitroindazoles: crystallographic and computational analyses of inhibitor potency.";

RT Biochemistry 41:13915-13925(2002).

RL [14]

RT X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 77-495.

RL MEDLINE=22351711; PubMed=12464241; DOI=10.1016/S0003-9861(02)00555-6;

RX RA Fedorov R.J., Ghosh D.K., Schlichting I.;

RA "Crystal structures of cyanide complexes of P450cam and the oxygenase domain of inducible nitric oxide synthase - structural models of the short-lived oxygen complexes.";

RT Arch. Biochem. Biophys. 409:25-31(2003).

RL -/- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule with diverse functions throughout the body. In macrophages, NO mediates tumoricidal and bactericidal actions.

CC -/- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline + nitric oxide + n NADP(+).

CC -/- COFACTOR: Heme.

CC -/- COFACTOR: FAD. Binds 1 mole of FAD.

CC -/- COFACTOR: FMN. Binds 1 mole of FMN.

CC -/- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric form of the enzyme.

CC -/- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin inhibits expression and function of this enzyme and effects may be exerted at the level of translational/posttranslational modification and directly on the catalytic activity.

CC -/- SUBUNIT: Homodimer. Binds SLCA3R1 (By similarity).

CC -/- TISSUE SPECIFICITY: Macrophages.

CC -/- INDUCTION: By treatment with endotoxins or cytokines.

CC -/- SIMILARITY: Belongs to the NOS family.

CC -/- SIMILARITY: Contains 1 flavodoxin-like domain.

RT This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR EMBL: M87039; AAA39315.1; -; mRNA.

DR EMBL: M92849; -; NOT ANNOTATED CDS; mRNA.

DR EMBL: M84373; AAA39834.1; -; mRNA.

DR EMBL: U43428; AAC52356.1; -; mRNA.

DR EMBL: AF065919; AAC17914.1; -; mRNA.

DR EMBL: AF065920; AAC17915.1; -; mRNA.

DR EMBL: AF065921; AAC17916.2; -; mRNA.

DR EMBL: AF065922; AAC17917.2; -; mRNA.

DR EMBL: AF065923; AAC17918.2; -; mRNA.

DR PIR: A43271; A43271.

DR PDB: 1DD7; X-ray; A=114-498.

DR PDB: 1DF1; X-ray; A/B=77-499.

DR PDB: 1DWJ; X-ray; A/B=77-496.

DR PDB: 1DWX; X-ray; A/B=77-496.

DR PDB: 1DWX; X-ray; A/B=77-496.

DR PDB: 1DWJ; X-ray; A/B=66-498.

DR PDB: 1LWK; X-ray; A/B=66-498.

DR PDB: 1W8D; X-ray; A/B=65-498.

AC O9GLV6;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE RNA helicase.
 GN Name=RHIV-1;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20261798; PubMed=10799277; DOI=10.1006/mpat.1999.0349;
 RA Zhang X., Wang C., Schook L.B., Hawken R.J., Rutherford M.S.;
 RT "An RNA helicase, RHIV -1, induced by porcine reproductive and
 RT respiratory syndrome virus (PRRSV) is mapped on porcine chromosome
 RT 10q13.";
 RL Microb. Pathog. 28:267-278(2000).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AF181119; AACG9428.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR011545; DEAD/DEAH N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 KW Helicase; Hydrolase; Nuclear protein; Repeat.
 SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 940;
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIVFFA 6
 Db 290 KIVFFA 295
 RESULT 40
 ID NOS2 MOUSE STANDARD; PRT; 1144 AA.
 AC P29477; O70515; O70516;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
 GN Name=Nos2; Synonyms=Inos1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92229444; PubMed=1373522;
 RA Xie Q.-W., Cho H.J., Calaycay J.; Munford R.A., Swiderek K.M.,
 RA Lee T.-D., Ding A., Troso T., Nathan C.;
 RT "Cloning and characterization of inducible nitric oxide synthase from
 RT mouse macrophages.";
 RL Science 256:225-228(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92357701; PubMed=1379716;
 RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
 RT "Cloned and expressed macrophage nitric oxide synthase contrasts with
 RT the brain enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
 RN [3]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92210618; PubMed=1372907;
 RA Lyons C.R., Orloff G.J., Cunningham J.M.;
 RT "Molecular cloning and functional expression of an inducible nitric
 RT oxide synthase from a murine macrophage cell line.";
 RL J. Biol. Chem. 267:6370-6374(1992).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96088781; PubMed=7503239;
 RA Kone B.C., Schwebel J., Turner P., Mohaupt M.G., Cangro C.B.;
 RT "Role of NF-kappa B in the regulation of inducible nitric oxide
 RT synthase in an MTL cell line.";
 RL Am. J. Physiol. 269:F718-F729(1995).
 RN [5]
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.
 RC STRAIN=B10.S/J, BALB/cBYJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
 RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2262-2266(1999).
 RN [6]
 RP EFFECT OF ASPIRIN.
 RC TISSUE=Macrophage;
 RX MEDLINE=95372392; PubMed=7544010;
 RA Anin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
 RA Weismann G., Abramson S.B.;
 RT "The mode of action of aspirin-like drugs: effect on inducible nitric
 RT oxide synthase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
 RX MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;
 RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,
 RA Stuehr D.J., Tainer J.A.;
 RT "The structure of nitric oxide synthase oxygenase domain and inhibitor
 RT complexes.";
 RL Science 278:425-431(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
 RX MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;
 RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RT "Structure of nitric oxide synthase oxygenase dimer with pterin and
 RT substrate.";
 RL Science 279:2121-2126(1998).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20031637; PubMed=10562538; DOI=10.1093/emboj/18.22.6260;
 RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
 RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
 RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
 RT hook and pterin-binding segment in dimerization and
 RT tetrahydrobiopterin interaction.";
 RL EMBO J. 18:6260-6270(1999).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
 RX MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;
 RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,
 RA Tainer J.A., Stuehr D.J., Getzoff E.D.;
 RT "N-terminal domain swapping and metal ion binding in nitric oxide
 RT synthase dimerization.";
 RL EMBO J. 18:6271-6281(1999).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20233702; PubMed=10769116; DOI=10.1021/bi992409a;
 RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible
 RT nitric oxide synthase oxygenase dimer with active and inactive

```

O95786 HUMAN
ID O95786 HUMAN PRELIMINARY; PRT; 925 AA.
AC O95786;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=DDX58; Synonyms=RIG-I;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Sun Y.W.;
RT "RIG-I, a human homolog gene of RNA helicase, is induced by retinoic
acid during the differentiation of acute promyelocytic leukemia
cell.";
RL Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
Shanghai Second Medical University.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yi-Wu S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038963; AAD19826.1; -; mRNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR HGNC; HGNC:19102; DDX58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0001661; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase.
SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3DD0F00D4 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 292 KVVFFA 297
|:|||||

RESULT 37
Q5VYTL_HUMAN
ID Q5VYTL_HUMAN PRELIMINARY; PRT; 925 AA.
AC Q5VYTL;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OTHUMP00000021185.
GN Names=RP11-334P12.2; ORFNames=RP11-334P12.2-001;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

```

RA Sehra H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL353671; CAH71251.1; -; Genomic DNA.
DR EMBL; AL161783; CAH72600.1; -; Genomic DNA.
DR EMBL; AL161783; CAH71251.1; JOINED; Genomic DNA.
DR EMBL; AL353671; CAH72600.1; JOINED; Genomic DNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase; Hydrolase; Nuclear protein.
KW Helicase; 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;
SQ SEQUENCE 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 292 KVVFFA 297
|:|||||

RESULT 38
Q6Q899_MOUSE
ID Q6Q899_MOUSE PRELIMINARY; PRT; 926 AA.
AC Q6Q899;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DEAD/H box polypeptide RIG-I.
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Wei J.; Gu J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY553221; AAS59532.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR006935; ResIII.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF04851; ResIII; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase.
SQ SEQUENCE 926 AA; 105877 MW; 632462010107698E CRC64;

Query Match 96.6%; Score 28; DB 2; Length 926;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 293 KVVFFA 298
|:|||||

RESULT 39
Q9GLV6_PIG
ID Q9GLV6_PIG PRELIMINARY; PRT; 940 AA.

```


QY 1 KIVFFA 6
 DB 564 KIVFFA 569

RESULT 35

QSQ82 DROME PRELIMINARY; PRT; 785 AA.

AC QSQ82; DROME

DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)

DE Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).

GN Name=Aaph; ORFNames=CG8421;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;

RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,

RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,

RA Friedman P.A.,

RA "Aspartyl beta -hydroxylase (Aaph) and an evolutionarily conserved

RT isoform of Aaph missing the catalytic domain share exons with

RT junctin.";

RL J. Biol. Chem. 275:39543-39554(2000).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballweir L.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Buesam D.A., Butler H., Cadiieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.B., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laoko P., Lei Y., Levitaky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kimios I., Simpson M.C., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22436070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,

RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RX Berkeley Drosophila Genome Project;

RA Celniker S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,

RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,

RA Yu C., Rubin G.;

RT "Drosophila melanogaster release 4 sequence.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [7]

RP NUCLEOTIDE SEQUENCE.

RX Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF289493; AAG40806.1; -; mRNA.

DR EMBL; AE003808; AAM70947.1; -; Genomic DNA.

DR Ensembl; CG8421; Drosophila melanogaster.

DR FlyBase; FBgn0034075; Asph.

DR FlyBase; FBgn0034075; CG8421.

DR GO; GO:0030376; C: integral to endoplasmic reticulum membrane; IEA.

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0005488; F: binding; IEA.

DR GO; GO:0004597; F: peptidyl-aspartate beta-dioxygenase activity; IEA.

DR GO; GO:0018193; F: peptidyl-amino acid modification; IEA.

DR InterPro; IPR007803; Asp Arg Hydrol.

DR InterPro; IPR006025; Pept_M_Zn_BS.

DR InterPro; IPR001440; TPR.

DR InterPro; IPR011990; TPR-like helical.

DR Pfam; PF05118; Asp Arg Hydrol; 1.

DR PROSITE; PS0293; TPR_REGION; 1.

DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.

SQ SEQUENCE 785 AA; 89843 MW; 30ABDFCD6836F7F1 CRC64;

Query Match 96.6% Score 28; DB 2; Length 785;
 Best Local Similarity 83.3% Pred. No. 6.6e+02;
 *Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 DB 53 KIVFFA 58

RESULT 36

```

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RL melanogaster euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaas R.,
RA Patel S., Priebe E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskaas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- INTERACTION:
CC O46085:HG:63B12.5; NExp=1; IntAct=EBI-123244, EBI-151469;
DR EMBL; AB003808; AAF58064.2; -; Genomic_DNA.
DR IntAct; Q9V719; -.
DR Ensembl; CG8421; Drosophila melanogaster.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 556 AA; 63144 MW; B420980CBDE6C357A CRC64;

Query Match 96.6%; Score 28; DB 2; Length 556;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |||||
DB 53 KIIFFA 58

RESULT 33
QSHYEL HUMAN
ID QSHYEL1 HUMAN PRELIMINARY; PRT; 703 AA.
AC QSHYEL1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686N19181 (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa;
OC Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RT TISSUE=Skin endothel;

```

```

RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX647917; CAI46068.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
KW Hypothetical protein.
FT NON TER 703
SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 703;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFEA 6
   |||||
DB 247 KVVFEA 252

RESULT 34
QNG35 LEIXX
ID Q6AG25 LEIXX PRELIMINARY; PRT; 721 AA.
AC Q6AG25;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATP-dependent RNA helicase.
GN OrderedLocustNames=LXX07490;
OS Leifsonia xyl (subsp. xyl).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furian L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F., Jr., Carrier H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
xyl subsp. xyl.";
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAT88670.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; DNA-binding; Helicase; Hydrolase.
SQ SEQUENCE 721 AA; 78860 MW; 73F5D2A8435BADE3 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 721;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 30
O59243_PYRHO
ID O59243_PYRHO PRELIMINARY; PRT; 447 AA.
AC O59243;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PH1606.
GN OrderedLocusNames=PH1606;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus
OX NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Savada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hoshiyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka T., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:53-76(1998).
DR EMBL; BA000001; BAA30718.1; -; Genomic_DNA.
DR PIR; F71039; F71039.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005355; F:glucose transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000803; Gluc_transporter.
DR PRINTS; PR00172; GLUCTRNSPORT.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
Db 207 KIIFFA 212

RESULT 31
Q95S93_DROME
ID Q95S93_DROME PRELIMINARY; PRT; 556 AA.
AC Q95S93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM052229p.
GN Name=Aeph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RX Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RX Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RX Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RX Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060905; AAL28453.1; -; mRNA.
DR FlyBase; FBgn0034075; Aeph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11FE8 CRC64;

```

```

Query Match 96.6%; Score 28; DB 2; Length 556;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
Db 53 KIIFFA 58

RESULT 32
Q9V719_DROME
ID Q9V719_DROME PRELIMINARY; PRT; 556 AA.
AC Q9V719;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Aeph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RX Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RX Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RX Brandon R.C., Rogers Y.-H.C., Blaese R.G., Champe M., Pfeiffer B.D.,
RX Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RX Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RX Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RX Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RX Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RX Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RX de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RX Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RX Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,
RX Foele C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RX Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RX Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RX Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RX Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RX Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RX Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RX Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RX Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RX Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RX Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RX Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RX Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RX Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RX Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RX Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RX Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RX Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RX Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RX Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RX Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RX Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RX George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RX Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RX Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

```

NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning.";
RT Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20185660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu V., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bargh G.,
RA Brownstein M.J., Bult C., Fletcher C., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli R., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium,
RL "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RL "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RL "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Haehizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Okazaki Y.,

```

DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transpore; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FBA3 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 184 KVVFFA 189

RESULT 26
Q81SK9 BACAN
ID Q81SK9_BACAN PRELIMINARY; PRT; 387 AA.
AC Q81SK9_Q610U3; Q6KUP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Germination protein gerX.
GN OrderedLocNames=Ba1639, BAS1521, GBAA1639;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson N.J., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.B., Tettelin S.H., Fouts D.E., Elesen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri I.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Dewey S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-Sterne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017029; AAP25572.1; -; Genomic DNA.
DR EMBL; AE017334; AAT30749.1; -; Genomic DNA.
DR EMBL; AE017225; AAT53839.1; -; Genomic DNA.
DR TIGR; BA1639; -.
DR TIGR; GBAA1639; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; P:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transpore; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 184 KVVFFA 189

RESULT 27
Q6L2B4 PICTO
ID Q6L2B4_PICTO PRELIMINARY; PRT; 410 AA.
AC Q6L2B4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lipopolysaccharide N-acetylglucosaminyltransferase.
GN OrderedLocNames=PT00303;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9095(2004).
DR EMBL; AE017261; AAT42888.1; -; Genomic DNA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl. .; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 410 AA; 48120 MW; C192F0152E66E9B0 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 410;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 235 KIVFFA 240

RESULT 28
Q8CS13 MOUSE
ID Q8CS13_MOUSE PRELIMINARY; PRT; 410 AA.
AC Q8CS13;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box
DE helicase containing protein, full insert sequence.
GN Name=bdx38;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.

```

```

OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax."
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA001000008; EAL15336.1; -; Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79B12C38 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KJVFPA 6
DB 184 KJVFPA 189

RESULT 23
Q63DD4_BACCZ
ID Q63DD4_BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=286861;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006865; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRfams; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991FDD63F33 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KJVFPA 6
DB 184 KJVFPA 189

RESULT 24
Q6HKU6_BACHK
ID Q6HKU6_BACHK PRELIMINARY; PRT; 387 AA.
AC Q6HKU6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN; OrderedLocusNames=BT9727_1493;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT63168.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006865; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRfams; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41076 MW; DFECAD90985F951 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KJVFPA 6
DB 184 KJVFPA 189

RESULT 25
Q73AP3_BACCI
ID Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
AC Q73AP3;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Germination protein gerN.
GN OrderedLocusNames=BCEI1729;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI."
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AA940658.1; -; Genomic DNA.
DR TIGR; BCEI1729; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.

```

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibgwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.N., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RN Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
 RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
 RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
 RA Friedman P.A.;

RT "Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
 RT isoform of Asph missing the catalytic domain share exons with
 RT junction.";
 RL J. Biol. Chem. 275:39543-39554(2000).
 DR EMBL; AF003808; AAF58063.2; -; Genomic_DNA.
 DR EMBL; AF289494; AAG40807.1; -; mRNA.
 DR Ensembl; CG8421; Drosophila melanogaster.
 DR FlyBase; FBgn0034075; Asph.
 DR FlyBase; FBgn0034075; CG8421.
 SQ SEQUENCE 382 AA; 43287 MW; 60ESC03AEBFC6EBB CRC64;

Query Match 96.6%; Score 28; DB 2; Length 382;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 53 KIIFFA 58

RESULT 21

ID Q9K110_BACCE PRELIMINARY; PRT; 387 AA.
 AC Q9K110;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GerN.
 GN Name=gerN;
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=1396;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC10876;
 RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
 RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;
 RT "GerN, an antiporter homologue important in germination of *Bacillus*
 RT cereus endospores.";
 RL J. Bacteriol. 183:476-482(2001).
 DR EMBL; AF246294; AAF91326.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; F:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRPFAMs; TIGR00932; 2a37; 1.
 KW Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41093 MW; 40DB45B71B715D01 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 184 KIVFFA 189

RESULT 22

ID Q4WT39_BACCE PRELIMINARY; PRT; 387 AA.
 AC Q4WT39;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Na+/H+ antiporter
 GN ORFNames=BCE_G3241_1647;

```

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.T., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AFUJ01000002; BAF53713.1; -; Genomic DNA.
SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12D60CAED CRC64;

Query Match 96.6%; Score 28; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KIVFFA 6
Db 132 KIVFFA 137

RESULT 18
Q6D7U3_ERWCT PRELIMINARY; PRT; 372 AA.
AC Q6D7U3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hydrogenase isoenzymes formation protein.
GN Name=hypD; OrderedLocusNames=ECA1232;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).
DR EMBL; BX50851; CAG74142.1; -; Genomic DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
SQ SEQUENCE 372 AA; 41130 MW; A001A18AC015E620 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 372;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 139 KIVFFA 144

```

```

RESULT 19
Q7M9N5_WOLSU PRELIMINARY; PRT; 373 AA.
AC Q7M9N5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HYDROGENASE PROTEIN.
GN Name=hypD; OrderedLocusNames=WS0793;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).
DR EMBL; BX571659; CAB09906.1; -; Genomic DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 373;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 138 KIVFFA 143

RESULT 20
Q9V7J0_DROME PRELIMINARY; PRT; 382 AA.
AC Q9V7J0; Q9G081;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG8421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

```


RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml P., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX STRAIN=C57BL/6J; TISSUE=Heart;
RA The RIKEN Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11041159; DOI=10.1101/gr.145100;
RA Carninci P., Aizawa K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipette sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ichii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nunazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the ENBL/GenBank/DBJ databases.
RL

DR EMBL; AK052871; BAC35183.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD. 1.
DR SMART; SM00487; DEXdc. 1.
KW Helicase, Hypothetical protein.
FT NON TER 231 232
SQ SEQUENCE 231 AA; 1D191607390D7FBB CRC64;

Query Match 96.6%; Score 28; DB 2; Length 231;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 145 KIVFFA 150
|:|:|:|
|:|:|:|

RESULT 16
Q61C67 CAEBR
ID Q61C67 CAEBR PRELIMINARY; PRT; 315 AA.
AC Q61C67;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG13055 (Fragment).
GN Name=CBG13055;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC01000061; CAB67532.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
FT NON TER 1 1
FT NON TER 315 315
SQ SEQUENCE 315 AA; 579B590D01874512 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 315;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 117 KIVFFA 122
|:|:|:|
|:|:|:|

RESULT 17
Q4HSJ7 CAMUP
ID Q4HSJ7 CAMUP PRELIMINARY; PRT; 362 AA.
AC Q4HSJ7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hydrogenase expression/formation protein HypD.
GN Name=HypD; ORFNames=CUP0294;
OS Campylobacter upsaliensis RM3195.

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 19 kDa globulin precursor (Alpha-globulin).
 OS Oryza sativa (Rice)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
 RC STRAIN=cv. Japonica / Nipponbare; TISSUE=Endosperm;
 RX MEDLINE=92119226; PubMed=8501935;
 RA Tanaka K., Muthukrishnan S., Reek G.R.;
 RA "A novel cereal storage protein: molecular genetics of the 19 kDa
 RT globulin of rice";
 RT Plant Mol. Biol. 18:151-154 (1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 5-186.
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;
 RX MEDLINE=93277591; PubMed=8501935;
 RA Krishnan H.B., Pueppke S.G.;
 RA "Nucleotide sequence of an abundant rice seed globulin: homology with
 RT the high molecular weight glutelins of wheat, rye and triticale";
 RL Biochem. Biophys. Res. Commun. 193:460-466 (1993).
 CC 1- FUNCTION: Seed storage protein.
 CC 1- SIMILARITY: Belongs to the 2S seed storage albumins family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; X63990; CAA45400.1; -; mRNA.
 DR EMBL; L12252; AAN72362.1; ALT_INIT; mRNA.
 DR PIR; S20024; WNR219.
 DR HSP; P24565; 1PNB.
 DR Gramene; P29835; -.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR PANTHER; PTHR14054; Glutenin; 1.
 DR Pfam; PF00234; Tryp alpha amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 DR Direct protein sequencing; Seed storage protein; Signal;
 KW Storage protein.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 186 19 kDa globulin.
 FT SEQUENCE 186 AA; 21050 MW; 9E09BA74CB0B6810 CRC64;
 SQ
 Query Match 96.6%; Score 28; DB 1; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 4 KVVFFA 9
 RESULT 14
 P93414 Oryza
 ID P93414 Oryza PRELIMINARY; PRT; 186 AA.
 AC P93414;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE 26 kDa globulin (Alpha-globulin).
 GN Name=P010D04.16; Synonyms=OJ1057_B02.5;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Endosperm;
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,
 RA Tanaka K., Matsuda T.;
 RA "Cloning of the rice seed alpha-globulin-encoding gene: sequence
 RT similarity of the 5'-flanking region to those of the genes encoding
 RT wheat high molecular-weight glutenin and barley D hordein";
 RL Gene 170:223-226 (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RA "Oryza sativa BAC OJ1057 B02 genomic sequence";
 RT Submitted (AUG-2004) to The EMBL/GenBank/DBJ databases.
 DR EMBL; D50643; BAA09308.1; -; Genomic_DNA.
 DR EMBL; AC130605; AAT44292.1; -; Genomic_DNA.
 DR EMBL; AC113332; AAT93857.1; -; Genomic_DNA.
 DR PIR; JC4784; JC4784.
 DR HSP; P24565; 1PNB.
 DR Gramene; P93414; -.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR Pfam; PF00234; Tryp alpha amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 DR SEQUENCE 186 AA; 21055 MW; AE2B8F1107C8BC94 CRC64;
 SQ
 Query Match 96.6%; Score 28; DB 2; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 4 KVVFFA 9
 RESULT 15
 Q8C6Y8 MOUSE
 ID Q8C6Y8 MOUSE PRELIMINARY; PRT; 231 AA.
 AC Q8C6Y8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
 DE library, clone:D83015B12 product:hypothetical DEAD/DEAH box helicase
 DE containing protein, full insert sequence. (Fragment).
 GN Name=Ddx58;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

```

FT NON TER 1 1
SQ SEQUENCE 1265 AA; 143403 MW; C9C157ABE90FF928 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1265;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1081 KIVFFA 1086

RESULT 10
O5F3M1_CHICK PRELIMINARY; PRT; 1412 AA.
AC O5F3M1;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=RCJWB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayaishizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH65263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40. 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS50082; WD REPEATS_2; 1.
DR PROSITE; PS50294; WD REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 1412 AA; 158448 MW; FA0050885B274747 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1412;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1225 KIVFFA 1230

RESULT 11
O4LBQ8_SODGL PRELIMINARY; PRT; 88 AA.
AC O4LBQ8;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE CheY protein.
GN Name=cheY;
OS Sodalis glossinidius.
OC Plasmid pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtsis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius.";

```

```

RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic DNA.
KW Plasmid.
SQ SEQUENCE 88 AA; 10177 MW; F4168F2A56B8D0AC CRC64;

Query Match 96.6%; Score 28; DB 2; Length 88;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 42 KIIFFA 47

RESULT 12
Q9RQ09_BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09; O7C422;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidales (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=99380605; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic DNA.
DR EMBL; AE016931; AAO76385.1; -; Genomic DNA.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF04542; Sigma70_r2; 1.
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Sigma factor; Transcription;
KW Transcription regulation; Transferase.
SQ SEQUENCE 183 AA; 22042 MW; 6B24DABC99BEC643 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 172 KIIFFA 177

RESULT 13
GL19_ORYSA STANDARD; PRT; 186 AA.
ID GL19_ORYSA
AC P29835;
DT 01-APR-1993 (Rel. 25, Created)

```

```

ID Q6RUU2_MOUSE PRELIMINARY; PRT; 663 AA.
AC Q6RUU2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brathwaite M., Waelst P., Dudekula D., Nagaraja R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY491413; RAS21643.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3BED356F1C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
DB 433 KIVFFFA 438

RESULT 7
Q83IB2_TROW8
ID Q83IB2_TROW8 PRELIMINARY; PRT; 690 AA.
AC Q83IB2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative helicase regulator.
GN OrderedLocNames=TW130;
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Beera G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Rellman D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whipplei.";
RL Lancet 361:637-644(2003).
DR EMBL; BK251410; CAD66810.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; Helicase.
SQ SEQUENCE 690 AA; 76266 MW; CD3633B94B669E32 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
DB 526 KIVFFFA 531

```

```

RESULT 8
Q83GW3_TROWT
ID Q83GW3_TROWT PRELIMINARY; PRT; 698 AA.
AC Q83GW3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA helicase.
GN OrderedLocNames=TW118;
OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Twist;
RX MEDLINE=22784088; PubMed=12902375;
RA Raoult D., Ogata H., Audic S., Robert C., Suhr K., Drancourt M.,
RA Claverie J.-M.;
RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
reduced genome.";
RL Genome Res. 13:1800-1809(2003).
DR EMBL; AE016850; AA044215.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; Helicase.
SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDDE72 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
DB 534 KIVFFFA 539

RESULT 9
Q6ZQ91_MOUSE
ID Q6ZQ91_MOUSE PRELIMINARY; PRT; 1265 AA.
AC Q6ZQ91;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KIAA0590 protein (Fragment).
GN Name=KIAA0590;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
III. the complete nucleotide sequences of 500 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129167; BAC97977.1; -; mRNA.

```

AC Q4TRF8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Membrane protein.
 GN ORFNames=ELI0568;
 OS Erythrobacter litoralis HTCC2594.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 OC Sphingomonadaceae; Erythrobacter.
 OX NCBI_TaxID=314225;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HTCC2594;
 RA Giovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S.,
 RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
 RA Friedman R., Venter J.C.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAGG0100001; EAL76762.1; -; Genomic DNA.
 SQ SEQUENCE 450 AA; 50280 MW; 077F448E75ADF977 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 116 KIVFFA 121
 RESULT 4
 ID Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
 AC Q4S4T5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 2 SCAFI4738, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00024047001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellan S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McRwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAG01014738; CAG04347.1; -; Genomic DNA.

FT NON TER 464 464
 SQ SEQUENCE 464 AA; 53213 MW; 0F9FF81DB193CE5C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 464;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 304 KIVFFA 309
 RESULT 5
 ID Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
 AC Q91VU5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Wtcc2 protein.
 GN Name=AI661311; Synonyms=Wtcc2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RC NIH WGC Project;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009019; AAH09019.1; -; mRNA.
 DR Ensembl; ENSMUSG0000024169; Mus musculus.
 DR MGI; MGI:2146906; AI661311.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like_helical.
 SQ SEQUENCE 606 AA; 70992 MW; 4BB6057E07ADA16C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 606;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 376 KIVFFA 381
 RESULT 6
 ID Q6RUU2_MOUSE

251 25 86.2 26 2 Q4XGPI PLACH
 252 25 86.2 46 2 Q4YT9 PLABE
 253 25 86.2 47 2 Q8EXM4 LEPIN
 254 25 86.2 46 2 Q8QY9 FUGRU
 255 25 86.2 49 2 Q4XA79 PLACH
 256 25 86.2 51 2 Q7F81 PLAYO
 257 25 86.2 51 2 Q4YGS7 PLABE
 258 25 86.2 55 2 Q42VG8 NITEU
 259 25 86.2 59 2 Q4XGP8 PLABE
 260 25 86.2 62 1 Y078 HELRU
 261 25 86.2 62 1 Y085 HELPV
 262 25 86.2 63 2 Q64S36 BACFR
 263 25 86.2 72 2 Q4HSS4 CAMUP
 264 25 86.2 77 2 Q5K6Q9 CRAGI
 265 25 86.2 79 2 Q5WJL6 BACSK
 266 25 86.2 81 1 MORAD ECOLI
 267 25 86.2 81 2 Q9APP7 9BACT
 268 25 86.2 81 2 Q57RF2 SALCH
 269 25 86.2 81 2 Q65TTO MANSN
 270 25 86.2 81 2 Q7N6P4 PHOLL
 271 25 86.2 81 2 Q8D897 VIBVU
 272 25 86.2 81 2 Q9KT78 VIBCH
 273 25 86.2 81 2 Q8S38 SHIFL
 274 25 86.2 81 2 Q7MM72 VIBVU
 275 25 86.2 81 2 Q8X807 ECO57
 276 25 86.2 83 2 Q8CLV3 YERPE
 277 25 86.2 83 2 Q5PG40 SALPA
 278 25 86.2 83 2 Q8Z886 SALT1
 279 25 86.2 83 2 Q8ZQQ0 SALTY
 280 25 86.2 85 2 Q87MY3 VIBPA
 281 25 86.2 108 1 Y3403 METJA
 282 25 86.2 109 2 Q6VYX4 ORYSA
 283 25 86.2 111 2 Q9A126 ECOLI
 284 25 86.2 116 2 Q49347 MYCGE
 285 25 86.2 121 2 Q4V6R3 BRARE
 286 25 86.2 128 2 Q6DUB9 PSEFL
 287 25 86.2 128 1 Y613 PASMU
 288 25 86.2 130 1 Q6BXU4 DEBHA
 289 25 86.2 131 2 Q9LIH4 ARATH
 290 25 86.2 135 2 Q5LGT9 BACFN
 291 25 86.2 141 2 Q67684 AQUAE
 292 25 86.2 141 2 Q64XP1 BACFR
 293 25 86.2 143 1 COFI YEAST
 294 25 86.2 143 2 Q6BWX4 DEBHA
 295 25 86.2 143 2 Q6CQ22 KLJLA
 296 25 86.2 143 2 Q6FV81 CANGA
 297 25 86.2 143 2 Q9HF97 ZYGRO
 298 25 86.2 143 2 Q759P0 ASHGO
 299 25 86.2 143 2 Q8EMC6 OCEIH
 300 25 86.2

ALIGNMENTS

RESULT 1
 Q7N39 TREDE
 ID Q7N39 TREDE PRELIMINARY; PRT; 164 AA.
 AC Q7N39;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocustNames=DEI1317;
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OC NCBI_TaxID=158;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 35405 / DSM 14222;
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
 RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 RA Gebregorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
 RA Shatsman S., McLeod M.P., Smajls D., Howell J.K., Pal S., Amin A.,
 RA Vaishish P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
 RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.,
 RT "Comparison of the genome of the oral pathogen Treponema denticola
 with other spirochete genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
 DR EMBL; AE017250; AAS11834.1; -; Genomic_DNA.
 DR TIGR; TDE1317; -;
 KW Complete proteome.
 SQ SEQUENCE 164 AA; 18968 MW; 27E92778DDA9117C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 164;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 50 KIVFFA 55
 RESULT 2
 Q81FH5 BACCR
 ID Q81FH5 BACCR PRELIMINARY; PRT; 387 AA.
 AC Q81FH5;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Na+/H+ antiporter NnpA (inosine-dependent germination).
 GN OrderedLocustNames=BC1612;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=226900;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
 RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Ponstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 Bacillus anthracis.";
 RL Nature 423:87-91 (2003).
 DR EMBL; AE017003; AAP08591.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; F:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGR; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41037 MW; 907C03E6B150B4A CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 184 KIVFFA 189
 RESULT 3
 Q4TRF8_9SPHN
 ID Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.

105	27	93.1	714	2	Q56JK4 CANFA	Q56jk4	canis famil	178	26	89.7	248	2	Q813W8 PLAF7	Q813w8	plasmodium
106	27	93.1	733	2	Q8P605_RAT	Q8p6q5	rattus norv	179	26	89.7	253	2	Q9KL60_VIBCH	Q9kl60	vibrio chol
107	27	93.1	737	1	A4_FUGRU	Q91279	fugu rubrip	180	26	89.7	270	2	Q7MW75_FORGI	Q7mw75	porphyromon
108	27	93.1	738	2	Q6NU21_BARE	Q6nu21	brachydanio	181	26	89.7	279	2	Q4ILF1_GIBBEZ	Q4ilf1	gibberella
109	27	93.1	738	2	Q90W28_BARE	Q90w28	brachydanio	182	26	89.7	281	2	Q51231_MAGGR	Q512j1	magnaporthe
110	27	93.1	747	2	Q91963_9PIPI	Q91963	xenopus. ap	183	26	89.7	281	2	Q4XSI1_PLACH	Q4xsi1	plasmodium
111	27	93.1	749	2	Q56JK2_SNECO	Q56jk2	stenella co	184	26	89.7	284	2	Q4XZ22_PSESY	Q4xx22	pseudomonas
112	27	93.1	749	2	Q6NR11_XENLA	Q6nr11	xenopus lae	185	26	89.7	292	2	Q4WK19_ASFFU	Q4wk19	aspergillus
113	27	93.1	750	2	Q6DJB6_XENTR	Q6djb6	xenopus tro	186	26	89.7	300	2	Q9XU61_CABEL	Q9xu61	caenorhabdi
114	27	93.1	751	1	A4_SAISC	Q95241	s amyloid b	187	26	89.7	301	2	Q5B613_EHEMI	Q5b613	aspergillus
115	27	93.1	751	2	Q6GSC0_HUMAN	Q6gsc0	homo sapien	188	26	89.7	306	2	Q68RL2_9HEMI	Q68rl2	glycaspis b
116	27	93.1	751	2	Q6RH28_CANFA	Q6ch28	canis famil	189	26	89.7	312	2	Q9ZU4_9CAEN	Q9zu4	littorina s
117	27	93.1	751	2	Q56JK5_CANFA	Q56jk5	canis famil	190	26	89.7	321	1	Y189_RICPR	Q8zdx5	rickettsia
118	27	93.1	751	2	Q4R48R_MACFA	Q4r48	macaca fasc	191	26	89.7	333	2	Y6TG00_HELZE	Q6tg00	heliothis z
119	27	93.1	751	2	Q9DGJ7_CHICK	Q9dgj7	gallus gall	192	26	89.7	336	1	RSMC_BUCAP	Q8k915	buchnera ap
120	27	93.1	754	2	Q4RY33_TETNG	Q4ry33	tetradodon n	193	26	89.7	337	2	Q54NZ2_DICDI	Q54nz2	dictyosteli
121	27	93.1	759	2	Q4S0J4_TETNG	Q4s0j4	tetradodon n	194	26	89.7	347	2	Q87PM3_VIBPA	Q87pm3	vibrio para
122	27	93.1	760	2	Q55HW1_CRYNE	Q55hw1	cryptococcu	195	26	89.7	349	2	Q9XU59_CABEL	Q9xu59	caenorhabdi
123	27	93.1	770	1	A4_CAVFO	Q60495	c amyloid b	196	26	89.7	352	2	Q8YUK9_ANASP	Q8yuk9	anabaena sp
124	27	93.1	770	1	A4_HUMAN	P5067	h amyloid b	197	26	89.7	360	2	Q7NMZ9_GLOVI	Q7nm29	gloeobacter
125	27	93.1	770	1	A4_MACFA	P53601	m amyloid b	198	26	89.7	366	2	Q8DIZ5_SYNEL	Q8diz5	synechococc
126	27	93.1	770	1	A4_MOUSE	P12023	p amyloid b	199	26	89.7	380	2	Q7VJC1_HELHP	Q7vjc1	helicobacte
127	27	93.1	770	1	A4_PANTR	Q51s80	p amyloid b	200	26	89.7	382	2	Q9KDB2_BACHD	Q9kdb2	bacillus ha
128	27	93.1	770	1	A4_PIG	P79307	s amyloid b	201	26	89.7	390	2	Q5WLG1_BACSK	Q5wlg1	bacillus cl
129	27	93.1	770	1	A4_RAT	P08592	r amyloid b	202	26	89.7	391	2	Q8A2G6_BACTN	Q8a2g6	bacteroides
130	27	93.1	770	2	Q6RH30_CANFA	Q6rh30	canis famil	203	26	89.7	400	2	Q7PXH6_ANOGA	Q7pxh6	anopheles g
131	27	93.1	770	2	Q56JRK_CANFA	Q56jk6	canis famil	204	26	89.7	402	2	Q9ZIT8_ECOLI	Q9zit8	escherichia
132	27	93.1	770	2	Q53ZT3_MOUSE	Q53zt3	mus musculus	205	26	89.7	402	2	Q7DB96_ECOS7	Q7db96	escherichia
133	27	93.1	770	2	Q547B7_RAT	Q547b7	rattus norv	206	26	89.7	402	2	Q83PE1_SHIFL	Q83ppi	shigella fl
134	27	93.1	780	1	A4_TETFL	Q73683	tetradodon f	207	26	89.7	405	1	SVY_BORBU	SVY	borrelia bu
135	27	93.1	955	2	Q8GR22_9POTV	Q80r22	calla lily	208	26	89.7	405	2	Q661P9_BORGA	Q661p9	borrelia ga
136	27	93.1	962	2	Q8NTK2_9BELT	Q8ntk2	anaeromyxob	209	26	89.7	421	2	Q9LH60_ARATH	Q9lh60	arabidopsis
137	27	93.1	1016	2	Q59912_9POTV	Q59912	zucchini ye	210	26	89.7	468	2	Q616J7_CAEER	Q616j7	caenorhabdi
138	27	93.1	1056	2	Q6FKH6_CANGA	Q6fkh6	candida gla	211	26	89.7	472	2	Q4WEZ5_ASFFU	Q4wez5	aspergillus
139	27	93.1	1655	2	Q4Q5Q4_LEIMA	Q4q5q4	leishmania	212	26	89.7	479	2	Q9QDL5_9POTV	Q9qdl5	sarcophilus
140	27	93.1	1916	2	Q8QKQ4_9POTV	Q8qkq4	zucchini ye	213	26	89.7	479	2	Q4F979_9POTV	Q4f979	eustrephus
141	27	93.1	3080	1	POLG_ZYMYC	P18479	z genome po	214	26	89.7	480	2	Q4N8N8_THEPA	Q4n8n8	theileria p
142	27	93.1	3080	2	Q6WN47_9POTV	Q6wn47	zucchini ye	215	26	89.7	496	2	Q5K4D0_9POTV	Q5k4d0	dasheen mos
143	27	93.1	3080	2	Q6WN48_9POTV	Q6wn48	zucchini ye	216	26	89.7	502	2	Q5LIS5_GEOKA	Q5lis5	geobacillus
144	27	93.1	3080	2	Q6WN49_9POTV	Q6wn49	zucchini ye	217	26	89.7	522	2	Q4XPM5_PLACH	Q4xpm5	plasmodium
145	27	93.1	3080	2	Q6Y2U7_9POTV	Q6y2u7	zucchini ye	218	26	89.7	524	2	Q912R1_9POTV	Q912r1	dasheen mos
146	27	93.1	3080	2	Q7T908_9POTV	Q7t908	zucchini ye	219	26	89.7	539	2	Q9Q999_9POTV	Q9q999	dasheen mos
147	27	93.1	3080	2	Q7T914_9POTV	Q7t914	zucchini ye	220	26	89.7	557	2	Q4UGZ4_THEAN	Q4ugz4	theileria a
148	27	93.1	3083	1	POLG_ZYMYVS	Q36979	z genome po	221	26	89.7	598	2	Q644G8_9SALA	Q644g8	gyrinophilu
149	27	93.1	3105	2	Q70XR2_9POTV	Q70xr2	soybean mos	222	26	89.7	604	2	Q645F2_9SALA	Q645f2	stereochilu
150	26	89.7	40	2	Q91FF3_IRV6	Q91ff3	chilo iride	223	26	89.7	606	2	Q8SJI9_URSAM	Q8sj19	ursus ameri
151	26	89.7	66	2	Q728F0_DESVFV	Q728f0	desulfovibr	224	26	89.7	607	2	Q644P6_9SALA	Q644p6	thorius n.
152	26	89.7	74	1	Y131_MYCGE	P47377	mycoplasma	225	26	89.7	611	2	Q6ZLV9_9TELE	Q6zlv9	ophisurus m
153	26	89.7	81	2	Q8D3D0_ERWCT	Q6d3d0	erwinia car	226	26	89.7	613	2	Q4ZG30_9TELE	Q4zgg0	scieropages
154	26	89.7	89	2	Q83VF2_LACLC	Q83vf2	lactococcus	227	26	89.7	620	2	Q29198_ARCFU	Q29198	archaeoglob
155	26	89.7	105	2	Q64CV5_9ARCH	Q64cv5	uncultured	228	26	89.7	624	2	Q6FBJ6_ACIAD	Q6fbj6	acinetobact
156	26	89.7	109	2	Q9X292_THEMEA	Q9x292	thermotoga	229	26	89.7	626	2	Q8RM01_ACIAD	Q8rm01	acinetobact
157	26	89.7	145	2	Q5USA9_9PEZI	Q5usa9	monacrospor	230	26	89.7	685	1	MDL1_CANAL	P97998	candida alb
158	26	89.7	156	2	Q8DN20_STRPN	Q8dn20	streptococc	231	26	89.7	685	2	Q5A951_CANAL	Q5a951	candida alb
159	26	89.7	156	2	Q97N92_STRPN	Q97n92	streptococc	232	26	89.7	726	2	Q4Y7D6_PLACH	Q4y7d6	plasmodium
160	26	89.7	164	2	Q81Y15_BACAN	Q81y15	bacillus an	233	26	89.7	738	2	Q5A445_CANAL	Q5a445	candida alb
161	26	89.7	190	2	Q92WB8_RHIME	Q92wb8	rhizobium m	234	26	89.7	743	2	Q6BM34_DEBHA	Q6bm34	debaromyce
162	26	89.7	194	2	Q97G46_CLOAB	Q97g46	clostridium	235	26	89.7	771	2	Q4SD14_TETNG	Q4sd14	tetradodon n
163	26	89.7	196	2	Q6HVS9_BACAN	Q6hvs9	bacillus an	236	26	89.7	774	2	Q64777_ARATH	Q64777	arabidopsis
164	26	89.7	202	2	Q7P578_FUSNV	Q7p578	fusobacteri	237	26	89.7	787	2	Q4XMD0_PLACH	Q4xmd0	plasmodium
165	26	89.7	202	2	Q8RE19_FUSNN	Q8re19	fusobacteri	238	26	89.7	804	2	Q64770_ARATH	Q64770	arabidopsis
166	26	89.7	218	2	Q5CYB3_CRIPV	Q5cyb3	cryptospori	239	26	89.7	881	2	Q6BM22_DEBHA	Q6bm22	debaromyce
167	26	89.7	218	2	Q5CIV9_CRYHO	Q5civ9	cryptospori	240	26	89.7	911	2	Q6MUF5_MYCMS	Q6muf5	mycophasma
168	26	89.7	220	2	Q52ZT4_PEMVM	Q52zt4	peanut mott	241	26	89.7	957	2	Q7T3T7_OREMO	Q7t3t7	oreochromis
169	26	89.7	230	2	Q7RDM9_PLAYO	Q7rdm9	plasmodium	242	26	89.7	969	2	Q71953_9POTV	Q71953	dasheen mos
170	26	89.7	231	2	Q637W5_BACZ	Q637w5	bacillus ce	243	26	89.7	973	2	Q9VTH1_DROME	Q9vth1	drosophila
171	26	89.7	241	2	Q4XAZ2_PLACH	Q4xaz2	plasmodium	244	26	89.7	1094	2	Q4Q4Z7_LEIMA	Q4q4z7	leishmania
172	26	89.7	241	2	Q4MXQ0_BACCE	Q4mxq0	bacillus ce	245	26	89.7	1119	2	Q9LM79_ARATH	Q9lm79	arabidopsis
173	26	89.7	241	2	Q638P6_BACZ	Q638p6	bacillus ce	246	26	89.7	1273	2	Q9LM82_ARATH	Q9lm82	arabidopsis
174	26	89.7	241	2	Q6HG76_BACHK	Q6hg76	bacillus th	247	26	89.7	3099	1	POLG_PEMVM	POLG	p genome po
175	26	89.7	241	2	Q734P7_BACCL	Q734p7	bacillus ce	248	26	89.7	3191	2	Q912R2_9POTV	Q912r2	dasheen mos
176	26	89.7	241	2	Q81B59_BACCR	Q81b59	bacillus ce	249	26	89.7	3381	2	Q81DK4_PLAF7	Q81dk4	plasmodium
177	26	89.7	241	2	Q81N30_BACAN	Q81n30	bacillus an	250	25	86.2	20	2	Q8CYA3_STRRE6	Q8cya3	streptococc

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	164	2 Q73N39	TREDE
2	29	100.0	387	2 Q81PH5	BACCR
3	29	100.0	450	2 Q4TFP8	9SPHN
4	29	100.0	464	2 Q4S4T5	TETNG
5	29	100.0	606	2 Q91VU5	MOUSE
6	29	100.0	663	2 Q6RUU2	MOUSE
7	29	100.0	690	2 Q831B2	TROW8
8	29	100.0	698	2 Q83GW3	TROWT
9	29	100.0	1265	2 Q6ZQ91	MOUSE
10	29	100.0	1412	2 Q5F3M1	CHICK
11	28	96.6	88	2 Q4LBQ8	SODGL
12	28	96.6	183	2 Q9RQ09	BACTN
13	28	96.6	186	1 GL19	ORYSA
14	28	96.6	186	2 P93414	ORYSA
15	28	96.6	211	2 Q8C5V8	MOUSE
16	28	96.6	315	2 Q61C67	CAEBR
17	28	96.6	362	2 Q4HSJ7	CAMUP
18	28	96.6	372	2 Q6D7U3	ERWCT
19	28	96.6	373	2 Q7M9N5	WOLSU
20	28	96.6	382	2 Q9V7J0	DROME
21	28	96.6	387	2 Q9K110	BACCE
22	28	96.6	387	2 Q4MT39	BACCC
23	28	96.6	387	2 Q63DD4	BACCC
24	28	96.6	387	2 Q6HKU6	BACHK
25	28	96.6	387	2 Q73AP3	BACCI
26	28	96.6	387	2 Q81SK9	BACAN
27	28	96.6	410	2 Q6L2B4	PICTO
28	28	96.6	410	2 Q8C513	MOUSE
29	28	96.6	442	2 Q9PHV5	CAMJE
30	28	96.6	447	2 Q59243	PYROC
31	28	96.6	556	2 Q95893	DROME

Q9V7I9	DROSOPHILA	556	2	Q9V7I9	DROME
Q5HYE1	HOMO SAPIEN	703	2	Q5HYE1	HUMAN
Q6AG25	LEIFSONIA X	721	2	Q6AG25	LEIXX
Q9GQ82	DROSOPHILA	785	2	Q9GQ82	DROME
Q95786	HOMO SAPIEN	925	2	Q95786	HUMAN
Q5VYT1	HOMO SAPIEN	925	2	Q5VYT1	HUMAN
Q6Q899	MUS MUSCULUS	926	2	Q6Q899	MOUSE
Q9GLV6	SUS SCROFA	940	2	Q9GLV6	PIG
P29477	MUS MUSCULUS	1144	1	NOS2	MOUSE
Q5EXT3	MUS MUSCULUS	1144	2	Q5EXT3	MOUSE
Q8410	MUS MUSCULUS	1145	2	Q8410	MOUSE
Q6P6A0	MUS MUSCULUS	1145	2	Q6P6A0	MOUSE
Q68K27	CHILAMYDOMON	1384	2	Q68K27	CHLRE
Q7QEF0	ANOPHELES G	1408	2	Q7QEF0	ANOAG
Q5B164	DROSOPHILA	1443	2	Q5B164	DROME
Q7KTZ4	DROSOPHILA	1503	2	Q7KTZ4	DROME
Q8A6R7	BACTERIOIDES	1676	2	Q8A6R7	BACTN
Q9UC33	HOMO SAPIEN	33	2	Q9UC33	HUMAN
Q5EJJ6	GRAMPUS GRI	42	2	Q5EJJ6	GRAGR
Q56JJ7	TURSIOPS TR	42	2	Q56JJ7	TURTR
Q7M088	CAVIA PORCE	42	2	Q7M088	CAVPO
Q8WZ99	HOMO SAPIEN	52	2	Q8WZ99	HUMAN
Q29149	U ALZHEIMER	57	1	A4	URSWA
Q28280	C ALZHEIMER	58	1	A4	CANFA
Q28748	O ALZHEIMER	58	1	A4	RABIT
Q28053	B ALZHEIMER	58	1	A4	SHEEP
Q35463	CRICETULUS	59	1	A4	BOVIN
Q81H58	CHELYDRA SE	79	2	Q81H58	CHESE
Q7UPR1	RHODOPIRELL	113	2	Q7UPR1	RHOBA
Q98TZ9	ARABIDOPSIS	137	2	Q98TZ9	ARATH
Q6AKE9	DESBOS	152	2	Q6AKE9	DESPS
Q8BPV5	MOUSE	203	2	Q8BPV5	MOUSE
Q8VY56	ARATH	218	2	Q8VY56	ARATH
Q9SV79	ARATH	229	2	Q9SV79	ARATH
Q9XGY6	SIMMONDSIA	231	2	Q9XGY6	SIMCH
Q8U460	PYROCOCUS	352	2	Q8U460	PYFCH
Q8UUI8	BRARE	357	2	Q8UUI8	BRARE
Q8PPL1	XANAC	366	2	Q8PPL1	XANAC
Q67225	AQUAE	366	2	Q67225	AQUAE
Q8BPC7	MOUSE	380	2	Q8BPC7	MOUSE
Q4NSU7	THELERIA P	391	2	Q4NSU7	THEPA
Q5WPU9	LUTLO	391	2	Q5WPU9	LUTLO
Q5L117	GEOKA	399	2	Q5L117	GEOKA
Q4UY55	XANCP	403	2	Q4UY55	XANCP
Q8P597	XANCP	404	2	Q8P597	XANCP
Q9M1Q8	ARABIDOPSIS	404	2	Q9M1Q8	ARATH
Q89329	9POTV	428	2	Q89329	9POTV
Q7T910	9POTV	461	2	Q7T910	9POTV
Q8UU50	BRARE	470	2	Q8UU50	BRARE
Q52NV6	9POTV	472	2	Q52NV6	9POTV
Q7T911	9POTV	488	2	Q7T911	9POTV
Q7T912	9POTV	490	2	Q7T912	9POTV
Q5K4D4	9POTV	490	2	Q5K4D4	9POTV
Q5K4D5	9POTV	493	2	Q5K4D5	9POTV
Q5GVS5	XANOR	493	2	Q5GVS5	XANOR
Q93296	CHICK	508	2	Q93296	CHICK
Q9PVL1	CHICK	534	2	Q9PVL1	CHICK
Q919E7	BRARE	569	2	Q919E7	BRARE
Q50Z85	ENTHI	612	2	Q50Z85	ENTHI
Q4WBU2	ASPFU	615	2	Q4WBU2	ASPFU
Q5B2V4	EMENI	623	2	Q5B2V4	EMENI
Q7ZT1	BRARE	630	2	Q7ZT1	BRARE
Q98SG0	XENIA	678	2	Q98SG0	XENIA
Q5R477	PONPY	678	2	Q5R477	PONPY
Q6RH29	CANFA	695	2	Q6RH29	CANFA
Q56JK3	CANIS FAMIL	695	2	Q56JK3	CANFA
Q6GR78	MUS MUSCULUS	695	2	Q6GR78	MOUSE
Q9DJ78	GALLUS GALL	695	2	Q9DJ78	CHICK
Q98SF9	XENIA	695	2	Q98SF9	XENIA
Q7ZXQ0	XENIA	695	2	Q7ZXQ0	XENIA

Q9V7I9	DROSOPHILA	556	2	Q9V7I9	DROME
Q5HYE1	HOMO SAPIEN	703	2	Q5HYE1	HUMAN
Q6AG25	LEIFSONIA X	721	2	Q6AG25	LEIXX
Q9GQ82	DROSOPHILA	785	2	Q9GQ82	DROME
Q95786	HOMO SAPIEN	925	2	Q95786	HUMAN
Q5VYT1	HOMO SAPIEN	925	2	Q5VYT1	HUMAN
Q6Q899	MUS MUSCULUS	926	2	Q6Q899	MOUSE
Q9GLV6	SUS SCROFA	940	2	Q9GLV6	PIG
P29477	MUS MUSCULUS	1144	1	NOS2	MOUSE
Q5EXT3	MUS MUSCULUS	1144	2	Q5EXT3	MOUSE
Q8410	MUS MUSCULUS	1145	2	Q8410	MOUSE
Q6P6A0	MUS MUSCULUS	1145	2	Q6P6A0	MOUSE
Q68K27	CHILAMYDOMON	1384	2	Q68K27	CHLRE
Q7QEF0	ANOPHELES G	1408	2	Q7QEF0	ANOAG
Q5B164	DROSOPHILA	1443	2	Q5B164	DROME
Q7KTZ4	DROSOPHILA	1503	2	Q7KTZ4	DROME
Q8A6R7	BACTERIOIDES	1676	2	Q8A6R7	BACTN
Q9UC33	HOMO SAPIEN	33	2	Q9UC33	HUMAN
Q5EJJ6	GRAMPUS GRI	42	2	Q5EJJ6	GRAGR
Q56JJ7	TURSIOPS TR	42	2	Q56JJ7	TURTR
Q7M088	CAVIA PORCE	42	2	Q7M088	CAVPO
Q8WZ99	HOMO SAPIEN	52	2	Q8WZ99	HUMAN
Q29149	U ALZHEIMER	57	1	A4	URSWA
Q28280	C ALZHEIMER	58	1	A4	CANFA
Q28748	O ALZHEIMER	58	1	A4	RABIT
Q28053	B ALZHEIMER	58	1	A4	SHEEP
Q35463	CRICETULUS	59	1	A4	BOVIN
Q81H58	CHELYDRA SE	79	2	Q81H58	CHESE
Q7UPR1	RHODOPIRELL	113	2	Q7UPR1	RHOBA
Q98TZ9	ARABIDOPSIS	137	2	Q98TZ9	ARATH
Q6AKE9	DESBOS	152	2	Q6AKE9	DESPS
Q8BPV5	MOUSE	203	2	Q8BPV5	MOUSE
Q8VY56	ARATH	218	2	Q8VY56	ARATH
Q9SV79	ARATH	229	2	Q9SV79	ARATH
Q9XGY6	SIMMONDSIA	231	2	Q9XGY6	SIMCH
Q8U460	PYROCOCUS	352	2	Q8U460	PYFCH
Q8UUI8	BRARE	357	2	Q8UUI8	BRARE
Q8PPL1	XANAC	366	2	Q8PPL1	XANAC
Q67225	AQUAE	366	2	Q67225	AQUAE
Q8BPC7	MOUSE	380	2	Q8BPC7	MOUSE
Q4NSU7	THELERIA P	391	2	Q4NSU7	THEPA
Q5WPU9	LUTLO	391	2	Q5WPU9	LUTLO
Q5L117	GEOKA	399	2	Q5L117	GEOKA
Q4UY55	XANCP	403	2	Q4UY55	XANCP
Q8P597	XANCP	404	2	Q8P597	XANCP
Q9M1Q8	ARABIDOPSIS	404	2	Q9M1Q8	ARATH
Q89329	9POTV	428	2	Q89329	9POTV
Q7T910	9POTV	461	2	Q7T910	9POTV
Q8UU50	BRARE	470	2	Q8UU50	BRARE
Q52NV6	9POTV	472	2	Q52NV6	9POTV
Q7T911	9POTV	488	2	Q7T911	9POTV
Q7T912	9POTV	490	2	Q7T912	9POTV
Q5K4D4	9POTV	490	2	Q5K4D4	9POTV
Q5K4D5	9POTV	493	2	Q5K4D5	9POTV
Q5GVS5	XANOR	493	2	Q5GVS5	XANOR
Q93296	CHICK	508	2	Q93296	CHICK
Q9PVL1	CHICK	534	2	Q9PVL1	CHICK
Q919E7	BRARE	569	2	Q919E7	BRARE
Q50Z85	ENTHI	612	2	Q50Z85	ENTHI
Q4WBU2	ASPFU	615	2	Q4WBU2	ASPFU
Q5B2V4	EMENI	623	2	Q5B2V4	EMENI
Q7ZT1	BRARE	630	2	Q7ZT1	BRARE
Q98SG0	XENIA	678	2	Q98SG0	XENIA
Q5R477	PONPY	678	2	Q5R477	PONPY
Q6RH29	CANFA	695	2	Q6RH29	CANFA
Q56JK3	CANIS FAMIL	695	2	Q56JK3	CANFA
Q6GR78	MUS MUSCULUS	695	2	Q6GR78	MOUSE
Q9DJ78	GALLUS GALL	695	2	Q9DJ78	CHICK
Q98SF9	XENIA	695	2	Q98SF9	XENIA
Q7ZXQ0	XENIA	695	2	Q7ZXQ0	XENIA

THIS PAGE BLANK (USPTO)

R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90318
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <KUR>
A;Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI0000064436; GB:AE006641; NID:gl3814829; E
C;Genetics:
A;Gene: glpK-1

Query Match 86.2%; Score 25; DB 2; Length 294;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|:|
Db 184 KVVYFA 189

RESULT 75
D64240
methionyl-tRNA formyltransferase (EC 2.1.1.2.9) homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: D64240
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: D64240
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-311 <TIGR>
A;Cross-references: UNIPROT:P47605; UNIPARC:UPI000012AAEE; GB:U39721; GB:I43967; NID:gl
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: methionyl-tRNA formyltransferase; phosphoribosylglycinamide formyltransfe
C;Keywords: protein biosynthesis; transferase

Query Match 86.2%; Score 25; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 3 KIVFF 7

Search completed: December 29, 2005, 17:49:02
Job time : 19.9677 secs

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Verra, J.; et al.
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: AB1000; MUID:20175755; PMID:10710307

A;Accession: AB1056
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-262 <TET>
 A;Cross-references: UNIPROT:Q9JVB3; UNIPARC:UPI000000C4774; GB:AE002517; GB:AE002098; NID:10710307
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB1663

Query Match 86.2%; Score 25; DB 2; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 Db 4 KIVFF 8

RESULT 70
 AB1820
 conserved hypothetical protein NMA1921 [imported] - *Neisseria meningitidis* (strain Z2491)
 C;Species: *Neisseria meningitidis*
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: AB1820
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Kles, S.R.; Morel, P.; et al.
 Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A;Reference number: AB1775; MUID:20222556; PMID:10761919
 A;Accession: AB1820
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-269 <PAR>
 A;Cross-references: UNIPROT:Q9JTB4; UNIPARC:UPI000000C4CCE; GB:AL162757; GB:AL157959; NID:10761919
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: NMA1921

Query Match 86.2%; Score 25; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 Db 11 KIVFF 15

RESULT 71
 S05343
 NAD ADP-ribosyltransferase (EC 2.4.2.30) - *Rhodospirillum rubrum*
 C;Species: *Rhodospirillum rubrum*
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C;Accession: S05343; J05335
 R;Pitzmaurice, W.P.; Saari, L.L.; Lowery, R.G.; Ludden, P.W.; Roberts, G.P.
 Mol. Gen. Genet. 218, 340-347, 1989
 A;Title: Genes coding for the reversible ADP-ribosylation system of dinitrogenase reductase in *Rhodospirillum rubrum*.
 A;Reference number: JQ0446; MUID:89384461; PMID:2506427
 A;Accession: S05343
 A;Molecule type: DNA
 A;Residues: 1-276 <FIT>
 A;Cross-references: UNIPROT:P14299; UNIPARC:UPI0000129874; EMBL:X16187; NID:G46389; PIDN:10761919
 A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by sequencing.
 C;Genetics:
 A;Gene: drat
 A;Start codon: TTG
 C;Superfamily: Azospirillum NAD-nitrogenase ADP-D-ribosyltransferase
 C;Keywords: Glycosyltransferase; NAD; pentosyltransferase
 Query Match 86.2%; Score 25; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIVFF 5
 Db 243 KIVFF 247

RESULT 72
 AI2038
 carboxyphosphoenolpyruvate phosphonmutase [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp. PCC 7120
 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AI2038
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, S.; et al.
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AI2038
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-287 <KUR>
 A;Cross-references: UNIPROT:Q8YVW0; UNIPARC:UPI000000CE22D; GB:BA000019; PIDN:BA073562.1;
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: all1863
 C;Superfamily: carboxyphosphoenolpyruvate phosphonmutase

Query Match 86.2%; Score 25; DB 2; Length 287;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 Db 228 KIVFF 232

RESULT 73
 D69355
 hypothetical protein AF0844 - *Archaeoglobus fulgidus*
 C;Species: *Archaeoglobus fulgidus*
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: D69355
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; et al.
 Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; et al.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: D69355
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-293 <KLE>
 A;Cross-references: UNIPROT:O29414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; NID:9389475

Query Match 86.2%; Score 25; DB 2; Length 293;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 140 KLVFFA 145

RESULT 74
 H90318
 glycerol kinase (glpK-1) [imported] - *Sulfolobus solfataricus*
 C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: H90318

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	208 KIVFF 212
RESULT 65	
C64666	
glutamine transport protein glnQ - Helicobacter pylori (strain 26695)	
C:Species: Helicobacter pylori	
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004	
C:Accession: C64666	
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L. Nature 388, 539-547, 1997	
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.	
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.	
A:Reference number: A64520; MUID:97394467; PMID:9252185	
A:Accession: C64666	
A>Status: nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-248 <TOM>	
A:Cross-references: UNIPROT:Q25785; UNIPARC:UPI0000D31A1; GB:AE000623; GB:AE000511; NID	
A:Experimental source: strain 26695	
C:Genetics:	
A:Gene: glnQ; HPI171	
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology	
C:Keywords: ATP; glutamine transport; nucleotide binding; P-loop	
F:20-215/Domain: ATP-binding cassette homology <ABC>	
F:37-44/Region: nucleotide-binding motif A (P-loop)	
F:160-164/Region: nucleotide-binding motif B	
Query Match 86.2%; Score 25; DB 2; Length 248;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	208 KIVFF 212
RESULT 66	
T28170	
hypothetical protein ORF9 - Melanoplus sanguinipes entomopoxvirus (strain Tuscon)	
C:Species: Melanoplus sanguinipes entomopoxvirus	
A:Variety: strain Tuscon	
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004	
C:Accession: T28170	
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.	
J. Virol. 73, 533-552, 1999	
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.	
A:Reference number: Z20484; MUID:99102612; PMID:9847359	
A:Accession: T28170	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: DNA	
A:Residues: 1-254 <AFO>	
A:Cross-references: UNIPROT:Q9YW83; UNIPARC:UPI00000F390B; EMBL:AF063866; NID:94049647;	
A:Experimental source: strain Tuscon	
C:Genetics:	
A:Note: MSV009	
Query Match 86.2%; Score 25; DB 2; Length 254;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	95 KIVFF 99
RESULT 67	

AC1561	
conserved hypothetical protein homolog lml028 [imported] - Listeria innocua (strain Cl)	
C:Species: Listeria innocua	
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C:Accession: AC1561	
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker	
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.	
D.; Jones, L.M.; Karst, U.	
Science 294, 849-852, 2001	
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma	
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,	
A:Title: Comparative genomics of Listeria species.	
A:Reference number: AB1077; MUID:21537279; PMID:11679669	
A:Accession: AC1561	
A>Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-256 <GLA>	
A:Cross-references: UNIPROT:Q92C23; UNIPARC:UPI00000CC42D; GB:AL592022; PIDN:CAC96259.1;	
A:Experimental source: strain Clp11262	
C:Genetics:	
A:Gene: lml028	
Query Match 86.2%; Score 25; DB 2; Length 256;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	3 KIVFF 7
RESULT 68	
AE1203	
conserved hypothetical proteins homolog lml029 [imported] - Listeria monocytogenes (st	
C:Species: Listeria monocytogenes	
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C:Accession: AE1203	
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke	
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.	
D.; Jones, L.M.; Karst, U.	
Science 294, 849-852, 2001	
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M	
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland	
A:Title: Comparative genomics of Listeria species.	
A:Reference number: AB1077; MUID:21537279; PMID:11679669	
A:Accession: AE1203	
A>Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-256 <GLA>	
A:Cross-references: UNIPROT:Q8Y888; UNIPARC:UPI0000055436; GB:NC_003210; PIDN:CAC99107.	
A:Experimental source: strain EGD-e	
C:Genetics:	
A:Gene: lml029	
Query Match 86.2%; Score 25; DB 2; Length 256;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	3 KIVFF 7
RESULT 69	
AB1056	
conserved hypothetical protein NMB1663 [imported] - Neisseria meningitidis (strain MC58	
C:Species: Neisseria meningitidis	
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004	
C:Accession: AB1056	
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.	
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.	
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.	
Science 287, 1809-1815, 2000	

Db 185 KIAFFA 190
|||
|||

RESULT 60
A75004
hypothetical protein PAB1033 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A75004
R:anonymous, Genoscope
A:Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: A75004
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <KAW>
A:Cross-references: UNIPROT:Q9UYE1; UNIPARC:UPI000006347D; GB:AJ248288; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1033

Query Match 86.2%; Score 25; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 109 KIVFF 113

RESULT 61
G72322
glutaredoxin-related protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: G72322
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72322
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <ARN>
A:Cross-references: UNIPROT:Q9WZX2; UNIPARC:UPI00000D396F; GB:AE001753; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0868

Query Match 86.2%; Score 25; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 25 KIVFF 29

RESULT 62
T47768
hypothetical protein F24I3.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47768
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A:Reference number: 224475
A:Accession: T47768
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-222 <NTA>
A:Cross-references: UNIPROT:Q9M1J2; UNIPARC:UPI000000C63B; EMBL:AL138655
A:Experimental source: cultivar Columbia; BAC clone F24I3
C:Genetics:
A:Map position: 3
A:Introns: 84/3; 143/3; 181/3
A:Note: F24I3.160
C:Superfamily: DNA-directed RNA polymerase, RPBS subunit

Query Match 86.2%; Score 25; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 86 KIVFF 90

RESULT 63
A90260
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: A90260
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.;
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90260
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <KUR>
A:Cross-references: UNIPROT:Q97Z59; UNIPARC:UPI0000064342; GB:AE006641; NID:G13814264; P
C:Genetics:
A:Gene: SS01074

Query Match 86.2%; Score 25; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 4 KIVFF 8

RESULT 64
F71849
amino acid ABC transporter, ATP-binding protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: F71849
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: F71849
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <ARN>
A:Cross-references: UNIPROT:Q9ZK44; UNIPARC:UPI00000D36EE; GB:AE001537; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1098
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
F;20-215/Domain: ATP-binding cassette homology <ABC>

Query Match 86.2%; Score 25; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

A;Molecule type: DNA
A;Residues: 1-143 <WED>
A;Cross-references: UNIPARC:UPI0000110C55; EMBL:273155; NID:g1360250; PIDN:CAA97502.1; E
A;Note: experimental source strain S288C
R;Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence of a 37 kb DNA fragment from chromosome XII of *Saccharomyces cerevisiae*
A;Reference number: S50950
A;Accession: S50970
A;Molecule type: DNA
A;Residues: 'MWGKKFIRSGNWKFLCS', 6-143 <WEW>
A;Cross-references: UNIPARC:UPI000069A87; EMBL:247973; NID:g642313; PIDN:CAA88007.1; PI
A;Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C;Genetics:
A;Gene: SGD:COF1; MIPS:YLL050C
A;Cross-references: SGD:S0003973; MIPS:YLL050C
A;Map position: 12L
A;Introns: 5/2
C;Superfamily: cofilin
C;Keywords: actin binding
F;88-118/Region: actin binding #status predicted

Query Match 86.2%; Score 25; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFP 5
|:|:|:
82 KIVFFP 86

Db

RESULT 57
B90157
hypothetical protein SSO0168 [imported] - *Sulfolobus solfataricus*
C;Species: *Sulfolobus solfataricus*
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
A;Accession: B90157
R;She, Q.; Singh, R. K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M. J.; Chan-
Jong, I.; Jeffries, A. C.; Kozera, C. J.; Medina, N.; Peng, X.; Thi-Ngoc, H. P.; Redder, R.
arrett, R. A.; Ragan, M. A.; Sensen, C. W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: *Sulfolobus solfataricus* complete genome.
A;Reference number: A99139
A;Accession: B90157
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <KUR>
A;Cross-references: UNIPROT:Q980V9; UNIPARC:UPI00000641A8; GB:AE006641; NID:g13813299; E
C;Genetics:
A;Gene: SSO0168

Query Match 86.2%; Score 25; DB 2; Length 193;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFP 6
|:|:|:
117 KIVFFP 122

Db

RESULT 58
B81256
phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81256
R;Parkhill, J.; Wren, B. W.; Mungall, K.; Ketley, J. M.; Churcher, C.; Basham, D.; Chillin
C. W.; Quail, M.; Rajandream, M. A.; Rutherford, K. M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81256
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-207 <PAR>
A;Cross-references: UNIPROT:Q9PW71; UNIPARC:UPI000012C76D; GB:AL139079; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: hisI; Cj1604
C;Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein
C;Keywords: hydrolase

Query Match 86.2%; Score 25; DB 2; Length 207;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFP 6
|:|:|:
51 KIVFFP 56

Db

RESULT 59
A35617
HDEL receptor ERD2 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: 26K endoplasmic reticulum retention receptor; ER lumen protein-retain
C;Species: *Saccharomyces cerevisiae*
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: A35617; S45774; S50290; S42504
R;Semenza, J. C.; Hardwick, K. G.; Dean, N.; Pelham, H. R. B.
Cell 61, 1349-1357, 1990
A;Title: ERD2, a yeast gene required for the receptor-mediated retrieval of luminal ER f
A;Reference number: A35617; MUID:90304893; PMID:2194670
A;Accession: A35617
A;Molecule type: DNA
A;Residues: 1-219 <SEM>
A;Cross-references: UNIPROT:P18414; UNIPARC:UPI000012A121; GB:M34777; NID:g171466; PIDN
R;Goffeau, A.; Jonniaux, J. L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45745
A;Accession: S45774
A;Molecule type: DNA
A;Residues: 1-219 <GOF>
A;Cross-references: UNIPARC:UPI000012A121; EMBL:Z35801; NID:g536054; PIDN:CAA84860.1; P
R;de Wergifosse, P.; Jacques, B.; Jonniaux, J. L.; Purnelle, B.; Skala, J.; Goffeau, A.
Yeast 10, 1489-1496, 1994
A;Title: The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome I
NA-binding protein.
A;Reference number: S50284; MUID:95176707; PMID:7871888
A;Accession: S50290
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 64-219 <DEF>
A;Cross-references: UNIPARC:UPI0000168A10; EMBL:X78214; NID:g463261; PIDN:CAA55054.1; P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
C;Genetics:
A;Gene: SGD:ERD2; MIPS:YBL040C
A;Cross-references: SGD:S0000136; MIPS:YBL040C
A;Map position: 2L
A;Introns: 8/1
C;Function:
A;Description: achieves retention of proteins specific to the lumen of the endoplasmic
usually KDEL in animal cells and HDEL in budding yeasts
C;Superfamily: KDEL receptor
C;Keywords: Golgi apparatus; protein trafficking; sorting signal recognition; transmembr
F;4-20/Domain: transmembrane #status predicted <TM1>
F;38-54/Domain: transmembrane #status predicted <TM2>
F;61-82/Domain: transmembrane #status predicted <TM3>
F;99-115/Domain: transmembrane #status predicted <TM4>
F;122-138/Domain: transmembrane #status predicted <TM5>
F;186-202/Domain: transmembrane #status predicted <TM6>

Query Match 86.2%; Score 25; DB 1; Length 219;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFP 6

A:Gene: moad

A:Map position: 17.7 min
 A:Complex: heterodimer with D chain (PIR:S31883) [validated, MUID:93293873]
 C:Function:
 A:Description: required for the addition of the Mo-binding dithiolene group to a molybdo
 C:Superfamily: Molybdopter in biosynthesis sulfur carrier protein
 C:Keywords: heterodimer; molybdopter in biosynthesis
 F:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 86.2%; Score 25; DB 2; Length 81;
 Best Local Similarity 66.7%; Pred. No. 56;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|
 Db 3 KVLFFA 8

RESULT 53

AC0598
 molybdopter in converting factor, chain 1 [imported] - Salmonella enterica subsp. enteric
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
 C:Accession: AC0598
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connerston, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AC0598
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-83 <PAR>
 A:Cross-references: UNIPARC:UPI000005A0EA; GB:AL513382; PIDN:CAD05253.1; PID:gl6502022;
 C:Genetics:
 A:Gene: STY0839
 C:Superfamily: Molybdopter in biosynthesis sulfur carrier protein

Query Match 86.2%; Score 25; DB 2; Length 83;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|
 Db 5 KVLFFA 10

RESULT 54

C64516
 hypothetical protein MJEC503 - Methanococcus jannaschii plasmid pURB801
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: C64516
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 Reisch, C.I.; Overbeek, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: C64516
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <BUL>
 A:Cross-references: UNIPROT:Q60302; UNIPARC:UPI000013C25B; GB:L77119; NID:gl500688; TIGR
 C:Genetics:
 A:Map position: ECSREV5174-4848
 A:Genome: plasmid
 A:Note: this stable 16-kilobase pair plasmid is also designated ECS (small extrachromoso
 C:Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|
 Db 2 KILFFA 7

RESULT 55

B70457
 gliding motility protein MglA - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: B70457
 R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
 V.

Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: B70457

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-141 <AQF>

A:Cross-references: UNIPROT:O67684; UNIPARC:UPI000005670A; GB:AE000757; GB:AE000657; NID
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: mglA2
 C:Superfamily: gliding motility protein

Query Match 86.2%; Score 25; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 |:|:|
 Db 4 KIVFF 8

RESULT 56

A44397
 cofillin - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein L0595; protein YLL050C
 C:Species: Saccharomyces cerevisiae
 C:Date: 31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C:Accession: A44397; B44397; JN0529; S64802; S50970; S31309; S36087
 R:Moore, A.L.; Janney, P.A.; Louie, K.A.; Drubin, D.G.
 J. Cell Biol. 120, 421-435, 1993
 A:Title: Cofilin is an essential component of the yeast cortical cytoskeleton.
 A:Reference number: A44397; MUID:93132073; PMID:8421056
 A:Accession: A44397
 A:Molecule type: DNA
 A:Residues: 1-143 <MOO>
 A:Cross-references: UNIPROT:Q03048; UNIPARC:UPI0000110C55; EMBL:Z14971; NID:g3563; PIDN:
 A:Note: sequence extracted from NCBI backbone (NCBIN:122683, NCBI:P:122684)

A:Accession: B44397

A:Molecule type: protein

A:Residues: 43-56; 83-96, 'X', 98; 106-129, 'DS', 132-141 <MO2>

A:Cross-references: UNIPARC:UPI0000173E79; UNIPARC:UPI0000173E7A; UNIPARC:UPI0000173E7B

A:Note: sequence extracted from NCBI backbone

R:Ida, K.; Moriyama, K.; Matsumoto, S.; Kawasaki, H.; Nishida, E.; Yahara, I.

Gene 124, 115-120, 1993

A:Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mammalian

A:Reference number: JN0529; MUID:93178959; PMID:8440472

A:Accession: JN0529

A:Molecule type: DNA

A:Residues: 1-143 <IID>

A:Cross-references: UNIPARC:UPI0000110C55; GB:DL3230; NID:g287599; PIDN:BAA02514.1; PID:

R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64792

A:Accession: S64802

A;Cross-references: UNIPARC:UPI0000139223; GB:AE001447; GB:AE001439; NID:94154583; PIDN:
A;Experimental source: strain J99
C;Genetics:
A;Gene: HP0085; jhp0078

Query Match 86.2%; Score 25; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|||||
Db 16 KIVFF 20

RESULT 49
F90736
molybdopterin biosynthesis protein D chain [imported] - Escherichia coli (strain O157:H7
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C;Accession: F90736
R;Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90736
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <HAY>
A;Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; GB:BA000007; PIDN:BA834285.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0862
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 86.2%; Score 25; DB 2; Length 81;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 6
|||||
Db 3 KVLFFA 8

RESULT 50
A82251
molybdenum cofactor biosynthesis protein D VC1027 [imported] - Vibrio cholerae (strain N
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2004
C;Accession: A82251
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <HEI>
A;Cross-references: UNIPROT:Q9KVT8; UNIPARC:UPI00000C2E5B; GB:AE004184; GB:AE003852; NID
F;81/Modified site: 1-thioglycine (Gly) #status predicted
C;Genetics:
A;Gene: VC1027
A;Map position: 1
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 86.2%; Score 25; DB 2; Length 81;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 6

Db 3 KVLFFA 8
|.:|||
|.:|||

RESULT 51
G85586
molybdopterin biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: G85586
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouais, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85586
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <STO>
A;Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; GB:AE005174; NID:912513773; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: moad
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 86.2%; Score 25; DB 2; Length 81;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 6
|.:|||
Db 3 KVLFFA 8

RESULT 52
H64814
molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)
N;Alternate names: moaD protein; molybdopterin-converting factor 10K chain; molybdopterin
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: H64814; S35001; A46585; S31882
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64814
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-81 <BLAT>
A;Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE0000181; GB:U00096; NID:
A;Experimental source: strain K-12, substrain MG1655
R;Kiviers, S.L.; McNamee, E.; Blasco, F.; Giordano, G.; Boxer, D.H.
Mol. Microbiol. 8, 1071-1081, 1993
A;Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required
A;Reference number: S34998; MUID:93368423; PMID:8361352
A;Accession: S35001
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-44, 'R', 46-81 <RIV>
A;Cross-references: UNIPARC:UPI000016F2FD; EMBL:X70420; NID:942007; PIDN:CAA49864.1; PI
A;Experimental source: strain K12
R;Pitterle, D.M.; Rajagopalan, K.V.
J. Biol. Chem. 268, 13499-13505, 1993
A;Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and charac
A;Reference number: A46585; MUID:93293873; PMID:8514782
A;Accession: A46585
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8, 'E', 10-15 <PIT>
A;Cross-references: UNIPARC:UPI0000178EC3
A;Note: sequence extracted from NCBI backbone (NCBIP:134491)
C;Genetics:

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: P96639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-774 <STO>
A;Cross-references: UNIPROT:O64777; UNIPARC:UPI00000A26B1; GB:AE005173; NID:g3056587; PI
C;Genetics:
A;Gene: T1P9.8
A;Map position: 1
C;Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-specific

Query Match 89.7%; Score 26; DB 2; Length 774;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 5 RIVFFA 10

RESULT 45
A86340
protein F2D10.24 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86340
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86340
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1119 <STO>
A;Cross-references: UNIPROT:Q9LM79; UNIPARC:UPI00000A3B0B; GB:AE005172; NID:g8886947; PI
C;Genetics:
A;Gene: F2D10.24
A;Map position: 1

Query Match 89.7%; Score 26; DB 2; Length 1119;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 1045 KILFFA 1050

RESULT 46
JU0330
hypothetical protein, 2.4K (lytA 5' region) - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JU0330
R;Diaz, E.; Garcia, J.L.
Gene 90, 157-162, 1990
A;Title: Characterization of the transcription unit encoding the major pneumococcal auto
A;Reference number: JU0329; MUID:90337339; PMID:1974230
A;Accession: JU0330
A;Molecule type: DNA

A;Residues: 1-20 <DIP>
A;Cross-references: UNIPROT:Q8CYA3; UNIPARC:UPI000000E477A
A;Experimental source: strain M31
C;Genetics:
A;Start codon: GTG

Query Match 86.2%; Score 25; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:|||||
Db 14 KIVFF 18

RESULT 47

A99091

hypothetical protein spr1755 [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C;Accession: A99091

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: A99091

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-20 <KUR>

A;Cross-references: UNIPROT:Q8CYA3; UNIPARC:UPI000000E477A; GB:AE007317; PIDN:AAL00558.1;
C;Genetics:
A;Gene: spr1755

Query Match

86.2%; Score 25; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:|||||
Db 14 KIVFF 18

RESULT 48

E64530

hypothetical protein (HP0085, jhp0078) - Helicobacter pylori

C;Species: Helicobacter pylori

A;Variety: strains J99, 26695

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: E64530; A71976

R;Tomb, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.;

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: E64530

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-62 <TON>

A;Cross-references: UNIPROT:O24912; UNIPARC:UPI0000139223; GB:AE000530; GB:AE000511; NID

A;Experimental source: strain 26695

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: A71976

A;Molecule type: DNA

A;Residues: 1-62 <ARN>

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH1271

C;Superfamily: yceG protein

Query Match 89.7%; Score 26; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||:
25 KIVFFS 30

Db

RESULT 40

ES6038 Probable LPS biosynthesis enzyme waal [imported] - Escherichia coli (strain O157:H7, sub

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: E86038

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: E86038

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-402 <STO>

A;Cross-references: UNIPROT:Q92IT8; UNIPARC:UPI00000D00DF; GB:AE0051174; NID:gl2518378; F

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: waal

Query Match 89.7%; Score 26; DB 2; Length 402;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||:
126 KIVFFS 131

Db

RESULT 41

D91191 lipid A-core surface polymer ligase [imported] - Escherichia coli (strain O157:H7, sub

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: D91191

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: D91191

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-402 <HAY>

A;Cross-references: UNIPROT:Q92IT8; UNIPARC:UPI00000D00DF; GB:BA000007; PIDN:BA037923.1;

A;Experimental source: strain O157:H7, substrain RMD 0509952

C;Genetics:

A;Gene: ECs4500

Query Match 89.7%; Score 26; DB 2; Length 402;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||:
126 KIVFFS 131

Db

RESULT 42

A70146 tyrosine-tRNA ligase (EC 6.1.1.1) tyrS - Lyme disease spirochete

N;Alternate names: tyrosyl-tRNA synthetase

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C;Accession: A70146

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White

son, D.; Peterson, J.; Karlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: A70146

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-405 <KLB>

A;Cross-references: UNIPROT:O51343; UNIPARC:UPI000005745B; GB:AE001142; GB:AE000783; NID

A;Experimental source: strain B31

C;Superfamily: tyrosine-tRNA ligase

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 89.7%; Score 26; DB 2; Length 405;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||:
31 KIVFFA 36

Db

RESULT 43

H69382

ABC transporter, ATP-binding protein homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004

C;Accession: H69382

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodeso

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69382

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-620 <KLB>

A;Cross-references: UNIPROT:O29198; UNIPARC:UPI0000056E80; GB:AE001029; GB:AE000782; NI

C;Keywords: ATP; nucleotide binding; P-loop

F;428-612/Domain: ATP-binding cassette homology <ABC>

F;445-452/Region: nucleotide-binding motif A (P-loop)

Query Match 89.7%; Score 26; DB 2; Length 620;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||:
59 KILFFA 64

Db

RESULT 44

F96639

protein TIF9.8 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004

C;Accession: F96639

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Gene: CESP:C02E7.12
A:Map position: 5
A:Introns: 45/2; 146/3

Query Match 89.7%; Score 26; DB 2; Length 277;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||:|
Db 112 KIVFFA 117

RESULT 35

T26245

hypothetical protein W06G6.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26245

R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z20180

A:Accession: T26245

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-300 <WIL>

A:Cross-references: UNIPROT:Q9XU61; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN:CAB05641.1;

A:Experimental source: clone W06G6

C:Genetics:

A:Gene: CESP:W06G6.6

A:Map position: 5

A:Introns: 171/2; 204/2

Query Match 89.7%; Score 26; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||:|
Db 281 KIVFFA 286

RESULT 36

H71729

hypothetical protein RP189 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C:Accession: H71729

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A>Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71729

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-321 <AND>

A:Cross-references: UNIPROT:Q9ZDX5; UNIPARC:UPI0000139421; GB:AJ235270; GB:AJ235269; NID

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: RP189

C:Superfamily: Rickettsia prowazekii hypothetical protein RP189

Query Match 89.7%; Score 26; DB 2; Length 321;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||:|
Db 178 KIVFFA 183

RESULT 37

T26247

hypothetical protein W06G6.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26247

R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z20180

A:Accession: T26247

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-349 <WIL>

A:Cross-references: UNIPROT:Q9XU59; UNIPARC:UPI0000061209; EMBL:Z83129; PIDN:CAB05643.1;

A:Experimental source: clone W06G6

C:Genetics:

A:Gene: CESP:W06G6.8

A:Map position: 5

A:Introns: 172/2; 210/3; 247/2

Query Match 89.7%; Score 26; DB 2; Length 349;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||:|
Db 324 KIVFFA 329

RESULT 38

AH2097

sorbitol dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

C>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AH2097

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2097

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-352 <KUR>

A:Cross-references: UNIPROT:Q8YUK9; UNIPARC:UPI000000CE3D5; GB:BA000019; PIDN:BA074034.1;

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr2335

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||:|
Db 262 KIVFFA 267

RESULT 39

G83808

hypothetical protein BH1271 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: G83808

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira,

Nucleic Acids Res. 28, 4317-4331, 2000

A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: G83808

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-382 <STO>

A:Cross-references: UNIPROT:Q9KDE2; UNIPARC:UPI000000C3B44; GB:AP001511; GB:BA000004; NID

RESULT 30
A:Accession: A95895
A:Title: probable permease protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95895
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: A95895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <KUR>
A:Cross-references: UNIPROT:Q92WB8; UNIPARC:UPI00000CB514; GB:AL591985; PIDN:CAC48825.1;
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20443
A:Genome: plasmid

Query Match 89.7%; Score 26; DB 2; Length 190;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 116 KIVFFA 121

RESULT 31
B97211
A:Title: uncharacterized conserved membrane protein CAC2524 [imported] - Clostridium acetobutylic
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97211
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <KUR>
A:Cross-references: UNIPROT:Q97G46; UNIPARC:UPI00000CA55C; GB:AE001437; PIDN:AAK80477.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2524

Query Match 89.7%; Score 26; DB 2; Length 194;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 165 KIVFFA 170

RESULT 32
T32514
A:Title: hypothetical protein C44B12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004

C:Accession: T32514
R:Tin-Wollam, A.
A:Description: The sequence of C. elegans cosmid C44B12.
A:Reference number: Z21183
A:Accession: T32514
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-247 <TIN>
A:Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AAB88324.
A:Experimental source: strain Bristol N2; clone C44B12
C:Genetics:
A:Gene: CESP:C44B12.1
A:Map position: 4
A:Introns: 28/3; 82/1; 164/1; 192/1
Query Match 89.7%; Score 26; DB 2; Length 247;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 224 KIVFFS 229

RESULT 33
D82405
A:Title: transcription regulator LuxR family VCA0888 [imported] - Vibrio cholerae (strain N16961
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
A:Accession: D82405
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, I.;
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <HEI>
A:Cross-references: UNIPROT:Q9KL60; UNIPARC:UPI00000C36AA; GB:AE004416; GB:AE003853; NI
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0888
A:Map position: 2

Query Match 89.7%; Score 26; DB 2; Length 253;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 51 KIVFFS 56

RESULT 34
T31855
A:Title: hypothetical protein C02E7.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
A:Accession: T31855
R:Fulton, B.; Wohldmann, P.
Submitted to the EMBL Data Library, June 1998
A:Description: The sequence of C. elegans cosmid C02E7.
A:Reference number: Z21093
A:Accession: T31855
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-277 <PUL>
A:Cross-references: UNIPARC:UPI000017B71A; EMBL:AF016446; PIDN:AAC24170.1; GSPDB:GN0002
A:Experimental source: strain Bristol N2; clone C02E7
C:Genetics:

A;Accession: S30236
 A;Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A;Residues: 1-1016 <WUM>
 A;Cross-references: UNIPROT:Q05912; UNIPARC:UPI00000ECC69; EMBL:X68509; NID:G288233; PID
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992
 C;Superfamily: tobacco etch virus genome polyprotein
 C;Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein;
 P;9-61/Product: VPg protein #status predicted <VPG>
 P;62-494/Product: nuclear inclusion protein a #status predicted <NIA>
 P;495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>
 P;1011-1016/Product: coat protein (fragment) #status predicted <COP>
 P;125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 93.1%; Score 27; DB 2; Length 1016;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 837 KLVFFA 842
 :|||||
 :|||||

RESULT 26
 E64214
 Hypothetical protein homolog MG131 - Mycoplasma genitalium
 C;Species: Mycoplasma genitalium
 C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: E64214
 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
 C.A.; Venter, J.C.
 Science 270, 397-403, 1995
 A;Title: The minimal gene complement of Mycoplasma genitalium.
 A;Reference number: A64200; MUID:96026346; PMID:7569993
 A;Accession: E64214
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A;Residues: 1-74 <TIGR>
 A;Cross-references: UNIPROT:P47377; UNIPARC:UPI000013931D; GB:U39691; GB:L43967; NID:g10
 A;Experimental source: strain G-37
 C;Genetics:
 A;Genetic code: SGC3

Query Match 89.7%; Score 26; DB 2; Length 74;
 Best Local Similarity 83.3%; Pred. No. 30;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 34 KLVFFA 39
 :|||||
 :|||||

RESULT 27
 B72213
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: B72213
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
 C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:95287316; PMID:10360571
 A;Accession: B72213
 A;Status: preliminary
 A:Molecule type: DNA
 A;Residues: 1-109 <ARN>
 A;Cross-references: UNIPROT:Q9X292; UNIPARC:UPI00000C120B; GB:AE001815; GB:AE000512; NID
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TM1771

C;Superfamily: Bacillus subtilis conserved hypothetical protein yqhY

Query Match 89.7%; Score 26; DB 2; Length 109;
 Best Local Similarity 83.3%; Pred. No. 43;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 19 KIVFFA 24
 :|||||
 :|||||

RESULT 28

H95252
 PTS system, IIB component [imported] - Streptococcus pneumoniae (strain TIGR4)
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C;Accession: H95252
 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: H95252
 A;Status: preliminary
 A:Molecule type: DNA
 A;Residues: 1-156 <KUR>
 A;Cross-references: UNIPROT:Q97N92; UNIPARC:UPI0000051B4E; GB:AE005672; PIDN:AAK76217.1;
 A;Experimental source: strain TIGR4
 C;Genetics:
 A;Gene: SP2163

C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 89.7%; Score 26; DB 2; Length 156;
 Best Local Similarity 83.3%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 56 KIVFFS 61
 :|||||
 :|||||

RESULT 29

F98117

hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 23-Oct-2001 #text_change 09-Jul-2004

C;Accession: F98117

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: F98117

A;Status: preliminary

A:Molecule type: DNA

A;Residues: 1-156 <KUR>

A;Cross-references: UNIPROT:Q8DN20; UNIPARC:UPI00000E3754; GB:AE007317; PIDN:AAI00771.1;

C;Genetics:

A;Gene: PTS-EII

C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 89.7%; Score 26; DB 2; Length 156;
 Best Local Similarity 83.3%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 56 KIVFFS 61
 :|||||
 :|||||

R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I9562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:9236720; PIDN:AAB19991.1; PID:
R;Kamino, K.; Orr, H.T.; Payami, H.; Wajsmann, E.M.; Alonso, M.E.; Pullet, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAM1>
A;Cross-references: UNIPARC:UPI000011F7EB; GB:S45135; NID:9257377; PIDN:AAB23645.1; PID:
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:9257379; PIDN:AAB23646.1; PID:
A;Experimental source: familial Alzheimer disease family Lit
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: UNIPARC:UPI000002A2P2; GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:9
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <ROB>
A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:9178539; PIDN:AAA51722.1; PID:
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <COL>
A;Cross-references: UNIPARC:UPI00001420B5; GB:M15533; NID:9178706; PIDN:AAA35540.1; PID:
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.P.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TANI>
A;Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYP>
A;Cross-references: UNIPARC:UPI0000035AB0
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.P.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat

A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA3
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:928816; PIDN:CAA30041.1; PID:
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtoi
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three i
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288, 'V', 365-770 <VIT2>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
A;Cross-references: UNIPARC:UPI0000174094
R;Zain, S.B.; Salim, M.; Chou, W.G.; Saidel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA

Query Match 93.1%; Score 27; DB 1; Length 770;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 687 KLVFFA 692

RESULT 25
S30236
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)
N;Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC
C;Species: zucchini yellow mosaic virus, ZYMV
A;Variety: strain Singapore
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S30236
R;Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.
Nucleic Acids Res. 21, 1317, 1993
A;Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore
A;Reference number: S30236; MUID:93219099; PMID:8464715

A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A;Cross-references: UNIPARC:UPI00001777FD
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
PEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Cross-references: UNIPARC:UPI00001777FE
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TM>

Query Match 93.1%; Score 27; DB 2; Length 695;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 612 KLVFFA 617

RESULT 23
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 93.1%; Score 27; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 664 KLVFFA 669

RESULT 24
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
A;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor
N;Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
C;Keywords: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
466; A28583; A29302; A50805; J00038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Baynes, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288, 'V', 365-770 <LEM1>
A;Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14, 'VM', 17-288, 'V', 365-770 <LEM2>
A;Cross-references: UNIPARC:UPI000016A6FC; EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:
A;Note: alternative splice form APP(695)
R;La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAP>
A;Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:G341202; PIDN:AAAC13
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Cross-references: UNIPARC:UPI0000148176
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMPVPAFWKVGVR' <YOS2>
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G178618; PIDN:AAA51727.1; PID:
A;Note: a mutation with 693-Gln is presented

C;Accession: F70399
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70399
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <AQF>
A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:g2983612; PI
A;Experimental source: strain VF5
C;Genetics:
C;Superfamily: [NifE]-hydrogenase maturation factor, HypD type
Query Match 93.1%; Score 27; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 141 KIVFFA 146
RESULT 19
T48008
Hypothetical protein T17J13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: T48008
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482
A;Accession: T48008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <RIE>
A;Cross-references: UNIPROT:Q9M108; UNIPARC:UPI00000488B7; EMBL:AL1138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
C;Genetics:
A;Map position: 3
A;Introns: 137/3
A;Note: T17J13.120
C;Superfamily: N-hydroxycinnamoyl/benzoyl transferase
Query Match 93.1%; Score 27; DB 2; Length 428;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 271 KIVFFA 276
RESULT 20
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PID-
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing

Query Match 93.1%; Score 27; DB 1; Length 695;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 612 KIVFFA 617
RESULT 21
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid; transmembrane protein
Query Match 93.1%; Score 27; DB 2; Length 695;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 612 KIVFFA 617
RESULT 22
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2EB; EMBL:X07648; NID:g55616; PID
R;Schubert, D.; Schroeder, R.; Lacorbriere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C;Species: Ursus maritimus (polar bear)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
 C;Accession: B60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: B60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:G2165; PIDN:
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|:|
 Db 21 KLVFFA 26

RESULT 14
 PQ0438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C;Accession: PQ0438; C60045
 R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A;Reference number: PQ0438; MUID:93075180; PMID:1445331
 A;Accession: PQ0438
 A;Molecule type: DNA
 A;Residues: 1-82 <DAV>
 A;Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: C60045
 A;Molecule type: mRNA
 A;Residues: 12-68 <JOH>
 A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 93.1%; Score 27; DB 2; Length 82;
 Best Local Similarity 83.3%; Pred. No. 19;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|:|
 Db 32 KLVFFA 37

RESULT 15
 T06645
 hypothetical protein T20K18.220 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06645
 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Men
 submitted to the Protein Sequence Database, April 1999
 A;Reference number: Z15790
 A;Accession: T06645
 A;Molecule type: DNA
 A;Residues: 1-152 <BEV>
 A;Cross-references: UNIPROT:Q9ST29; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GN000062;
 A;Experimental source: cultivar Columbia; BAC clone T20K18
 C;Genetics:

A;Gene: ATSP:T20K18.220
 A;Map position: 4
 A;Introns: 87/3; 109/3
 C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 93.1%; Score 27; DB 2; Length 152;
 Best Local Similarity 83.3%; Pred. No. 33;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|:|
 Db 9 KLVFFA 14

RESULT 16

H85138
 hypothetical protein AT4g12900 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: H85138

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: H85138

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-231 <STO>

A;Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001268; NID:G7267992; P

C;Genetics:

A;Gene: AT4g12900

A;Map position: 4

C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 93.1%; Score 27; DB 2; Length 231;
 Best Local Similarity 83.3%; Pred. No. 49;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|:|
 Db 12 KLVFFA 17

RESULT 17

T48903

wax synthase [imported] - Simmondsia chinensis

C;Species: Simmondsia chinensis

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C;Accession: T48903

R;Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.

Plant Physiol. 122, 645-655, 2000

A;Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and productio

A;Reference number: Z25002

A;Accession: T48903

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-352 <LAR>

A;Cross-references: UNIPROT:Q9XGY6; UNIPARC:UPI00000A1C81; EMBL:AF149919; PIDN:AAD38041.

Query Match 93.1%; Score 27; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 72;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|:|
 Db 135 KLVFFA 140

RESULT 18

F70399

hydrogenase expression/formation protein HypD - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

A;Residues: 1-42 <SHI>
A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI0000031588
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
Db 16 KLVFFFA 21

RESULT 8
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
Db 21 KLVFFFA 26

RESULT 9
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
Db 21 KLVFFFA 26

RESULT 10
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
Db 21 KLVFFFA 26

RESULT 11
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
Db 21 KLVFFFA 26

RESULT 12
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
Db 21 KLVFFFA 26

RESULT 13
B60045

A;Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI00000C217E; GB:AL139075; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0560

Query Match 96.6%; Score 28; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 313 KVVFFA 318

RESULT 4
F71039
hypothetical protein PH1606 - *Pyrococcus horikoshii*
C;Species: *Pyrococcus horikoshii*
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C;Accession: F71039
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71039
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-447 <KAW>
A;Cross-references: UNIPROT:Q59243; UNIPARC:UPI00000630DE; GB:AP000006; NID:G3236133; PI
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1606
C;Superfamily: *Pyrococcus horikoshii* hypothetical protein PH142

Query Match 96.6%; Score 28; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 207 KIIFFA 212

RESULT 5
A43271
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A43271; A42166; JN0458; A46186
R;Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.;
Science 256, 225-228, 1992
A;Title: Cloning and characterization of inducible nitric oxide synthase from mouse macr
A;Reference number: A43271; MUID:92229444; PMID:1373522
A;Accession: A43271
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <XIE>
A;Cross-references: UNIPROT:P29477; UNIPARC:UPI0000000D36; GB:M87039; NID:G198406; PIDN:
R;Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.
J. Biol. Chem. 267, 6370-6374, 1992
A;Title: Molecular cloning and functional expression of an inducible nitric oxide syntha
A;Reference number: A42166; MUID:92210618; PMID:1372907
A;Accession: A42166
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <LYO>
A;Cross-references: UNIPARC:UPI0000000D36; GB:M84373; NID:G200095; PIDN:AA39834.1; PID:
R;Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Biophys. Res. Commun. 191, 767-774, 1993
A;Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxid
A;Reference number: JN0457; MUID:93221515; PMID:7682072

A;Accession: JN0458
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-278, 'F', 280-682, 'H', 684-937, 939-1144 <WOO>
A;Cross-references: UNIPARC:UPI000017223A
A;Experimental source: liver
R;Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992
A;Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain
A;Reference number: A46186; MUID:92357701; PMID:1379716
A;Accession: A46186
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <LOW>
A;Cross-references: UNIPARC:UPI000017223B; GB:M92649; NID:G200109
A;Experimental source: BALB/c, RAW 264.7 cells, macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:113541)
C;Genetics:
A;Gene: NOS
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; PAD; flavoprotein; FMN; heme; iron; metal
F;533-1121/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;535-671/Domain: flavodoxin homology <FLX>
F;194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 6
S23094
beta-amyloid protein precursor - rat
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
A;Cross-references: UNIPARC:UPI000001777FB
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 93.1%; Score 27; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 7
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: *Cavia porcellus* (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PN0512
R;Shimomigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragmen
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein

249 24 82.8 438 2 E97583 bicyclomycin resis
 250 24 82.8 442 2 S62569 probable transmem
 251 24 82.8 444 2 A82962 proton-glutamate s
 252 24 82.8 446 2 S01187 NADH2 dehydrogenas
 253 24 82.8 450 2 F71351 probable preprotei
 254 24 82.8 469 2 T02325 probable selenium-
 255 24 82.8 476 2 G70175 aminoacyl-histidin
 256 24 82.8 477 2 T02505 probable beta-alan
 257 24 82.8 495 2 G70593 probable cationic
 258 24 82.8 512 2 T19806 hypothetical prote
 259 24 82.8 513 2 B90050 DNA damage-inducib
 260 24 82.8 515 2 B84391 ADP/ATP translocas
 261 24 82.8 515 2 E86534 ADF, ATP carrier p
 262 24 82.8 515 2 E72089 probable membrane
 263 24 82.8 521 2 G84864 probable AMP-bind
 264 24 82.8 572 2 H96685 ABC transporter re
 265 24 82.8 574 2 A1414 ABC transporter re
 266 24 82.8 574 2 A1790 ABC transporter re
 267 24 82.8 587 2 A3519 2,3-dihydroxybenzo
 268 24 82.8 601 2 H69274 probable long-chai
 269 24 82.8 604 1 OX15M NADH2 dehydrogenas
 270 24 82.8 646 2 A3409 ABC transporter AT
 271 24 82.8 657 2 G8590 exinuclease ABC su
 272 24 82.8 657 2 B72034 exinuclease ABC,
 273 24 82.8 657 2 H90523 exinuclease ABC s
 274 24 82.8 660 1 A28153 gelatinase A (EC 3
 275 24 82.8 660 2 A81704 DNA ligase TC0423
 276 24 82.8 662 2 S70365 gelatinase A (EC 3
 277 24 82.8 662 2 A42496 gelatinase A (EC 3
 278 24 82.8 662 2 S34780 gelatinase A (EC 3
 279 24 82.8 663 1 S46492 gelatinase A (EC 3
 280 24 82.8 663 2 C71551 probable DNA ligas
 281 24 82.8 663 2 A86626 hypothetical prote
 282 24 82.8 665 2 D90092 hypothetical prote
 283 24 82.8 676 2 D81654 exinuclease ABC c
 284 24 82.8 680 2 T01403 hypothetical prote
 285 24 82.8 681 2 T39814 hypothetical prote
 286 24 82.8 690 2 H82923 conserved hypothet
 287 24 82.8 706 2 A86350 F8K7.10 protein -
 288 24 82.8 726 2 E90084 similarity to A.th
 289 24 82.8 754 2 T08249 protoporphyrin IX
 290 24 82.8 758 2 T02925 protoporphyrin IX
 291 24 82.8 774 2 T34496 hypothetical prote
 292 24 82.8 774 2 T21459 hypothetical prote
 293 24 82.8 778 2 B86218 protein T27G7.20 l
 294 24 82.8 785 2 H85036 hypothetical prote
 295 24 82.8 791 2 T30687 probable RNA polym
 296 24 82.8 804 2 G71546 probable DNA gyras
 297 24 82.8 812 2 H87386 hypothetical prote
 298 24 82.8 828 2 C96639 protein TIP9.14 [i
 299 24 82.8 844 2 T23656 hypothetical prote
 300 24 82.8 858 2 JC2308 chitin synthase (E

ALIGNMENTS

RESULT 1
 WMR219
 19K globulin precursor - rice
 N:Alternate names: alpha-globulin
 C:Species: Oryza sativa (rice)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004
 C:Accession: S20024; S25735; FN0497
 R;Shorrosh, B.S.; Wen, L.; Zen, K.C.; Huang, J.K.; Pan, J.S.; Hermodson, M.A.; Tanaka, K
 Plant Mol. Biol. 18, 151-154, 1992
 A:Title: A novel cereal storage protein: molecular genetics of the 19 kDa globulin of ri
 A:Reference number: S20024; MUID:92119226; PMID:1731968
 A:Accession: S20024
 A:Molecule type: mRNA
 A:Residues: 1-186 <SHO>
 A:Cross-references: UNIPROT:P29835; UNIPARC:UPI000012B4D1; EMBL:X63990; NID:g20158; PIDN
 A:Accession: S25735

A:Molecule type: protein
 A:Residues: 66-74;108-133;171-186 <SH2>
 A:Cross-references: UNIPARC:UPI0000173296; UNIPARC:UPI0000173297; UNIPARC:UPI0000173298
 R;Krishnan, H.B.; Pueppke, S.G.
 Biochem. Biophys. Res. Commun. 193, 460-466, 1993
 A:Title: Nucleotide sequence of an abundant rice seed globulin: homology with the high m
 A:Reference number: FN0497; MUID:93277591; PMID:8503935
 A:Accession: FN0497
 A:Molecule type: mRNA
 A:Residues: 6-186 <KRI>
 A:Cross-references: UNIPARC:UPI0000173299; GB:L12252
 A:Experimental source: seed
 C:Superfamily: Alpha amylase inhibitor
 C:Keywords: storage protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-186/Product: 19K globulin #status predicted <MAT>
 Query Match 96.6%; Score 28; DB 1; Length 186;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 4 KVVFFA 9
 |:|||||
 |:|||||
 RESULT 2
 JC4784
 alpha-globulin precursor - rice
 C:Species: Oryza sativa (rice)
 C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 31-Dec-2004
 C:Accession: JC4784
 R;Nakase, M.; Hotta, H.; Adachi, T.; Aoki, N.; Nakamura, R.; Masumura, T.; Tanaka, K.; t
 Gene 170, 223-226, 1996
 A:Title: Cloning of the rice seed alpha-globulin-encoding gene: Sequence similarity of t

A:Reference number: JC4784; MUID:96235139; PMID:8666249
 A:Accession: JC4784
 A:Molecule type: DNA
 A:Residues: 1-186 <NAK>
 A:Cross-references: UNIPROT:P93414; UNIPARC:UPI00000A4C3C; DDBJ:D50643; NID:g840704; PTI
 A:Experimental source: seed
 C:Genetics:
 A:Gene: Glb
 C:Superfamily: Alpha amylase inhibitor
 C:Keywords: globulin; seed
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-186/Product: alpha-globulin #status predicted <MAT>
 Query Match 96.6%; Score 28; DB 2; Length 186;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 4 KVVFFA 9
 |:|||||
 |:|||||

RESULT 3
 H81402
 Probable integral membrane protein Cj0560 [imported] - Campylobacter jejuni (strain NCTC
 C:Species: Campylobacter jejuni
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: H81402
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barre
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
 A:Reference number: A81250; MUID:20150912; PMID:10688204
 A:Accession: H81402
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-442 <PAR>

103 25 86.2 606 2 S41830
104 25 86.2 606 2 T45560
105 25 86.2 606 2 T11373
106 25 86.2 606 2 T10982
107 25 86.2 606 2 T11060
108 25 86.2 617 2 A72123
109 25 86.2 655 2 T13691
110 25 86.2 726 2 T15810
111 25 86.2 732 2 T32023
112 25 86.2 763 2 T21006
113 25 86.2 817 2 A82511
114 25 86.2 825 2 T46311
115 25 86.2 935 2 T40715
116 25 86.2 1121 2 T21303
117 25 86.2 1133 2 T30302
118 25 86.2 1270 2 T21269
119 25 86.2 1291 2 T21267
120 25 86.2 1316 2 D87145
121 25 86.2 1316 2 S31146
122 25 86.2 1316 2 T20535
123 25 86.2 1318 2 T21266
124 25 86.2 1327 2 T21268
125 25 86.2 1462 2 T00345
126 24 82.8 20 2 C60894
127 24 82.8 61 2 H71329
128 24 82.8 77 2 A01750
129 24 82.8 85 2 A63408
130 24 82.8 101 2 T26641
131 24 82.8 104 2 C75046
132 24 82.8 110 2 A10493
133 24 82.8 115 2 B25120
134 24 82.8 132 2 G84717
135 24 82.8 136 2 T19479
136 24 82.8 140 2 B95049
137 24 82.8 140 2 H97919
138 24 82.8 144 2 A86722
139 24 82.8 146 2 E75134
140 24 82.8 148 2 T32362
141 24 82.8 149 2 J80167
142 24 82.8 153 2 A80099
143 24 82.8 155 2 S59155
144 24 82.8 159 2 C71080
145 24 82.8 162 2 T13659
146 24 82.8 162 2 T13656
147 24 82.8 162 2 T13563
148 24 82.8 162 2 T13487
149 24 82.8 164 2 T13562
150 24 82.8 168 2 A25522
151 24 82.8 187 2 A99124
152 24 82.8 188 2 G70475
153 24 82.8 188 2 T25683
154 24 82.8 200 2 A81632
155 24 82.8 208 2 T05859
156 24 82.8 211 2 J45450
157 24 82.8 211 2 S14920
158 24 82.8 212 2 B75109
159 24 82.8 214 2 T47892
160 24 82.8 220 2 A64141
161 24 82.8 224 2 E95223
162 24 82.8 224 2 H98087
163 24 82.8 226 2 S62550
164 24 82.8 231 1 E84982
165 24 82.8 231 2 B91008
166 24 82.8 231 2 D85852
167 24 82.8 231 2 C64703
168 24 82.8 232 2 A71495
169 24 82.8 233 2 A25814
170 24 82.8 233 2 T32680
171 24 82.8 234 2 T32466
172 24 82.8 238 2 T70107
173 24 82.8 255 2 C87434
174 24 82.8 257 2 C83982
175 24 82.8 261 2 D84166

176 24 82.8 263 2 C97198
177 24 82.8 268 2 D86736
178 24 82.8 272 2 T24709
179 24 82.8 274 2 T33371
180 24 82.8 276 2 T32682
181 24 82.8 281 2 B54498
182 24 82.8 286 2 C84857
183 24 82.8 294 2 A2941
184 24 82.8 294 2 D98341
185 24 82.8 295 2 JC4744
186 24 82.8 295 2 I39751
187 24 82.8 295 2 C70736
188 24 82.8 295 2 A36966
189 24 82.8 296 2 D82515
190 24 82.8 302 2 A99074
191 24 82.8 302 2 B35961
192 24 82.8 304 2 C90565
193 24 82.8 311 2 S73625
194 24 82.8 312 2 A46247
195 24 82.8 316 2 S61237
196 24 82.8 316 2 F81712
197 24 82.8 318 2 A75275
198 24 82.8 318 2 H71561
199 24 82.8 322 2 F84948
200 24 82.8 322 2 T24356
201 24 82.8 328 2 T11938
202 24 82.8 330 2 H75505
203 24 82.8 334 2 T20562
204 24 82.8 347 2 A81988
205 24 82.8 347 2 D81043
206 24 82.8 347 2 S35229
207 24 82.8 348 2 C64676
208 24 82.8 348 2 C71841
209 24 82.8 352 2 H97272
210 24 82.8 356 2 T13430
211 24 82.8 356 2 D84280
212 24 82.8 356 2 T18590
213 24 82.8 357 2 T16596
214 24 82.8 363 2 F70195
215 24 82.8 364 2 H85856
216 24 82.8 364 2 A10784
217 24 82.8 364 2 F91012
218 24 82.8 364 2 A64987
219 24 82.8 365 2 T33499
220 24 82.8 373 2 AE0847
221 24 82.8 373 2 A85922
222 24 82.8 373 2 A91077
223 24 82.8 373 2 S15200
224 24 82.8 379 2 I39743
225 24 82.8 381 2 A70454
226 24 82.8 384 2 H64161
227 24 82.8 385 2 S32877
228 24 82.8 397 2 F95352
229 24 82.8 398 2 C81729
230 24 82.8 399 2 G97727
231 24 82.8 399 2 D71728
232 24 82.8 399 2 A82842
233 24 82.8 402 2 AE2804
234 24 82.8 404 2 H96916
235 24 82.8 404 2 A97559
236 24 82.8 404 2 AE2779
237 24 82.8 407 2 B81914
238 24 82.8 417 2 T18769
239 24 82.8 420 2 B90553
240 24 82.8 421 2 H72492
241 24 82.8 422 2 E82904
242 24 82.8 423 2 JC7677
243 24 82.8 426 2 F81187
244 24 82.8 435 2 AD1340
245 24 82.8 435 2 H61711
246 24 82.8 437 2 A64251
247 24 82.8 437 2 S50006
248 24 82.8 437 2 JC5115

HAD superfamily hy
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
major merozoite su
hypothetical prote
hypothetical prote
lactose transport
NAD-dinitrogen-red
NAD-dinitrogen-red
hypothetical prote
probable dTPP-rham
ketoreductase XF27
hypothetical prote
hypothetical 21K p
hypothetical prote
methionyl-tRNA for
olfactory receptor
capsid protein - b
ABC transporter, p
methionyl-tRNA for
probable integral
NADH2 dehydrogenas
hypothetical prote
NADH2 dehydrogenas
tryptophanyl-tRNA
hypothetical prote
probable N-acetyl-
N-acetyl-gamma-glu
hyPD, protein - Br
oligopeptide ABC t
probable peptide A
histidinol-phospha
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
UDP-N-acetylglucos
probable binding-p
probable transport
probable transport
Hypothetical ABC t
hypothetical prote
hydrogenase isoenz
pleiotrophic effec
hydrogenase isoenz
hydrogenase expres
hydrogenase homolo
conserved hypothet
hypothetical prote
hyPD protein - Rhi
probable proline d
Mr/TnaB/TyO perm
proton/sodium-glut
proton/sodium-glut
conserved hypothet
MFS permease (impo
probable permease
hypothetical prote
acyltransferase li
probable transmemb
hypothetical prote
hypothetical prote
probable proton/ao
hypothetical prote
allatostatin recep
Glucose/galactose
maltodextrin ABC-t
maltodextrin ABC-t
replication initia
preprotein translo
preprotein translo

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-1
Perfect score: 29
Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	96.6	186	1 WMR219	19K globulin precu
2	28	96.6	186	2 JC4784	alpha-globulin pre
3	28	96.6	442	2 H81402	probable integral
4	28	96.6	447	2 F71039	hypothetical prote
5	28	96.6	1144	1 A43271	nitric-oxide synth
6	27	93.1	33	2 S23094	beta-amyloid prote
7	27	93.1	42	2 PN0512	beta-amyloid prote
8	27	93.1	57	2 A60045	Alzheimer's diseas
9	27	93.1	57	2 F60045	Alzheimer's diseas
10	27	93.1	57	2 D60045	Alzheimer's diseas
11	27	93.1	57	2 E60045	Alzheimer's diseas
12	27	93.1	57	2 G60045	Alzheimer's diseas
13	27	93.1	57	2 B60045	Alzheimer's diseas
14	27	93.1	82	2 PQ0438	Alzheimer's diseas
15	27	93.1	152	2 T06645	hypothetical prote
16	27	93.1	231	2 H85138	hypothetical prote
17	27	93.1	352	2 T48903	wax synthase [impo
18	27	93.1	380	2 F70399	hydrogenase expres
19	27	93.1	428	2 T48008	hypothetical prote
20	27	93.1	695	1 A49795	Alzheimer's diseas
21	27	93.1	695	2 A27485	Alzheimer's diseas
22	27	93.1	695	2 S00550	Alzheimer's diseas
23	27	93.1	747	2 JH0773	Alzheimer's diseas
24	27	93.1	770	1 QRHUA4	Alzheimer's diseas
25	27	93.1	1016	2 S30236	genome polyprotein
26	26	89.7	74	2 E64214	hypothetical prote
27	26	89.7	109	2 B72213	conserved hypotet
28	26	89.7	156	2 H95252	PTS system, IIB co
29	26	89.7	156	2 F98117	hypothetical prote

26	89.7	190	2	A95895	probable permease
26	89.7	194	2	B97211	uncharacterized co
26	89.7	247	2	T32514	hypothetical prote
26	89.7	253	2	D82405	transcription regu
26	89.7	277	2	T31855	hypothetical prote
26	89.7	300	2	T26245	hypothetical prote
26	89.7	321	2	H71729	hypothetical prote
26	89.7	349	2	T26247	hypothetical prote
26	89.7	352	2	AH2097	sorbitol dehydroge
26	89.7	382	2	G83808	hypothetical prote
26	89.7	402	2	E86038	probable LPS biosy
26	89.7	402	2	D91191	lipid A-core surfa
26	89.7	405	2	A70146	tyrosine-tRNA liga
26	89.7	620	2	H93382	ABC transporter, A
26	89.7	774	2	F96639	protein Tif9.8 [im
26	89.7	1119	2	A86340	protein F2D10.24 [
25	86.2	20	2	JU0330	hypothetical prote
25	86.2	20	2	A99091	hypothetical prote
25	86.2	62	2	E84530	hypothetical prote
25	86.2	81	2	F90736	molybdopterin bios
25	86.2	81	2	A82251	molybdenum cofacto
25	86.2	81	2	G85586	molybdopterin bios
25	86.2	81	2	H64814	molybdopterin bios
25	86.2	83	2	AC0598	molybdopterin conv
25	86.2	108	2	C84516	hypothetical prote
25	86.2	141	1	B70457	gliding motility p
25	86.2	143	1	A44397	cofilin - yeast (S
25	86.2	193	2	B90157	hypothetical prote
25	86.2	207	2	B81256	phosphoribosyl-AMP
25	86.2	219	1	A35617	HDEL receptor ERD2
25	86.2	219	2	A75004	hypothetical prote
25	86.2	221	2	G72322	glutaredoxin-relat
25	86.2	222	2	T47768	hypothetical prote
25	86.2	225	2	A90260	conserved hypotet
25	86.2	248	2	F71849	amino acid ABC tra
25	86.2	248	2	C64666	glutamine transpor
25	86.2	254	2	T28170	hypothetical prote
25	86.2	256	2	AC1561	conserved hypotet
25	86.2	256	2	AE1203	conserved hypotet
25	86.2	262	2	A81056	conserved hypotet
25	86.2	269	2	A81820	conserved hypotet
25	86.2	276	2	S05343	NAD ADP-ribosyltra
25	86.2	287	2	AI2038	carboxyphosphoen
25	86.2	293	2	D69355	hypothetical prote
25	86.2	294	2	H90318	glycerol kinase [g
25	86.2	311	2	D64240	methionyl-tRNA for
25	86.2	330	2	B82822	NADH2 dehydrogenas
25	86.2	337	2	AG0963	hypothetical prote
25	86.2	339	2	B72402	UDP-N-acetylglucos
25	86.2	340	1	MMBE5	cell fusion protei
25	86.2	342	2	AE2238	methionyl-tRNA for
25	86.2	363	2	S56273	probable LPS biosy
25	86.2	380	2	F86038	probable LPS biosy
25	86.2	380	2	E91191	probable LPS biosy
25	86.2	383	2	AF1893	hydrogenase expres
25	86.2	385	2	T31493	hypothetical prote
25	86.2	400	2	H69009	hypothetical prote
25	86.2	409	2	S29124	membrane glycoprot
25	86.2	455	2	T34366	hypothetical prote
25	86.2	466	2	A95179	hypothetical prote
25	86.2	466	2	B97030	LPS glycosyltransf
25	86.2	466	2	H98045	hypothetical prote
25	86.2	477	2	B28988	hypothetical prote
25	86.2	490	2	A35312	potassium channel
25	86.2	509	2	S51348	hypothetical prote
25	86.2	520	2	A81548	hypothetical prote
25	86.2	594	2	F86499	hypothetical prote
25	86.2	603	2	T11490	hypothetical prote
25	86.2	603	2	F72237	conserved hypotet
25	86.2	604	2	T11867	NADH2 dehydrogenas
25	86.2	606	1	QXBQ5M	NADH2 dehydrogenas
25	86.2	606	2	T11150	NADH2 dehydrogenas
25	86.2	606	2	C58851	NADH2 dehydrogenas

THIS PAGE BLANK (USP 10)

CC of the invention are useful in the manufacture of a medicament for
 CC inhibiting or treating amyloidosis or amyloid deposits e.g. Type I and
 CC Type II diabetes and/or for cytoprotection. They are also useful for
 CC treating secondary amyloidosis associated with chronic infection e.g.
 CC tuberculosis and chronic inflammation e.g. rheumatoid arthritis, and
 CC familial inflammation, fever, neurodegenerative diseases e.g. scrapie,
 CC bovine spongy form encephalitis, Creutzfeldt-Jacob disease, Alzheimer's
 CC disease, cerebral amyloid angiopathy
 XX
 SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 74

AAU11658
 ID AAU11658 standard; peptide; 6 AA.

XX AAU11658;

XX 09-APR-2002 (first entry)

XX Peptide #11, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 6
 FT /note= "C-terminal amide"

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 75

AAU11650
 ID AAU11650 standard; peptide; 6 AA.

XX AAU11650;

XX 09-APR-2002 (first entry)

XX Peptide #3, used as a carrier for amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:33:38
 Job time : 82.7742 secs

CC not only reduces the formation of neurotoxic aggregates but also have the
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
 CC present sequence represents a beta-AP peptide, which is used in the
 CC exemplification of the present invention

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
 | : | | |
 Db 1 KLVFFA 6

RESULT 72
 AAU96820
 ID AAU96820 standard; peptide; 6 AA.

XX AAU96820;

DT 30-JUL-2002 (first entry)

DB Amyloid targeting peptide #10.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1. .6

FT /note= "Preferably D-form residue"

FT Modified-site 6

FT /note= "Ala is amidated"

PN WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
 XX agent is of general formula A_t-(A_l n k)-z-A_l a_b (I) where z = 0-1;
 XX A_t = an amyloid targeting moiety; A_l n k = a linker moiety; and A_l a_b
 XX = a labelling moiety. Also included are imaging amyloid deposition or
 XX diagnosing an amyloid-related condition in a patient involving
 XX administering (I) to the patient, and ultrasound imaging (I) in the
 XX patient to determine the presence of amyloid or amyloid-related condition
 XX ; and a kit for preparing a radiopharmaceutical preparation comprising
 XX (I), a reducing agent, a buffering agent, a transchelating agent, and

CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
 | : | | |
 Db 1 KLVFFA 6

RESULT 73
 ABB83305
 ID ABB83305 standard; peptide; 6 AA.

XX ABB83305;

DT 29-AUG-2002 (first entry)

DE Amyloid-beta (Abeta) peptide fragment.

XX Human; islet amyloid polypeptide; IAPP; antidiabetic; amylin;
 KW fibrillar accumulation; amyloidosis; diabetes; cytoprotection; neurotropic;
 KW chronic infection; tuberculosis; inflammation; rheumatoid arthritis;
 KW fever; neurodegenerative disease; scrapie; neuroprotective; antipyrretic;
 KW bovine spongy form encephalitis; Creutzfeldt-Jacob disease; amyloid-beta;
 KW Alzheimer's disease; cerebral amyloid angiopathy; anti-diabetic;
 KW tuberculostatic; antiarthritic; antirheumatic; cerebroprotective.

XX Unidentified.

XX WO200224727-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-CA001333.

XX 19-SEP-2000; 2000US-0233482P.

XX (UTOR) UNIV TORONTO.

XX Fraser P;

XX WPI; 2002-519078/55.

XX New antidiabetic peptide useful for inhibiting amyloidosis and/or
 XX for cytoprotection in the treatment of amyloidosis disorders e.g. type I
 XX or type II.

XX Disclosure; Page 5; 77pp; English.

XX The present invention relates to antidiabetic agents (ABB83281-
 XX ABB83298), derived from human islet amyloid polypeptide (IAPP, ABB83307).
 XX The present sequence is a peptide fragment of the amyloid-beta (Abeta)
 XX peptide. Aggregation of IAPP, also known as amylin, or Abeta results in
 XX fibrillar accumulations, leading to amyloidosis. The antidiabetic
 XX peptides prevent fibril formation and amyloidosis and hence control
 XX folding or deposition of amyloid proteins. The antidiabetic peptides

DB 1 KLVFFA 6
|:|||||

RESULT 70
ABG71009
ID ABG71009 standard; peptide; 6 AA.
XX AC ABG71009;
XX XX
XX 05-DEC-2002 (first entry)
XX DE
XX Long form beta-amyloid protein fragment #6.
XX KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
XX KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
XX KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
XX KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
XX KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;
XX KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;
XX KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;
XX KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;
XX KW hereditary cerebral haemorrhage with amyloidosis; Nuckle-Wells syndrome;
XX KW hereditary non-neuropathic systemic amyloidosis;
XX KW familial Mediterranean fever.
XX OS Homo sapiens.
XX XX
XX US2002098173-A1.
XX XX
XX 25-JUL-2002.
XX XX
XX 04-OCT-2001; 2001US-00972475.
XX XX
XX 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX PR 14-MAR-1996; 96US-00617267.
XX XX
XX (PRAE-) PRAECIS PHARM INC.
XX XX
XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX XX
XX WPI; 2002-697709/75.
XX XX
XX Amyloid modulator useful for treating a disorder associated with
XX PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
XX PT coupled to a modifying group.
XX XX
XX Example 12; Page 35; 41pp; English.
XX XX
XX The invention describes an amyloid modulator comprising an amyloidogenic
XX CC protein and/or peptide fragment coupled to a modifying group so that the
XX CC compound modulates the aggregation of natural amyloid proteins or
XX CC peptides. The modulator is used for treating a disorder associated with
XX CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese
XX CC and Swedish types), familial amyloid cardiomyopathy (Danish type),
XX CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine
XX CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
XX CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated
XX CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
XX CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous
XX CC nodular amyloidosis associated with Sjogren's syndrome, reactive
XX CC (secondary) amyloidosis, familial Mediterranean fever and familial
XX CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
XX CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
XX CC amyloidosis associated with long term haemodialysis, hereditary non-
XX CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy III),
XX CC familial amyloidosis of Finnish type, amyloidosis associated with
XX CC renal carcinoma of the thyroid, fibrinogen-associated hereditary
XX CC amyloidosis and lysozyme-associated hereditary systemic
XX CC amyloidosis. The compound is capable of altering and inhibiting beta-

CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
CC or peptides when contacted with a molar excess amount of natural beta-APs
CC relative to the modulator. This sequence represents a fragment of the
CC long form of beta-amyloid used in the creation of an amyloid modulator
XX XX
XX Sequence 6 AA;
XX
Query Match 93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
|:|||||
DB 1 KLVFFA 6

RESULT 71
ABG05157
ID ABG05157 standard; peptide; 6 AA.
XX AC ABG05157;
XX XX
XX 02-APR-2002 (first entry)
XX XX
XX Beta amyloid peptide (16-21) SEQ ID NO:9.
XX KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
XX KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
XX KW neurotic; neuroprotective; immunosuppressive; antimicrobial; auditory;
XX KW antidiabetic; antipyrretic; dermatological; cardiovascular; nephrotropic;
XX KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
XX KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
XX KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
XX XX
XX Homo sapiens.
XX OS Synthetic.
XX XX
XX US6319498-B1.
XX XX
XX 20-NOV-2001.
XX XX
XX 14-MAR-1996; 96US-00617267.
XX XX
XX 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX XX
XX (PRAE-) PRAECIS PHARM INC.
XX XX
XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX XX
XX WPI; 2002-146668/19.
XX XX
XX Amyloid modulator compound useful for treatment of an amyloidogenic
XX PT disease such as Alzheimer's disease comprises an aggregation core domain
XX PT and a modifying group attached to it.
XX XX
XX Disclosure; Col 18; 54pp; English.
XX XX
XX The present invention describes an amyloid modulator compound (I)
XX CC comprising an aggregation core domain and a modifying group attached to
XX CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,
XX CC antidiabetic, antipyrretic, dermatological, cardiovascular, nephrotropic
XX CC and auditory activities, and can be used as a natural amyloid aggregation
XX CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
XX CC (beta-AP). (I) are used in the manufacture of a medicament for the
XX CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
XX CC disease and other clinical occurrences of beta amyloid deposition such as
XX CC Down's syndrome individuals and in patients with hereditary cerebral
XX CC haemorrhage with amyloidosis, and for treating a disorder associated with
XX CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the
XX CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)

```

CC protein
XX Sequence 6 AA;
SQ

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 1 KLVFFA 6

RESULT 68
AAB48476
ID AAB48476 standard; peptide; 6 AA.
XX
AC AAB48476;
XX
DT 02-MAR-2001 (first entry)
XX
DE Antifibrillogenic peptide #3.
XX
KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
FN WO200068263-A2.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-CA000515.
XX
PR 05-MAY-1999; 99US-0132592P.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Chalifour R, Gervais F, Gupta A;
XX
DR WPI; 2001-031852/04.
XX
PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic.
XX
PS Claim 7; Page 25; 46pp; English.
XX
SQ Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycoaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein
XX
SQ Sequence 6 AA;
Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 1 KLVFFA 6

RESULT 69
AAB82632
ID AAB82632 standard; peptide; 6 AA.
XX
AC AAB82632;
XX

```

```

XX 02-OCT-2001 (first entry)
DT
XX All-D peptide used in Alzheimer's disease vaccine.
DE
XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
XX therapy; antigen.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
XX Misc-difference 1..6
XX Modified-site 6 /note= "all D-form residues"
XX /note= "C-terminal amide"
XX WO200139796-A2.
XX
XX 07-JUN-2001.
XX
XX 29-NOV-2000; 2000WO-CA001413.
XX
XX 29-NOV-1999; 99US-0168594P.
XX
XX 28-NOV-2000; 2000US-00724842.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Chalifour R, Hebert L, Kong X, Gervais F;
XX WPI; 2001-441458/47.
XX
XX Preventing/treating amyloid-related disease, especially Alzheimer's
XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
XX which elicits production of antibodies to prevent fibrillogenesis and
XX associated cellular toxicity.
XX
XX Disclosure; Page 11; 31pp; English.
XX
XX The present sequence is that of an all-D peptide suitable for use for
XX preparing vaccines for preventing or treating Alzheimer's disease and
XX other amyloid related disorders in humans. It is based on a portion of
XX amyloid-beta peptide (see AAB82632), and may be modified by removing or
XX inserting 1 or more amino acid residues, or by substituting 1 or more
XX amino acid residues with other amino acid residues or non-amino acid
XX fragments. Vaccines of the invention are produced using 'non-self'
XX peptides synthesised from the unnatural D-configuration amino acids to
XX avoid the drawbacks of 'self' proteins. The all-D peptides need not be
XX aggregated to be operative or immunogenic. They preferably interact with
XX at least 1 region of an amyloid protein, e.g. the beta-sheet region or
XX CAG-binding site region, the amyloid-beta peptide, or their immunogenic
XX fragments, protein conjugates, immunogenic derivative peptides and
XX immunogenic peptidomimetics. Examples include all-D peptides
XX corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
XX 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
XX in AAB82632-64. The vaccine elicits a preferential TH-2 or TH-1 response,
XX preventing fibrillogenesis and associated cellular toxicity. The amyloid
XX related diseases may be localised amyloidosis, e.g. diabetes type II,
XX neurodegenerative diseases, e.g. bovine spongiform encephalitis,
XX Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
XX prion protein related disorders, or systemic amyloidosis associated with
XX chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
XX rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
XX amyloidosis found in long-term haemodialysis patients. The present all-D
XX peptide was demonstrated to elicit antibody production in rabbits, and
XX provided greater anti-fibrillogenic activity than its all-L equivalent
XX
XX Sequence 6 AA;
Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

```

XX AAW02310-W02332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients. The
 CC amyloid modulators of the invention comprise an amyloidogenic protein or
 CC peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as deca-, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease
 XX
 SQ Sequence 6 AA;
 Query Match 93.1%; Score 27; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6
 RESULT 66
 IAW89378
 ID AAW89378 standard; peptide; 6 AA.
 XX
 AC AAW89378;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Beta-amyloid peptide derivative A-beta-16-21.
 XX
 KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; bAP.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US5854204-A.
 XX
 PD 29-DEC-1998.
 XX
 PF 14-MAR-1996; 96US-00612785.
 XX
 PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Hundal A, Geffer ML, Kasman L, Musso G, Molineaux S, Benjamin H;
 PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
 PI Garnick MB, Kubasek W, Signer ER;
 XX
 DR WPI; 1999-094964/08.
 XX
 PT New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
 aggregation - and neurotoxicity, specifically for treatment and

PT prevention of Alzheimer's disease.
 XX
 PS Example 12; Col 64; 52pp; English.
 XX
 CC The present invention describes beta-amyloid peptide (bAP) derivatives.
 CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically bAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of bAP to
 CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
 CC even when bAP is present in molar excess. The present sequence represents
 CC a bAP derivative
 XX
 SQ Sequence 6 AA;
 Query Match 93.1%; Score 27; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6
 RESULT 67
 AAB48484
 ID AAB48484 standard; peptide; 6 AA.
 XX
 AC AAB48484;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #11.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX
 PN WO200068263-A2.
 XX
 PD 16-NOV-2000.
 XX
 PF 04-MAY-2000; 2000WO-CA0000515.
 XX
 PR 05-MAY-1999; 99US-0132592P.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalfour R, Gervais F, Gupta A;
 XX
 DR WPI; 2001-031852/04.
 XX
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX
 PS Claim 7; Page 25; 46pp; English.
 XX
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid

or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
DB 514 KVVFFFA 519

RESULT 62

ADJ76136
ID ADJ76136 standard; protein; 1144 AA.

AC ADJ76136;

XX 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.

XX Mus musculus.

XX EP1394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample

PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.

XX Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent;
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (1) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
DB 514 KVVFFFA 519

RESULT 63

AEA03075
ID AEA03075 standard; protein; 1144 AA.

XX AEA03075;

XX 28-JUL-2005 (first entry)

DE VEGF amino acid sequence SEQ ID NO:101.

XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
KW vascular endothelial cell growth factor.

XX Unidentified.

XX US2005112141-A1.

XX 26-MAY-2005.

XX 08-SEP-2004; 2004US-00937758.

XX 30-AUG-2000; 2000US-00650884.

XX (TERM/) TERMAN D S.

XX Terman DS;

PA (TERM/) Terman D S.
 XX Terman DS;
 FI WPI; 2003-787326/74.
 XX N-PSDB; ADF43403.
 DR
 DR
 PT New receptor in a mammalian cell that inhibits regular activation by
 PT receptors specific for lipid-based tumor associated antigens, useful for
 PT treating a neoplastic disease or tumor, and infectious diseases.
 XX
 XX Example 3; SEQ ID NO 124; 151pp; English.
 PS
 XX The invention describes a receptor in a mammalian cell that inhibits
 CC regular activation by receptors specific for lipid-based tumor
 CC associated antigen. The receptor has cytostatic and antimicrobial
 CC properties and is suitable for use in gene therapy. The receptors,
 CC methods and compositions are useful for treating a neoplastic disease or
 CC tumour (cancer), and infectious diseases. This sequence represents INOS
 CC polypeptide, a cell surface moiety, the DNA of which can be transfected
 CC into a cell with superantigen DNA to generate antitumour immunity.
 XX
 SQ Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 7; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 Db 514 KVVFFFA 519
 :|||||
 :|||||
 RESULT 60
 ADF77432
 ID ADF77432 standard; protein; 1144 AA.
 XX
 AC ADF77432;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase, INOS.
 XX
 KW Mouse; inducible nitric oxide synthase; iNOS; cardiant; vasodilator;
 KW cycostatic; gynaecological; restenotic response; angioplasty;
 KW vasodilation; angina; cancer; cell death; premature labour; tumour;
 KW nervous system; brain; erectile dysfunction; uterus; lung; vascular tone;
 KW regional blood flow.
 XX
 OS Mus musculus.
 XX
 XX US6620616-B1.
 XX
 XX 16-SEP-2003.
 XX
 XX 13-SEP-2000; 2000US-00661258.
 XX
 XX 13-SEP-2000; 2000US-00661258.
 XX
 XX (CLEV-) CLEVELAND CLINIC FOUND.
 XX
 XX Stuehr DJ, Adak S;
 XX WPI; 2003-895427/82.
 DR
 XX
 PT New isolated polynucleotide encoding a variant of a corresponding wild-
 PT type nitric oxide synthase, useful for reducing the restenotic response
 PT after angioplasty, or for inhibiting the development or onset of
 PT premature labor.
 XX
 PS Disclosure; SEQ ID NO 5; 35pp; English.
 XX
 XX The invention relates to an isolated polynucleotide encoding a variant of

CC a corresponding wild-type nitric oxide synthase (NOS). The variant has
 CC the tryptophan in the alpha 3 helix substituted by tyrosine or
 CC phenylalanine. Also included are a nucleic acid construct comprising the
 CC nucleotide sequence that encodes a variant of a corresponding wild-type
 CC nitric oxide synthase and a promoter operably linked to the encoding
 CC sequence of the variant and a transformed cell comprising the construct,
 CC where the cell expresses the nitric oxide synthase variant. The variant
 CC has an in vitro enzymatic activity that is greater than the in vitro
 CC enzymatic activity of the corresponding wild-type nitric oxide synthase.
 CC The variant can preferably be of a corresponding wild-type endothelial
 CC nitric oxide synthase (eNOS), neuronal nitric oxide synthase (nNOS), or
 CC inducible nitric oxide synthase (iNOS). The polynucleotides are useful
 CC for reducing the restenotic response after angioplasty, or related
 CC interventional procedures, or to enhance the vasodilation response in
 CC treating angina, for anticancer therapy to promote cell death, and for
 CC inhibiting the development or onset of premature labour. The
 CC polynucleotides are useful to achieve or augment expression of NOS
 CC variant proteins or polypeptides in vivo to increase NOS production in
 CC target tissue, tumour tissue, tissue of the nervous system, including
 CC brain, penis (e.g. in erectile dysfunction) and uterine tissue, and lung
 CC tissue. NOS is useful for maintaining vascular tone and regulating
 CC regional blood flow. The present sequence is wild-type mouse iNOS.
 XX
 SQ Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 7; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 Db 514 KVVFFFA 519
 :|||||
 :|||||
 RESULT 61
 ADJ76212
 ID ADJ76212 standard; protein; 1144 AA.
 XX
 AC ADJ76212;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:1464.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Mus musculus.
 XX
 XX EP1394274-A2.
 XX
 XX 03-MAR-2004.
 XX
 XX 04-AUG-2003; 2003EP-00254857.
 XX
 XX 06-AUG-2002; 2002JP-00229312.
 XX
 XX 20-MAR-2003; 2003JP-00077212.
 XX
 XX (GENO-) GENOX RES INC.
 XX
 XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 XX WPI; 2004-193155/19.
 DR
 XX
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Claim 16; SEQ ID NO 1464; 241pp; English.
 XX
 XX The present invention describes a method of testing for bronchial asthma

CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiac,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of
 CC mouse inducible nitric oxide synthase

XX SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 4; Length 1144;

Best Local Similarity 83.3%; Pred. No. 9.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6

Db 514 KVVFFA 519

RESULT 59

ABU79138

ID ABU79138 standard; protein; 1144 AA.

XX AC

XX ABU79138;

XX DT 18-JUN-2003 (first entry)

XX DE

XX Inducible nitric oxide synthase protein.

XX DE

XX Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;

XX gene therapy; mammalian cell receptor; cytostatic;

XX tumour associated lipid; anergy; T cell; antigen presenting cell; APC;

XX tumouricidal immunocyte; antitumour.

XX OS Unidentified.

XX FN US2002177551-A1.

XX PD 28-NOV-2002.

XX PF 30-MAY-2001; 2001US-00870759.

XX PR 31-MAY-2000; 2000US-0208128P.

XX PA (TERM/) TERMAN D S.

XX PI Terman DS;

XX DR WPI; 2003-361759/34.

XX DR N-PSDB; ACA64740.

XX A mammalian cell receptor, useful in the treatment of cancer by binding
 XX to tumor associated lipids where the binding induces anergy or apoptosis
 XX in T cells and antigen presenting cells.

XX Example 2; Page; 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the
 XX treatment of cancer, which binds to tumour associated lipids and induces
 XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 XX Also included are a mammalian cell useful in the treatment of cancer
 XX where the receptor which binds tumour associated lipids and induces
 XX cellular inactivation or death is deleted or functionally deactivated,
 XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 XX (by allowing tumour associated lipids to contact immunocytes in which
 XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 XX sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 XX deleted), a construct useful in the treatment of cancer comprising a

CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal APC
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 6; Length 1144;

Best Local Similarity 83.3%; Pred. No. 9.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6

Db 514 KVVFFA 519

RESULT 59

ADP43404

ID ADP43404 standard; protein; 1144 AA.

XX AC

XX ADP43404;

XX DT 12-FEB-2004 (first entry)

XX DE iNOS polypeptide seqid 124.

XX receptor; lipid-based tumour associated antigen; cytostatic;

XX antimicrobial; gene therapy; neoplastic disease; tumour; cancer;

XX infectious disease; iNOS.

XX OS Unidentified.

XX US2003157113-A1.

XX PD 21-AUG-2003.

XX PF 28-DEC-2000; 2000US-00751708.

XX PR 28-DEC-1999; 99US-0173371P.

XX XX

DE Inducible nitrogen monoxide synthase.
 XX nitrogen monoxide synthase; inducible; treatment; prevention;
 KW vascular disease; restenosis.
 XX
 OS Mus musculus.
 XX
 PN DE4411402-A1.
 XX
 PD 05-OCT-1995.
 XX
 XX 31-MAR-1994; 94DE-04411402.
 XX
 XX 31-MAR-1994; 94DE-04411402.
 XX
 PA (SCHR/) SCHRADER J.
 XX
 XX Schrader J, Goedecke A;
 XX
 XX WPI; 1995-345550/45.
 DR N-PSDB; AAQ94252.
 XX
 XX Eukaryotic expression vector for nitrogen-monoxide synthase gene -
 PT useful in the treatment and prevention of diseases of blood vessels by
 PT gene therapy.
 XX
 XX Claim 5; Fig 1; 28pp; German.
 XX
 XX Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and
 CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per
 CC subunit. The activity of iNOS is independent of calmodulin and cellular
 CC calcium levels. Vectors contg. the DNA are used in the treatment or
 CC prevention of vascular diseases, high blood pressure, arteriosclerosis,
 CC stenosis or restenosis of blood vessels, esp. coronary vessels after
 CC percutane transluminal coronary angioplasty. See AAR77363 and AAR77362
 CC for endothelial and brain-derived NOS
 XX
 XX Sequence 1144 AA;
 SQ

Query Match 96.6%; Score 28; DB 2; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIVFFA 6
 Db 514 KVVFFA 519
 |:|||||
 RESULT 56
 AAWS1246
 ID AAWS1246 standard; protein; 1144 AA.
 XX
 AC AAWS1246;
 XX
 XX 25-MAR-2003 (revised)
 DT 12-AUG-1998 (first entry)
 XX
 XX Inducible nitric oxide synthase, long isoform.
 XX
 XX Inducible nitric oxide synthase; iNOS; recombinant protein; cDNA library;
 KW isoform.
 XX
 XX Mus sp.
 OS
 XX US5766909-A.
 PN
 XX 16-JUN-1998.
 PD
 XX 05-NOV-1993; 93US-00147812.
 PF
 XX 04-FEB-1992; 92US-00841641.
 PR
 XX (MERI) MERCK & CO INC.
 PA

XX Mumford RA, Calaycay JR, Xie Q, Nathan CF;
 PI WPI; 1998-361696/31.
 XX
 DR N-PSDB; AAV07247.
 XX
 XX DNA encoding inducible nitric oxide synthase proteins - useful for
 PT producing recombinant proteins.
 XX
 XX Claim 1; Col 25-32; 39pp; English.
 PS
 XX The invention relates to two DNA molecules encoding inducible nitric
 CC oxide synthase (iNOS) proteins, where the DNA molecules comprise defined
 CC sequences of 4041 and 4165 base pairs given in the specification and the
 CC proteins have 1144 amino acids. Also claimed are expression vectors
 CC containing the DNA molecules, and recombinant host cells containing the
 CC vectors. The DNA molecules are useful for producing the recombinant
 CC proteins. The present sequence represents inducible nitric oxide, long
 CC isoform. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 1144 AA;
 SQ

Query Match 96.6%; Score 28; DB 2; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIVFFA 6
 Db 514 KVVFFA 519
 |:|||||
 RESULT 57
 AAG64500
 ID AAG64500 standard; protein; 1144 AA.
 XX
 AC AAG64500;
 XX
 XX 02-OCT-2001 (first entry)
 DT
 XX Mouse inducible nitric oxide synthase 2.
 DE
 XX Antisense oligonucleotide; inducible nitric oxide synthase;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotrophic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; mouse.
 XX
 XX Mus sp.
 OS
 XX WO200152902-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 15-JAN-2001; 2001WO-US001381.
 PF
 XX 24-JAN-2000; 2000US-00490208.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Dean NM, Cowsert LM;
 PI WPI; 2001-465340/50.
 XX
 DR N-PSDB; AAH47974.
 DR
 XX New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.
 PT
 XX Example 17; Page 110-114; 144pp; English.
 PS
 XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridise to and modulate

CC a small inhibitory dsRNA, or a ribozyme. As such, the compositions and
 CC methods are useful for diagnosing and treating diseases or conditions
 CC associated with abnormal apoptosis in mammalian tissues, such as cancer,
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and
 CC neuroprotective activities. These may also be used for drug screening
 CC purposes and in gene therapy. This polypeptide sequence is a human target
 CC protein, an enzyme associated with the regulation of apoptosis whose
 CC expression is modulated by novel agents of the invention.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|
 DB 292 KVVFFA 297

RESULT 53

ID ADY17516 standard; protein; 925 AA.

XX

AC ADY17516;

XX 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 3322.

DE Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 8; SEQ ID NO 3322; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 9; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|

DB 292 KVVFFA 297

RESULT 54

ID AEA23525 standard; protein; 925 AA.

XX AEA23525;

XX 11-AUG-2005 (first entry)

XX Human PRO polypeptide SEQ ID NO 67.

DE immune disorder; PRO; Antiinflammatory; Dermatological;
 KW Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic;
 KW Muscular-Gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant.

XX Homo sapiens.

XX WO2005051988-A2.

XX 09-JUN-2005.

XX 02-MAR-2004; 2004WO-US006460.

XX 03-MAR-2003; 2003US-0451884P.

XX (GETH) GENENTECH INC.

XX Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI,
 PI Wu TD;

XX WPI; 2005-417958/42.

XX N-PSDB; AEA23524.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or
 PT psoriasis.

XX Disclosure; SEQ ID NO 67; 966pp; English.

XX The invention relates to an isolated nucleic acid. The polypeptide,
 CC compound or composition, and methods are useful for diagnosing and
 CC treating an immune related disorder, e.g. systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,
 CC spondyloarthropathies, systemic sclerosis, idiopathic inflammatory
 CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases
 CC including bullous skin diseases, erythema multiforme and contact
 CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
 CC present sequence represents the amino acid sequence of a human PRO
 CC polypeptide.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 9; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|

DB 292 KVVFFA 297

RESULT 55

ID AAR77360 standard; protein; 1144 AA.

XX AAR77360;

XX 10-MAY-1996 (first entry)

XX

CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 292 KVVFFA 297
 |:|:|

RESULT 51
 ADP25011
 ID ADP25011 standard; protein; 925 AA.

AC ADP25011;

DT 18-NOV-2004 (first entry)

DE PRO polypeptide SEQ ID NO:2189.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WJ;
 PI Wu TD;

DR WPI; 2004-419628/39.

DR N-PSDB; ADP25010.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.

XX Claim 7; SEQ ID NO 2189; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 292 KVVFFA 297
 |:|:|

RESULT 52

ADR97294

ID ADR97294 standard; protein; 925 AA.

AC ADR97294;

DT 02-DEC-2004 (first entry)

DE Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX human; enzyme; apoptosis; cancer; inflammation; autoimmune;
 KW neurodegenerative disorder; cytostatic; antiinflammatory;
 KW immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX Homo sapiens.

XX WO2004078783-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-GB000957.

XX 07-MAR-2003; 2003GB-00005267.

XX (BIRX-) BIRX THERAPEUTICS LTD.

XX Murphy FJ, Sheehan DE, Keating KE, Hayes I, Seera L;

DR WPI; 2004-662402/64.

DR N-PSDB; ADR97293.

XX Identifying an agent that modulates the function of an apoptosis-
 PT associated polypeptide, useful for diagnosing or treating e.g. cancer,
 PT comprises comparing the binding of the polypeptide to the candidate agent
 PT and to a control agent.

XX Claim 1; SEQ ID NO 2; 304pp; English.

XX This invention relates to novel agents that modulates the function of
 CC human apoptosis-associated proteins specified within the specification.
 CC Specifically, it refers to a method for the identification of target
 CC genes whose expression is correlated with an early stage in the
 CC regulation of apoptosis. The present invention describes a method of
 CC contacting either candidate agents or control agents to the target genes
 CC and assessing the difference of binding and inhibitory activity, where
 CC the candidate agent is selected from a low molecular weight organic
 CC molecule, an antibody or fragment thereof, an antisense oligonucleotide,

CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|
 Db 292 KVVFFA 297

RESULT 49
 ADN04860
 ID ADN04860 standard; protein; 925 AA.

XX AC ADN04860;

XX DT 01-JUL-2004 (first entry)

XX DE Antipsoriatic protein sequence #610.

XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX OS Homo sapiens.

XX PN WO2004028479-A2.

XX PD 08-APR-2004.

XX PF 25-SEP-2003; 2003WO-US030907.

XX PR 25-SEP-2002; 2002US-0414006P.

XX PA (GETH) GENENTECH INC.

XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 XX Wu TD;

XX DR WPI: 2004-305105/28.

XX DR N-PSDB; ADN04859.

XX PT New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

XX PS Claim 9; SEQ ID NO 1254; 3069pp; English.

XX CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|
 Db 292 KVVFFA 297

Db

292 KVVFFA 297

RESULT 50

ADN14233

ID ADN14233 standard; protein; 925 AA.

XX AC ADN14233;

XX DT 21-OCT-2004 (first entry)

XX DE Human NF-kappaB pathway-associated protein SeqID234.

XX KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnery; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.

XX OS Homo sapiens.

XX PN WO2004065577-A2.

XX PD 05-AUG-2004.

XX PF 13-JAN-2004; 2004WO-US000798.

XX PR 14-JAN-2003; 2003US-0440068P.

XX PR 12-MAY-2003; 2003US-0469757P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Nadler SG, Neubauer MG, Feder JN, Carman J;

XX DR WPI: 2004-562168/54.

XX DR N-PSDB; ADN14232.

XX PT New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.

XX PS Claim 6; SEQ ID NO 234; 237pp; English.

XX CC This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antitumor, immunosuppressive or
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnery activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

SQ Sequence 925 AA;
Query Match 96.6%; Score 28; DB 7; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 47
ADJ75428
ID ADJ75428 standard; protein; 925 AA.
XX AC ADJ75428;
XX DT 20-MAY-2004 (first entry)
XX DE Marker gene related amino acid sequence SEQ ID NO:680.
XX KW bronchial asthma; chronic obstructive pulmonary disease;
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX KW gene therapy; marker.
XX OS Homo sapiens.
XX PN EP1394274-A2.
XX PD 03-MAR-2004.
XX PF 04-AUG-2003; 2003EP-00254857.
XX PR 06-AUG-2002; 2002JP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX PA (GENO-) GENOX RES INC.
XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX Example 11; SEQ ID NO 680; 241pp; English.

CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a

CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX SQ Sequence 925 AA;
Query Match 96.6%; Score 28; DB 8; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 48
ADJ75495
ID ADJ75495 standard; protein; 925 AA.
XX AC ADJ75495;
XX DT 20-MAY-2004 (first entry)
XX DE Marker gene related amino acid sequence SEQ ID NO:747.
XX KW bronchial asthma; chronic obstructive pulmonary disease;
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX KW gene therapy; marker.
XX OS Homo sapiens.
XX PN EP1394274-A2.
XX PD 03-MAR-2004.
XX PF 04-AUG-2003; 2003EP-00254857.
XX PR 06-AUG-2002; 2002JP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX PA (GENO-) GENOX RES INC.
XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX Example 11; SEQ ID NO 747; 241pp; English.

CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial

```
SQ Sequence 922 AA;
  Query Match          96.6%; Score 28; DB 8; Length 922;
  Best Local Similarity 83.3%; Pred. No. 7.9e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:|||||
Db 291 KIVFFA 296

RESULT 45
ADF76335
ID ADF76335 standard; protein; 925 AA.
XX
AC ADF76335;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SeqID 8.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN WO2003072035-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005241.
XX
PR 22-FEB-2002; 2002US-0359461P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
WPI; 2003-721702/68.
DR N-PSDB; ADF76334.
XX
XX New PRO polypeptides, useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
XX diabetes mellitus.
PS Claim 10; SEQ ID NO 8; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.
```

```
XX
SQ Sequence 925 AA;
  Query Match          96.6%; Score 28; DB 7; Length 925;
  Best Local Similarity 83.3%; Pred. No. 7.9e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:|||||
Db 292 KIVFFA 297

RESULT 46
ADJ70225
ID ADJ70225 standard; protein; 925 AA.
XX
AC ADJ70225;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2031.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy tagged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX comprises detecting a modified polypeptide in a sample and correlating
XX with the disease.
PS Claim 1; SEQ ID NO 2031; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC tagged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
```

XX PS Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent

XX CC capable of detecting 1000 or more genes from *Drosophila*. The invention is

XX CC useful in developmental biology and in elucidating cell signalling and

XX CC cell-cell interactions in higher eukaryotes for the development of

XX CC insecticides, therapeutics and pharmaceutical drugs. The invention

XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-

XX CC ABB72072). The sequence data for this patent did not form part of the

XX CC printed specification, but was obtained in electronic format directly

XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 564 AA;

Query Match 96.6%; Score 28; DB 4; Length 564;

Best Local Similarity 83.3%; Pred. NO. 4.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 53 KIIFFA 58

RESULT 43

ADQ66704

ID ADQ66704 standard; protein; 854 AA.

XX AC ADQ66704;

XX DT 07-OCT-2004 (first entry)

XX DE Novel human protein sequence #1677.

XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

XX KW gene therapy; diagnostic marker; morbid state; osteoporosis;

XX KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

XX KW cancer.

XX OS Homo sapiens.

XX FN EPI440981-A2.

XX PD 28-JUL-2004.

XX PF 21-JAN-2004; 2004EP-00001196.

XX PR 21-JAN-2003; 2003JP-00102206.

XX PR 09-MAY-2003; 2003JP-00131392.

XX FA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Iisogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX DR WPI; 2004-535376/52.

XX DR N-PSDB; ADQ64516.

XX PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,

XX PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX PS Claim 1; SEQ ID NO 3865; 2449pp; English.

XX CC The invention relates to 2495 novel polynucleotides (I) and their encoded

XX CC polypeptides, sequences hybridizing to these nucleotides, sequences

XX CC encoding partial polypeptides and sequences having 70% or 90% identity to

XX CC the nucleotide and protein sequences. The nucleotides and polypeptides

XX CC are useful as diagnostic markers or therapeutic target for the diseases

XX CC or morbid states. They are also useful for treating osteoporosis,

XX CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,

XX CC dementia and various cancers. This sequence corresponds to a protein

XX CC sequence of the invention.

XX SQ Sequence 854 AA;

Query Match 96.6%; Score 28; DB 8; Length 854;

Best Local Similarity 83.3%; Pred. NO. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 221 KVVFFA 226

RESULT 44

ABM83252

ID ABM83252 standard; protein; 922 AA.

XX AC ABM83252;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:3501.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX KW Homo sapiens.

XX FN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV;

XX PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

XX PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX PI Patury S, Shi X, Suarez CJ;

XX DR WPI; 2004-329368/30.

XX DR N-PSDB; ACN41904.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX PT in diagnosing a condition, disease or disorder associated with human

XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides

XX CC selected from one of the 2722 sequences defined in the specification. A

XX CC polynucleotide of the invention may have a use in gene therapy. The human

XX CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

XX CC used to diagnose a particular condition, disease or disorder associated

XX CC with human molecules, e.g. cell proliferative disorders,

XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine

XX CC disorder, neurological disorders, gastrointestinal disorders, or

XX CC infections caused by virus, bacteria, fungi or parasite. The dithp

XX CC molecules may also be used in genetic mapping in identifying individuals

XX CC from minute biological samples, in detecting single nucleotide

XX CC polymorphisms, as molecular weight markers, and for somatic or germline

XX CC gene therapy. The present sequence represents a dithp protein of the

XX CC invention. Note: The sequence data for this patent is not represented in

XX CC the printed specification, but was obtained in electronic format directly

XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

```

PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241788P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
XX
XX

PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
DR N-PSDB; AAK56573.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 11385; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 190 AA;
Query Match 96.6%; Score 28; DB 4; Length 190;
Best Local Similarity 83.3%; Pred. NO. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db |:|
14 KVVFFA 19
RESULT 42
ABB61977
ID ABB61977 standard; protein; 564 AA.
XX AC ABB61977;
XX 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 12723.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX OS Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL06080.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
```


KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
KW gene; ds; plant.
XX
OS Oryza sativa.
XX
XX WO2003000905-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-IB002450.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX 26-SEP-2001; 2001US-0325277P.
XX 20-DEC-2001; 2001US-0342327P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Glazebrook J, Katagiri F, Kreps J, Provart N, Rickel D;
XX
XX WPI; 2003-229341/22.
XX N-PSDB; ADC07947.
XX
XX New plant genes encoding polypeptides having an activity involved in or
PT associated with the synthesis, metabolism or degradation of carbohydrates
PT in the plant grain useful in generating plants having improved
PT nutritional properties.
XX
XX Claim 15; SEQ ID NO 214; 130pp; English.
XX
XX This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is the
CC amino acid sequence of a rice protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences.
XX
XX SQ Sequence 186 AA;

Query Match 96.6%; Score 28; DB 7; Length 186;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|:|
Db 4 KVFFFA 9

RESULT 41
AAM83792
ID AAM83792 standard; protein; 190 AA.
XX
AC AAM83792;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen SEQ ID NO:11385.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
XX Homo sapiens.
XX

XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205515P.
XX 07-JUN-2000; 2000US-0209467P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216800P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225266P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 14-AUG-2000; 2000US-0225759P.
XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
XX 22-AUG-2000; 2000US-0226682P.
XX 23-AUG-2000; 2000US-0227182P.
XX 23-AUG-2000; 2000US-0227009P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 06-SEP-2000; 2000US-0230437P.
XX 06-SEP-2000; 2000US-0230438P.
XX 08-SEP-2000; 2000US-0231242P.
XX 08-SEP-2000; 2000US-0231243P.
XX 08-SEP-2000; 2000US-0231244P.
XX 08-SEP-2000; 2000US-0231413P.
XX 08-SEP-2000; 2000US-0231414P.
XX 08-SEP-2000; 2000US-0232080P.
XX 08-SEP-2000; 2000US-0232081P.
XX 12-SEP-2000; 2000US-0231968P.
XX 14-SEP-2000; 2000US-0232397P.
XX 14-SEP-2000; 2000US-0232398P.
XX 14-SEP-2000; 2000US-0232399P.
XX 14-SEP-2000; 2000US-0232400P.
XX 14-SEP-2000; 2000US-0232401P.
XX 14-SEP-2000; 2000US-0233063P.
XX 14-SEP-2000; 2000US-0233064P.
XX 14-SEP-2000; 2000US-0233065P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.
XX 25-SEP-2000; 2000US-0234998P.
XX 26-SEP-2000; 2000US-0235484P.
XX 27-SEP-2000; 2000US-0235834P.

CC The polypeptide mutant, polynucleotide and methods are useful for
CC diagnosing or treating a condition associated with aberrant eNOS
CC activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
CC Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.
XX
SQ Sequence 37 AA;

Query Match 96.6%; Score 28; DB 8; Length 37;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 18 KVVFFA 23
|:|||||

RESULT 37
AAG02840
ID AAG02840 standard; protein; 77 AA.
XX
AC AAG02840;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 6921.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
DR N-PSDB; AAC02846.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 6921; 71pp + Sequence Listing; English.
XX

The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX

SQ Sequence 77 AA;

Query Match 96.6%; Score 28; DB 3; Length 77;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

CC encoding allergen specific T-cell epitope peptide, inserting a DNA into
 CC the variable region of storage protein of the plant and expressing the
 CC peptide in the transgenic plant. The invention describes the accumulation
 CC of human T cell epitope in rice albumen, a method of accumulating T cell
 CC epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp
 CC into the variable region of glutenin (the major storage protein of rice),
 CC and expressing and accumulating 7crp as part of the glutenin. The rice
 CC capable of producing the 7crp is useful as an edible vaccine against
 CC Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen
 CC is Cryj1 or Cryj2. The T-cell epitope is integrated on an edible region
 CC such as the seed of a plant. The method of the invention is useful for
 CC producing a plant accumulated with allergen specific T-cell epitope, and
 CC manufacturing a transgenic plant, preferably rice, integrated with T-cell
 CC epitope. The method is useful for preventing or treating allergic disease
 CC such as hay fever. The method enables the production of allergen specific
 CC T-cell epitope at a low cost and also reduces the amount for
 CC administration. The allergen specific T-cell epitope accumulated in a
 CC seed is stable for storage. This sequence represents rice 26 kDa peptide.
 XX
 XX
 SQ Sequence 23 AA;

Query Match 96.6%; Score 28; DB 8; Length 23;
 Best Local Similarity 83.3%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:||||
 Db 4 KVVFFA 9

RESULT 34
 AAB05910
 ID AAB05910 standard; peptide; 37 AA.
 XX
 AC AAB05910;
 XX
 DT 16-OCT-2000 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase calmodulin-binding region.
 XX
 XX Mouse; inducible nitric oxide synthase; iNOS;
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
 KW AMP-activated protein kinase; AMPK; calmodulin; CaM;
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
 KW obstructive airways disease.
 XX
 OS Mus sp.

XX WO200028076-A1.
 XX
 XX 18-MAY-2000.
 XX
 XX 05-NOV-1999; 99WO-AU000968.
 XX
 XX 06-NOV-1998; 98AU-00006976.
 XX
 XX (SVIN-) ST VINCENTS INST MEDICAL RES.
 XX
 XX Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;
 XX WPI; 2000-376583/32.
 XX
 XX Identifying modulators of AMP-activated protein kinase-mediated
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
 PT disease, comprises testing for the increase or decrease in
 PT phosphorylation of NOS.
 XX
 XX Example 4; Fig 5; 41pp; English.

XX The present sequence is the calmodulin (CaM)-binding region of mouse
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric

CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca²⁺-CaM. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca²⁺-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease

XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 3; Length 37;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:||||
 Db 18 KVVFFA 23

RESULT 35
 ADK34080
 ID ADK34080 standard; peptide; 37 AA.
 XX
 AC ADK34080;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human nNOS calmodulin binding domain peptide seqid 7.
 XX
 KW vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;
 KW microvascular dysfunction; human; calmodulin binding domain;
 KW neuronal nitric oxide; nNOS.
 XX
 OS Homo sapiens.
 XX
 XX WO2004016761-A2.
 XX
 XX 26-FEB-2004.
 XX
 XX 15-AUG-2003; 2003WO-US025626.
 XX
 XX 16-AUG-2002; 2002US-0403637P.
 XX
 XX (SCHD) SCHERING AG.
 XX
 XX Dole WP, Kauser K, Qian HS, Rubanyi G;
 XX WPI; 2004-203789/19.
 XX
 XX Treating critical limb ischemia (CLI), or angiogenesis comprises
 PT administering to a patient a polynucleotide encoding a mammalian
 PT endothelial nitric oxide synthase (eNOS) polypeptide.
 XX
 XX Example 1; SEQ ID NO 7; 82pp; English.

XX The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a human neuronal nitric synthase
 CC (nNOS) calmodulin binding domain peptide.

XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 8; Length 37;
 Best Local Similarity 83.3%; Pred. No. 32;

Query Match 96.6%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 32
ADQ09761
ID ADQ09761 standard; peptide; 22 AA.
XX
AC ADQ09761;
XX
DT 23-SEP-2004 (first entry)
XX
DE Rice 26kDa globulin signal sequence SEQ ID NO:117.
XX
KW prolamine; rice; plant; seed; transgenic plant; signal.
XX
OS Oryza sativa.
XX
PN WO2004056993-A1.
XX
PD 08-JUL-2004.
XX
PF 09-DEC-2003; 2003WO-JP015753.
XX
PR 20-DEC-2002; 2002JP-00369700.
XX
PA (NAA-) NAT AGRIC & BIO-ORIENTED RES ORG.
XX
PI Kuroda M;
XX
DR WPI; 2004-525439/50.
DR N-PSDB; ADQ09760.
XX
PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding
prolamine, useful for reducing expression dose of protein in seed, and
for producing transgenic plant, preferably rice plant having reduced
storage protein.
XX
PS Example 13; SEQ ID NO 117; 272pp; Japanese.
XX
CC The present invention describes a nucleic acid molecule (I) comprising a
consecutive nucleic acid sequence (SI) of at least 15 bp in length and
complementary with a nucleic acid sequence encoding a prolamine
polypeptide or a nucleic acid sequence having a homology of at least
about 70% to (SI). Also described: (1) a nucleic acid molecule (NI)
comprising a nucleic acid sequence (A) having about 70% homology to a
nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid
sequence (B) having about 70% homology to the complement of the nucleic
acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable
of causing RNA interference of the gene sequence encoding a prolamine
polypeptide; (3) a nucleic acid cassette (III) containing (I); (4)
producing (III); (5) a vector (IV) comprising (I); (6) a plant cell (V)
comprising (I); (7) a plant tissue (VI) comprising (V); (8) a plant (VII)
containing (I) or (V); (9) a seed (VIII) produced by (VII); (10) starch
preparation produced from (VII) or (VIII); and (11) a composition
containing gene product of foreign gene produced from (VII) or (VIII).
(I) is useful for decreasing the expression level of a protein in the
seed of a plant, for expressing a foreign gene in the seed of a plant and
for decreasing the expression of a natural protein in the seed of a
plant. The method of decreasing the amount of expression level of a
protein in the seed of a plant involves providing (I), introducing (I)
into the cell of the plant, redifferentiating the cell, producing a
transgenic plant, and obtaining the seed from the transgenic plant. The
method after the step of introduction, further involves selecting the
cell introduced with (I), by determining resistance with respect to
antibiotics. The method of expressing a foreign gene in the seed of a
plant, involves providing (I) and the nucleic acid molecule encoding a

CC foreign gene product, introducing (I) and the nucleic acid molecule
CC encoding a foreign gene product into cell of the plant, re-
CC differentiating the cell, producing a transgenic plant, and obtaining the
CC seed from the transgenic plant. The method further involves isolating the
CC gene product of the foreign gene from the seed. (I) is useful for
CC producing transgenic plants having reduced expression of storage proteins
CC and for reducing the expression dose of a protein in a seed of a plant.
CC The present sequence represents a rice 26kDa globulin signal sequence,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 22 AA;
XX
Query Match 96.6%; Score 28; DB 8; Length 22;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 33
ADT93984
ID ADT93984 standard; peptide; 23 AA.
XX
AC ADT93984;
XX
DT 27-JAN-2005 (first entry)
XX
DE Rice 26 kDa peptide.
XX
KW Storage protein; allergen specific T cell epitope;
KW vesicle anchoring signal; transgenic plant; rice albumen;
KW T cell epitope-attached peptide; 7crp; seed; glutelin; edible vaccine;
KW Japanese cedar pollen antigen; Cryj1; Cryj2; allergic disease; hay fever;
KW antiallergic; plant; 26 kDa.
XX
OS Oryza sativa.
XX
FN WO2004094637-A1.
XX
PD 04-NOV-2004.
XX
PF 23-APR-2004; 2004WO-JP005938.
XX
PR 24-APR-2003; 2003JP-00120639.
XX (NORQ) NAT INST AGROBIOLOGICAL SCI.
XX Takaiwa F, Takagi H;
XX WPI; 2004-784905/77.
XX
PT Novel DNA having sequence encoding allergen specific T-cell epitope
peptide, useful for accumulating T-cell epitope peptide in plants and for
treating allergic diseases such as pollinosis.
XX
PS Disclosure; SEQ ID NO 5; 79pp; Japanese.
XX
CC This invention relates to a DNA (I) having a sequence under the control
of a storage protein promoter, chosen from a sequence encoding storage
protein signal sequence at the 5' end of a sequence encoding allergen
specific T cell epitope peptide and/or a sequence encoding vesicle
anchoring signal sequence at the 3' end, and a DNA sequence encoding a
polypeptide having allergen specific T-cell epitope peptide inserted in
the variable region of a storage protein. Also disclosed is a vector (II)
for T-cell epitope accumulated plant preparation, and a method of
accumulating allergen specific T-cell epitope in a plant. The method
involves introducing (I) or (II) to a plant, obtaining DNA encoding
allergen specific T-cell epitope peptide, adding a DNA encoding a storage
protein signal sequence to the 5' end and/or a vesicle anchoring signal
sequence to the 3' end of the obtained DNA, and expressing the DNA in a
plant under the control of a storage protein promoter, or obtaining DNA

Qy 1 KIVEFA 6
|:||||
Db 1 KIVEFA 6

RESULT 30

ADY37928
ID ADY37928 standard; peptide; 6 AA.

XX AC ADY37928;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX DR WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-

XX PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform

XX PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 8; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

XX SQ Sequence 6 AA;

Query Match 96.8%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVEFA 6
|:||||
Db 1 KIVEFA 6

RESULT 31

ADY37936
ID ADY37936 standard; peptide; 6 AA.

XX AC ADY37936;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 6 /note= "C-terminal amide"

XX XX US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX XX (NEUR-) NEUROCHEM INT LTD.

XX XX Gervais F, Kong X, Chalifour R, Migneault D;

XX XX WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-

XX PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform

XX PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 16; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

XX SQ Sequence 6 AA;

agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser, uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVFVFA 6

RESULT 29

ADQ37329
ID ADQ37329 standard; peptide; 6 AA.

XX AC ADQ37329;

DT 07-OCT-2004 (first entry)

DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; nootropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquiliser; uteropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;

vacine antigen.
XX Synthetic.
OS Key Location/Qualifiers
FH Modified-site 6
FT /note= "amidated"
XX W02004058239-A1.
PN 15-JUL-2004.
XX 24-DEC-2003; 2003WO-CA002021.
PD 24-DEC-2002; 2002US-0436379P.
PF 23-JUN-2003; 2003US-0482214P.
XX (NEUR-) NEUROCHEM INT LTD.
XX Gervais F, Bellini F;
XX WPI; 2004-543342/52.
DR Composition for treating e.g. Alzheimer's disease comprises first agent
XX that prevents or treats amyloid-beta related disease and second agent
XX that is either a peptide or peptidomimetic or an immune system modulator.
PS Disclosure; Page 70; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)
XX a second agent (a2) that is: (i) a peptide or peptidomimetic that
XX modulates amyloid-beta fibril formation or induces a prophylactic or
XX therapeutic immune response against amyloid-beta fibril formation; or
XX (ii) an immune system modulator that prevents or inhibits amyloid-beta
XX fibril formation. Also described is a kit comprising (C). (C) have
XX nootropic, neuroprotective, cerebroprotective, haemostatic,
XX ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
XX uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
XX neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
XX and can be used as amyloid-beta fibril formation modulators, and as
XX immune system modulators. (C) can be used for preventing or treating an
XX amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
XX (non-hereditary) or familial (hereditary)), mild cognitive impairment,
XX amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
XX Down's syndrome, inclusion body myositis, age-related macular
XX degeneration, or a condition associated with Alzheimer's disease
XX (including hypothyroidism, cerebrovascular disease, cardiovascular
XX disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
XX aggression, or incontinence), a neurological condition (e.g. Huntington's
XX disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
XX Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
XX with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
XX field deficits, incoordination, gait disturbance, transient ischaemic
XX attack or stroke, transient alertness, attention deficit, frequent falls,
XX syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
XX haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
XX damage), or a psychological condition (e.g. depression, delusions,
XX illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
XX disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
XX ideation, depressed mood, irritability, anhedonia, social withdrawal, or
XX excessive guilt)) in a subject e.g. human having a genomic mutation in an
XX amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
XX having amyloid-beta deposits. The present sequence represents a peptide
XX that can be used as an antifibrillogenic amyloidosis inhibiting peptide
XX in the exemplification of the present invention.

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "amidated"
 FT
 FT
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC ophthalmological, antithyroid, cerebroprotective, haemostatic,
 CC neuroleptic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC uropathic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVPFA 6
 Db 1 KVPFPA 6

RESULT 28

ADQ37321
 ID ADQ37321 standard; peptide; 6 AA.

XX AC ADQ37321;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX KW amyloid-beta; amyloid-beta related disease;

XX KW amyloid-beta fibril formation; immune response; neurotropic;

XX KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

XX KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;

XX KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

XX KW cardiant; antidepressant; endocrine; hypnotic;

XX KW amyloid-beta fibril formation modulator; immune system modulator;

XX KW Alzheimer's disease; mild cognitive impairment;

XX KW mild-to-moderate cognitive impairment; vascular dementia;

XX KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

XX KW senile dementia; Down's syndrome; inclusion body myositis;

XX KW age-related macular degeneration; hypothyroidism;

XX KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;

XX KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

XX OS Synthetic.

XX XX WO2004058239-A1.

XX PN 15-JUL-2004.

XX PD 24-DEC-2003; 2003WO-CA002021.

XX PF 24-DEC-2002; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX XX (NEUR-) NEUROCHEM INT LTD.

XX PA Gervais F, Bellini F;

XX PI WPI; 2004-543342/52.

XX DR Composition for treating e.g. Alzheimer's disease comprises first agent
 XX PT that prevents or treats amyloid-beta related disease and second agent
 XX PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX XX Disclosure; Page 69; 143pp; English.
 XX PS The present invention describes compositions (C) comprising: (a) a first
 XX CC

RESULT 25
AAU11656
ID AAU11656 standard; peptide; 6 AA.
AC AAU11656;
XX
XX
DT 09-APR-2002 (first entry)
XX
DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
OS Synthetic.
XX
FN WO200185093-A2.
XX
XX
PD 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
FT inhibitor.
XX
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
CC amyloid angiopathy. The new method of the invention involves contacting a
CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
CC can be used for treating disease states characterised by cerebral amyloid
CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
CC The present sequence represents one of a group of peptides (AAU11648-
CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
CC was used in the invention to treat a disease state characterised by
CC cerebral amyloid angiopathy (CAA)
XX
SQ Sequence 6 AA;
Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KVVFFA 6
|:|||||
|:|||||
RESULT 26
AAE35452
ID AAE35452 standard; peptide; 6 AA.
XX
XX AAE35452;
XX
XX 17-JUN-2003 (first entry)
XX
XX Abeta peptide #23.
DE
XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
KW

psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotic;
KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1. .6
FT Modified-site 6 /note= "D-form residues"
FT Modified-site 6 /note= "C-terminal amide"
XX
XX WO200296937-A2.
PN
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-CA000763.
XX
XX 29-MAY-2001; 2001US-00867847.
PR
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Hebert L, Chalifour RJ, Kong X;
PI WPI; 2003-201269/19.
XX
XX Prevention and/or treatment of an amyloid-related disease e.g.
PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
XX
XX Claim 1; Page 59; 44pp; English.
XX
XX The invention relates to a method for prevention and/or treatment of an
CC amyloid-related disease which comprises administration of an all-D -
CC amyloid-beta peptide. The method is used for preventing and/or treating
CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
CC the mammal; and reducing or inhibiting the formation of plaques. It is
CC also used for treating AA (reactive) amyloid diseases including
CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
CC disease. AA deposits are also produced as a result of chronic microbial
CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
CC present sequence is an Abeta peptide used to illustrate the method of the
CC invention
XX
SQ Sequence 6 AA;
Query Match 96.6%; Score 28; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KVVFFA 6
|:|||||
|:|||||
RESULT 27
ADQ37277
ID ADQ37277 standard; peptide; 6 AA.
XX
XX ADQ37277;
AC
XX
XX 07-OCT-2004 (first entry)
DT
XX Vaccine antigen amyloid-beta related amino acid sequence.
DE

```

XX SQ Sequence 6 AA;
SQ
  Query Match          96.6%; Score 28; DB 5; Length 6;
  Best Local Similarity 83.3%; Pred. No. 2e+06;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFFA 6
   |:|
DB 1 KVVFFFA 6
   |:|
RESULT 24
AAU11664
ID AAU11664 standard; peptide; 6 AA.
XX
AC AAU11664;
XX
DT 09-APR-2002 (first entry)
XX
DE Peptide #17, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
KW CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
FT
XX WO200185093-A2.
XX
PD 15-NOV-2001.
XX
PF 22-DEC-2000; 2000WO-IB002078.
XX
PR 23-DEC-1999; 99US-0171877P.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Green AM, Gervais F;
XX
DR WPI; 2002-075222/10.
XX
PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
PT inhibitor.
XX
PS Disclosure; Page 10; 68pp; English.
XX
CC The present invention relates to a new method of inhibiting cerebral
CC amyloid angiopathy. The new method of the invention involves contacting a
CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
CC can be used for treating disease states characterised by cerebral amyloid
CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
CC The present sequence represents one of a group of peptides (AAU11648-
CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
CC was used in the invention to treat a disease state characterised by
CC cerebral amyloid angiopathy (CAA)
XX
SQ Sequence 6 AA;
SQ
  Query Match          96.6%; Score 28; DB 5; Length 6;
  Best Local Similarity 83.3%; Pred. No. 2e+06;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFFA 6
   |:|
DB 1 KVVFFFA 6
   |:|
RESULT 23
AAU96826
ID AAU96826 standard; peptide; 6 AA.
XX
AC AAU96826;
XX
DT 30-JUL-2002 (first entry)
XX
DE Amyloid targeting peptide #16.
XX
KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
KW transmissible cerebral amyloidosis; transmissible virus dementia;
KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
KW bovine spongiform encephalopathy; inflammation associated amyloid;
KW primary amyloidosis; feline spongiform encephalopathy;
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
KW dialysis-related amyloidosis; light chain-related amyloidosis;
KW cerebral amyloid angiopathy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "Preferably D-form residue"
FT Modified-site 6 /note= "Ala is amidated"
FT
XX WO200207781-A2.
XX
PD 31-JAN-2002.
XX
PF 25-JUL-2001; 2001WO-CA001071.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Gervais F, Kong X, Chalifour R, Migneault D;
XX
DR WPI; 2002-371447/40.
XX
PT New amyloid-targeting imaging agents useful for in vivo imaging amyloid
PT plaques and/or for the treatment of amyloidosis disorders.
XX
PS Claim 49; Page 21; 57pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent comprising an
CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
CC agent is of general formula A-t-(A1-n1-k1)-z-A2-l2-a2-b2 (I) where z = 0 - 1;
CC A1-t = an amyloid targeting moiety; A1-n1-k1 = a linker moiety; and A1-l2-a2-b2
CC = a labelling moiety. Also included are imaging amyloid deposition or
CC diagnosing an amyloid-related condition in a patient involving
CC administering (I) to the patient, and ultrasound imaging (I) in the
CC patient to determine the presence of amyloid or amyloid-related condition
CC ; and a kit for preparing a radiopharmaceutical preparation comprising
CC (I), a reducing agent, a buffering agent, a transchelating agent, and
CC instructions for the preparation and use of the radiopharmaceutical in
CC the imaging of amyloid or an amyloid-related condition. The agents are
CC used for imaging amyloid deposition and for diagnosing an amyloid related
CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
CC scrapie, transmissible mink encephalopathy, bovine spongiform
CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
CC amyloid angiopathy. The agents are capable of crossing the blood-brain
CC barrier and are capable of binding specifically to amyloid plaques. The
CC present sequence is a peptide forming the amyloid targeting moiety of the
CC agent of the invention

```

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6

FT Modified-site 6

FT /note= "all D-form residues"

FT /note= "C-terminal amide"

XX WO200139796-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA001413.

XX 29-NOV-1999; 99US-0168594P.

XX 28-NOV-2000; 2000US-00724842.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Hebert L, Kong X, Gervais F;

XX WPI; 2001-441458/47.

XX Preventing/treating amyloid-related disease, especially Alzheimer's disease, comprises administering antigenic all-D peptide, eg. as vaccine, which elicits production of antibodies to prevent fibrillogenesis and associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in preparing vaccines for preventing or treating Alzheimer's disease and other amyloid related disorders in humans. It is based on a portion of amyloid-beta peptide (see AAB2622), and may be modified by removing or inserting 1 or more amino acid residues, or by substituting 1 or more amino acid residues with other amino acid residues or non-amino acid fragments. Vaccines of the invention are produced using 'non-self' peptides synthesised from the unnatural D-configuration amino acids to avoid the drawbacks of 'self' proteins. The all-D peptides need not be aggregated to be operative or immunogenic. They preferably interact with at least 1 region of an amyloid protein, e.g. the beta-sheet region or GAG-binding site region, the amyloid-beta peptide, or their immunogenic fragments, protein conjugates, immunogenic derivative peptides and immunogenic peptidomimetics. Examples include all-D peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D derivative peptides given in AAB2623-64. The vaccine elicits a preferential TH-2 or TH-1 response, preventing fibrillogenesis and associated cellular toxicity. The amyloid related diseases may be localised amyloidosis, e.g. diabetes type II, neurodegenerative diseases, e.g. bovine spongiform encephalitis, and Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and prion protein related disorders, or systemic amyloidosis associated with chronic infection (e.g. tuberculosis) or chronic inflammation (e.g. rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;

Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 1 KVVFFA 6

RESULT 22

AAU96818

ID AAU96818 standard; peptide; 6 AA.

XX AAU96818;

XX

30-JUL-2002 (first entry)

XX Amyloid targeting peptide #8.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD; transmissible cerebral amyloidosis; transmissible virus dementia; scrapie; transmissible mink encephalopathy; BSE; type II diabetes; bovine spongiform encephalopathy; inflammation associated amyloid; primary amyloidosis; feline spongiform encephalopathy; Alzheimer's disease; prion-mediated disease; blood-brain barrier; dialysis-related amyloidosis; light chain-related amyloidosis; cerebral amyloid angiopathy.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6

FT /note= "Preferably D-form residue"

FT WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an amyloid targeting moiety, a linker moiety and a labelling moiety. The agent is of general formula A t-(A l n k) z-A l a b (I) where z = 0 - 1; A t = an amyloid targeting moiety; A l n k = a linker moiety; and A l a b = a labelling moiety. Also included are imaging amyloid deposition or diagnosing an amyloid-related condition in a patient involving administering (I) to the patient, and ultrasound imaging (I) in the patient to determine the presence of amyloid or amyloid-related condition; and a kit for preparing a radiopharmaceutical preparation comprising (I), a reducing agent, a buffering agent, a transchelating agent, and instructions for the preparation and use of the radiopharmaceutical in the imaging of amyloid or an amyloid-related condition. The agents are used for imaging amyloid deposition and for diagnosing an amyloid related condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible cerebral amyloidosis (transmissible virus dementia), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy. The agents are capable of crossing the blood-brain barrier and are capable of binding specifically to amyloid plaques. The present sequence is a peptide forming the amyloid targeting moiety of the agent of the invention

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;

Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 1 KVVFFA 6

AC AAB48490;
 XX
 XX 02-MAR-2001 (first entry)
 XX
 XX Antifibrillogenic peptide #17.
 DE
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "C-terminal amide"
 FT
 XX WO200068263-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 04-MAY-2000; 2000WO-CA000515.
 XX
 XX 05-MAY-1999; 99US-0132592P.
 PR
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Gervais F, Gupta A;
 XX
 XX WPI; 2001-031852/04.
 DR
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 PT
 XX Claim 7; Page 25; 46pp; English.
 PS
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 CC
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 DB 1 KVVFFFA 6
 RESULT 20
 AAB82630
 ID AAB82630 standard; peptide; 6 AA.
 XX
 XX AAB82630;
 AC
 XX 02-OCT-2001 (first entry)
 DT
 XX All-D peptide used in Alzheimer's disease vaccine.
 DE
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1. .6
 FT /note= "all D-form residues"
 FT

XX WO200139796-A2.
 XX
 XX 07-JUN-2001.
 PD
 XX 29-NOV-2000; 2000WO-CA001413.
 PF
 XX 29-NOV-1999; 99US-0168594P.
 XX
 XX 28-NOV-2000; 2000US-00724842.
 PR
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 PI
 XX WPI; 2001-441458/47.
 DR
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 PT
 XX Disclosure; Page 11; 31pp; English.
 PS
 XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC prion protein related disorders, scrapie, cerebral amyloid angiopathy, and
 CC Creutzfeldt-Jakob disease, scrapie, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 DB 1 KVVFFFA 6
 RESULT 21
 AAB82638
 ID AAB82638 standard; peptide; 6 AA.
 XX
 XX AAB82638;
 AC
 XX 02-OCT-2001 (first entry)
 DT
 XX All-D peptide used in Alzheimer's disease vaccine.
 DE
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 KW
 XX

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 1 KIVFFA 6

RESULT 17
 ABG26598
 ID ABG26598 standard; protein; 99 AA.

XX AC ABG26598;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #26589.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS90785.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 56957; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 99 AA;

Query Match 100.0%; Score 29; DB 4; Length 99;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 63 KIVFFA 68

RESULT 18
 AAB48482

ID AAB48482 standard; peptide; 6 AA.

XX AC AAB48482;

XX DT 02-MAR-2001 (first entry)

XX DE Antifibrillogenic peptide #9.

XX KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200068263-A2.

XX PD 16-NOV-2000.

XX PF 04-MAY-2000; 2000WO-CA000515.

XX PR 05-MAY-1999; 99US-0132592P.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Chalifour R, Gervais F, Gupta A;

XX DR WPI; 2001-031852/04.

XX PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.

XX PS Claim 7; Page 25; 46pp; English.

XX CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycoaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 1 KIVFFA 6

RESULT 19
 AAB48490

ID AAB48490 standard; peptide; 6 AA.

XX

```

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |||||
Db 1 KIVFFA 6

RESULT 15
ADV37921
ID ADV37921 standard; peptide; 6 AA.
XX
AC ADV37921;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
FN US2005048000-A1.
XX
PD 03-MAR-2005.
XX
PF 03-DEC-2003; 2003US-00728028.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
PA (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX
PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 1; 34pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADV37921-ADV37947 and ADV37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

```

```

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |||||
Db 1 KIVFFA 6

RESULT 16
ADV37929
ID ADV37929 standard; peptide; 6 AA.
XX
AC ADV37929;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
FN US2005048000-A1.
XX
PD 03-MAR-2005.
XX
PF 03-DEC-2003; 2003US-00728028.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
PA (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX
PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 9; 34pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-10

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:*

1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*

6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	93.1	19	6	US-10-923-605-5
2	27	93.1	19	6	US-10-934-818-5
3	27	93.1	40	7	US-11-016-706-36
4	27	93.1	40	7	US-11-098-674-12
5	27	93.1	42	6	US-10-923-605-1
6	27	93.1	42	6	US-10-934-818-1
7	27	93.1	42	6	US-11-016-706-37
8	27	93.1	43	6	US-10-934-818-6
9	27	93.1	43	6	US-10-250-581-1
10	27	93.1	43	6	US-10-580-581-1
11	27	93.1	770	6	US-10-982-545-15
12	27	93.1	269	6	US-10-789-273-38
13	25	86.2	269	6	US-10-467-657-330
14	25	86.2	400	6	US-10-793-626-1056
15	24	82.8	50	6	US-10-467-657-7892
16	24	82.8	347	6	US-10-467-657-2014
17	24	82.8	402	6	US-10-467-657-9070
18	24	82.8	426	6	US-10-467-657-2120
19	24	82.8	524	6	US-10-689-742-13
20	24	82.8	660	7	US-11-186-284-125
21	24	82.8	677	6	US-10-131-826A-230
22	24	82.8	708	6	US-10-821-234-917
23	24	82.8	5	7	US-11-098-674-1
24	23	79.3	229	6	US-10-131-826A-410
25	23	79.3	311	6	US-10-793-626-2450

26	23	79.3	481	6	US-10-995-561-959	Sequence 959, App
27	23	79.3	522	7	US-11-080-991-104	Sequence 104, App
28	23	79.3	528	6	US-10-793-626-1930	Sequence 1930, App
29	23	79.3	533	6	US-10-467-657-2868	Sequence 2868, App
30	23	79.3	3623	6	US-10-995-561-593	Sequence 593, App
31	22	75.9	47	6	US-10-467-657-5436	Sequence 5436, App
32	22	75.9	98	6	US-10-467-657-4746	Sequence 4746, App
33	22	75.9	167	7	US-11-210-316-18	Sequence 18, Appl
34	22	75.9	211	6	US-10-467-657-6932	Sequence 6932, App
35	22	75.9	215	6	US-10-131-826A-4	Sequence 4, Appl
36	22	75.9	228	6	US-10-467-657-568	Sequence 568, App
37	22	75.9	228	6	US-10-467-657-4838	Sequence 4838, App
38	22	75.9	233	6	US-10-821-234-1322	Sequence 1322, App
39	22	75.9	239	6	US-10-467-657-432	Sequence 432, App
40	22	75.9	265	6	US-10-793-626-2500	Sequence 2500, App
41	22	75.9	330	6	US-10-793-626-2476	Sequence 2476, App
42	22	75.9	330	6	US-10-793-626-2734	Sequence 2734, App
43	22	75.9	338	6	US-10-878-556A-19	Sequence 19, Appl
44	22	75.9	344	6	US-10-131-826A-376	Sequence 376, App
45	22	75.9	358	7	US-11-055-822-572	Sequence 572, App
46	22	75.9	358	7	US-11-055-822-836	Sequence 836, App
47	22	75.9	432	7	US-11-194-246-308	Sequence 308, App
48	22	75.9	449	6	US-10-467-657-678	Sequence 678, App
49	22	75.9	453	7	US-11-082-389-198	Sequence 198, App
50	22	75.9	510	7	US-11-210-316-22	Sequence 22, Appl
51	22	75.9	539	7	US-11-210-316-25	Sequence 26, Appl
52	22	75.9	601	6	US-10-467-657-7120	Sequence 7120, App
53	22	75.9	635	6	US-10-821-234-1673	Sequence 1673, App
54	22	75.9	858	6	US-10-613-744-6	Sequence 6, Appl
55	22	75.9	2233	6	US-10-873-528-2	Sequence 2, Appl
56	21	72.4	43	6	US-10-467-657-7886	Sequence 7886, App
57	21	72.4	52	6	US-10-467-657-2216	Sequence 2216, App
58	21	72.4	76	6	US-10-467-657-5690	Sequence 5690, App
59	21	72.4	91	6	US-10-821-234-1703	Sequence 1703, App
60	21	72.4	123	6	US-10-793-626-430	Sequence 430, App
61	21	72.4	134	6	US-10-467-657-5166	Sequence 5166, App
62	21	72.4	123	6	US-10-793-626-2374	Sequence 2374, App
63	21	72.4	155	6	US-10-467-657-2420	Sequence 2420, App
64	21	72.4	175	6	US-10-965-694-23	Sequence 23, Appl
65	21	72.4	182	6	US-10-793-626-2836	Sequence 2836, App
66	21	72.4	182	6	US-10-467-657-3510	Sequence 3510, App
67	21	72.4	190	6	US-10-467-657-3436	Sequence 3436, App
68	21	72.4	211	6	US-10-821-234-1372	Sequence 1372, App
69	21	72.4	216	6	US-10-467-657-8102	Sequence 8102, App
70	21	72.4	221	6	US-10-467-657-2390	Sequence 2390, App
71	21	72.4	221	6	US-10-467-657-5750	Sequence 5750, App
72	21	72.4	254	6	US-10-467-657-6144	Sequence 6144, App
73	21	72.4	272	6	US-10-632-150-46	Sequence 46, Appl
74	21	72.4	272	7	US-11-073-457-46	Sequence 46, Appl
75	21	72.4	272	7	US-11-073-460-46	Sequence 45, Appl
76	21	72.4	278	6	US-10-957-569-45	Sequence 45, Appl
77	21	72.4	370	6	US-10-821-234-1105	Sequence 1105, App
78	21	72.4	440	7	US-11-082-389-106	Sequence 106, App
79	21	72.4	463	6	US-10-467-657-6352	Sequence 6352, App
80	21	72.4	463	6	US-10-467-657-7604	Sequence 7604, App
81	21	72.4	482	6	US-10-793-626-24	Sequence 24, Appl
82	21	72.4	496	7	US-11-067-121-12	Sequence 12, Appl
83	21	72.4	522	6	US-10-995-561-1030	Sequence 1030, App
84	21	72.4	525	7	US-11-082-389-350	Sequence 350, App
85	21	72.4	569	7	US-11-082-389-104	Sequence 104, App
86	21	72.4	582	7	US-11-090-439-58	Sequence 58, Appl
87	21	72.4	592	6	US-10-467-657-4888	Sequence 4888, App
88	21	72.4	615	6	US-10-995-561-940	Sequence 940, App
89	21	72.4	662	6	US-10-995-561-943	Sequence 943, App
90	21	72.4	702	7	US-10-995-561-942	Sequence 942, App
91	21	72.4	738	7	US-11-147-047-48	Sequence 48, Appl
92	21	72.4	747	7	US-11-018-018-1	Sequence 1, Appl
93	21	72.4	747	7	US-11-047-757-1	Sequence 1, Appl
94	21	72.4	754	6	US-10-995-561-941	Sequence 941, App
95	21	72.4	1061	7	US-11-000-463-347	Sequence 49, Appl
96	21	72.4	1070	7	US-11-147-047-49	Sequence 49, Appl
97	21	72.4	1091	7	US-11-000-463-348	Sequence 348, App
98	21	72.4	3507	7	US-11-075-185-7	Sequence 7, Appl

99	20	69.0	19	6	US-10-467-657-8712	Sequence 8712, Ap	172	20	69.0	325	6	US-10-454-437-142	Sequence 142, App
100	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	173	20	69.0	329	6	US-10-793-626-1942	Sequence 1942, Ap
101	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	174	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
102	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	337	6	US-10-485-517-234	Sequence 234, App
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	342	7	US-11-082-389-214	Sequence 214, App
104	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	177	20	69.0	343	6	US-10-467-657-7824	Sequence 7824, Ap
105	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	178	20	69.0	343	6	US-10-467-657-7256	Sequence 7256, Ap
106	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	179	20	69.0	343	6	US-10-467-657-7256	Sequence 7256, Ap
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	343	6	US-10-467-657-7256	Sequence 7256, Ap
108	20	69.0	42	6	US-10-467-657-8811	Sequence 8811, Ap	181	20	69.0	355	6	US-10-467-657-7996	Sequence 7996, Ap
109	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	182	20	69.0	355	6	US-10-995-561-636	Sequence 636, App
110	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	183	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
111	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	184	20	69.0	357	6	US-10-467-657-2500	Sequence 2500, Ap
112	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	185	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
113	20	69.0	54	6	US-10-467-657-4978	Sequence 4978, Ap	186	20	69.0	362	6	US-10-995-561-637	Sequence 637, App
114	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	187	20	69.0	389	7	US-11-018-018-2	Sequence 2, Appli
115	20	69.0	83	6	US-10-510-386-114	Sequence 114, App	188	20	69.0	389	7	US-11-047-757-2	Sequence 2, Appli
116	20	69.0	95	6	US-10-467-657-3518	Sequence 2318, Ap	189	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
117	20	69.0	102	6	US-10-793-626-2592	Sequence 2592, Ap	190	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
118	20	69.0	105	6	US-10-467-657-9209	Sequence 9209, Ap	191	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
119	20	69.0	108	6	US-10-467-657-4266	Sequence 4266, Ap	192	20	69.0	399	7	US-11-018-018-3	Sequence 3, Appli
120	20	69.0	114	6	US-10-821-234-1140	Sequence 1140, Ap	193	20	69.0	399	7	US-11-047-757-3	Sequence 3, Appli
121	20	69.0	114	6	US-10-467-657-124	Sequence 124, App	194	20	69.0	406	6	US-10-467-657-7420	Sequence 7420, Ap
122	20	69.0	114	6	US-10-467-657-3414	Sequence 1414, Ap	195	20	69.0	409	6	US-10-821-234-1425	Sequence 1425, Ap
123	20	69.0	114	6	US-10-467-657-3162	Sequence 3162, Ap	196	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
124	20	69.0	114	6	US-10-467-657-3754	Sequence 3754, Ap	197	20	69.0	414	6	US-10-878-556A-1	Sequence 1, Appli
125	20	69.0	114	6	US-10-467-657-8674	Sequence 8674, Ap	198	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
126	20	69.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	199	20	69.0	432	7	US-11-113-424-186	Sequence 186, App
127	20	69.0	116	6	US-10-467-657-5514	Sequence 5514, Ap	200	20	69.0	436	7	US-10-467-657-7694	Sequence 7694, App
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	201	20	69.0	436	7	US-11-082-389-256	Sequence 256, App
129	20	69.0	127	7	US-11-106-796-10	Sequence 106, Appl	202	20	69.0	443	6	US-10-793-626-1860	Sequence 1860, Ap
130	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	203	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
131	20	69.0	131	6	US-10-467-657-5308	Sequence 5308, Ap	204	20	69.0	445	6	US-10-873-528-30	Sequence 30, Appl
132	20	69.0	137	6	US-10-821-234-1701	Sequence 1701, Ap	205	20	69.0	448	6	US-10-763-712A-69	Sequence 69, Appl
133	20	69.0	140	6	US-10-467-657-2486	Sequence 2486, Ap	206	20	69.0	448	6	US-10-763-712A-112	Sequence 112, App
134	20	69.0	144	6	US-10-793-626-1640	Sequence 1640, Ap	207	20	69.0	449	6	US-10-821-234-1075	Sequence 1075, Ap
135	20	69.0	144	6	US-10-793-626-1640	Sequence 1640, Ap	208	20	69.0	450	6	US-10-467-657-7094	Sequence 7094, Ap
136	20	69.0	156	6	US-10-467-657-1958	Sequence 1958, Ap	209	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
137	20	69.0	179	6	US-10-467-657-2232	Sequence 2232, Ap	210	20	69.0	450	6	US-10-763-712A-76	Sequence 76, Appl
138	20	69.0	182	6	US-10-980-388-89	Sequence 89, Appl	211	20	69.0	451	6	US-10-467-657-7104	Sequence 7104, Ap
139	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	212	20	69.0	456	7	US-10-467-657-4150	Sequence 4150, Ap
140	20	69.0	186	6	US-10-467-657-3918	Sequence 3918, Ap	213	20	69.0	466	7	US-11-102-240-104	Sequence 104, App
141	20	69.0	195	7	US-11-019-955-24	Sequence 24, Appl	214	20	69.0	470	6	US-11-186-284-123	Sequence 123, App
142	20	69.0	197	6	US-10-793-626-2856	Sequence 2856, Ap	215	20	69.0	471	6	US-10-995-561-901	Sequence 901, App
143	20	69.0	200	6	US-10-793-626-394	Sequence 394, App	216	20	69.0	477	6	US-10-131-826A-452	Sequence 452, App
144	20	69.0	200	6	US-10-793-626-1242	Sequence 1242, Ap	217	20	69.0	481	6	US-10-467-657-3124	Sequence 3124, Ap
145	20	69.0	204	6	US-10-980-388-102	Sequence 102, App	218	20	69.0	481	6	US-11-090-439-16	Sequence 16, Appl
146	20	69.0	210	6	US-10-467-657-6318	Sequence 6318, Ap	219	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appli
147	20	69.0	214	6	US-10-508-263-108	Sequence 108, App	220	20	69.0	488	6	US-10-821-234-1654	Sequence 1654, Ap
148	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	221	20	69.0	488	6	US-11-186-284-121	Sequence 121, App
149	20	69.0	239	6	US-10-467-657-8743	Sequence 8743, Ap	222	20	69.0	489	6	US-10-467-657-7846	Sequence 7846, Ap
150	20	69.0	241	7	US-11-019-955-27	Sequence 27, Appl	223	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
151	20	69.0	250	7	US-11-082-389-216	Sequence 216, App	224	20	69.0	495	7	US-11-074-176-316	Sequence 316, App
152	20	69.0	257	7	US-11-102-240-94	Sequence 94, Appl	225	20	69.0	508	7	US-11-082-389-178	Sequence 178, App
153	20	69.0	266	6	US-10-995-561-544	Sequence 544, App	226	20	69.0	514	6	US-10-793-626-12	Sequence 12, Appl
154	20	69.0	267	6	US-10-995-561-543	Sequence 543, App	227	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
155	20	69.0	268	7	US-11-019-955-28	Sequence 28, Appl	228	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
156	20	69.0	271	6	US-10-793-626-1156	Sequence 1156, Ap	229	20	69.0	558	7	US-11-078-189-19	Sequence 19, Appl
157	20	69.0	272	6	US-10-467-657-2520	Sequence 2520, Ap	230	20	69.0	560	6	US-10-623-155-225	Sequence 225, App
158	20	69.0	276	6	US-10-873-528-134	Sequence 134, App	231	20	69.0	563	6	US-10-821-234-1067	Sequence 1067, Ap
159	20	69.0	280	6	US-10-858-730-200	Sequence 200, App	232	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
160	20	69.0	280	6	US-10-467-657-2130	Sequence 2130, Ap	233	20	69.0	585	6	US-10-967-457-18	Sequence 18, Appl
161	20	69.0	285	7	US-11-082-389-324	Sequence 324, App	234	20	69.0	585	6	US-10-939-890-500	Sequence 500, App
162	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	235	20	69.0	585	7	US-11-078-663-18	Sequence 18, Appl
163	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	236	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
164	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	237	20	69.0	626	6	US-10-467-657-7618	Sequence 7618, Ap
165	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	238	20	69.0	626	6	US-10-467-657-7618	Sequence 7618, Ap
166	20	69.0	299	6	US-10-467-657-2190	Sequence 2190, Ap	239	20	69.0	637	6	US-10-873-528-53	Sequence 53, Appl
167	20	69.0	312	7	US-11-055-822-16	Sequence 16, Appl	240	20	69.0	647	7	US-11-080-991-32	Sequence 32, Appl
168	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appl	241	20	69.0	657	7	US-11-080-991-48	Sequence 48, Appl
169	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	242	20	69.0	659	7	US-11-119-683-2	Sequence 2, Appli
170	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	243	20	69.0	675	6	US-10-467-657-4004	Sequence 4004, Ap
171	20	69.0	324	6	US-10-467-657-8440	Sequence 8440, Ap	244	20	69.0	690	6	US-10-939-890-501	Sequence 501, App


```
245 20 69.0 692 7 US-11-103-957-29
246 20 69.0 708 7 US-11-174-150-25
247 20 69.0 721 7 US-11-078-189-18
248 20 69.0 710 6 US-10-467-962B-49
249 20 69.0 736 7 US-11-174-150-26
250 20 69.0 736 7 US-11-078-189-9
251 20 69.0 739 7 US-11-082-389-94
252 20 69.0 739 7 US-11-078-189-12
253 20 69.0 739 7 US-11-107-028-6
254 20 69.0 741 6 US-10-467-657-6266
255 20 69.0 745 7 US-11-147-109-2
256 20 69.0 748 6 US-10-821-234-1479
257 20 69.0 817 6 US-10-793-626-2948
258 20 69.0 852 6 US-10-467-657-5004
259 20 69.0 856 6 US-10-467-657-8534
260 20 69.0 874 6 US-10-510-386-28
261 20 69.0 896 7 US-11-192-219-3
262 20 69.0 898 7 US-11-166-730-3
263 20 69.0 902 7 US-11-057-058-64
264 20 69.0 916 6 US-10-467-657-4242
265 20 69.0 923 7 US-11-192-219-4
266 20 69.0 989 7 US-10-821-234-975
267 20 69.0 1013 7 US-11-103-957-9
268 20 69.0 1047 6 US-10-510-386-200
269 20 69.0 1165 7 US-11-192-219-2
270 20 69.0 1167 6 US-10-601-368-18
271 20 69.0 1217 7 US-11-074-176-252
272 20 69.0 1730 7 US-11-192-967-4
273 20 69.0 1730 6 US-11-193-715-4
274 20 69.0 2644 6 US-10-770-726-45
275 20 69.0 7968 7 US-11-186-731-5
276 19 65.5 13 7 US-11-016-706-29
277 19 65.5 27 7 US-11-157-930-14
278 19 65.5 35 6 US-10-821-234-1704
279 19 65.5 43 7 US-11-075-400-28
280 19 65.5 44 7 US-11-000-463-372
281 19 65.5 46 6 US-10-467-657-9119
282 19 65.5 47 6 US-10-467-657-9186
283 19 65.5 57 6 US-10-467-657-5448
284 19 65.5 71 7 US-11-000-463-772
285 19 65.5 80 6 US-10-986-501-200
286 19 65.5 83 6 US-10-467-657-5366
287 19 65.5 86 6 US-10-467-657-3962
288 19 65.5 98 6 US-10-467-657-3376
289 19 65.5 100 7 US-11-123-896-137
290 19 65.5 103 6 US-10-793-626-1708
291 19 65.5 103 6 US-10-793-626-2074
292 19 65.5 104 6 US-10-793-626-2512
293 19 65.5 106 7 US-11-064-174-50
294 19 65.5 107 6 US-10-793-626-1586
295 19 65.5 107 6 US-10-467-657-1018
296 19 65.5 107 6 US-10-467-657-2102
297 19 65.5 107 7 US-11-000-463-300
298 19 65.5 115 6 US-10-432-483-10
299 19 65.5 117 6 US-10-467-657-2282
300 19 65.5 122 6 US-10-467-657-606

SEQUENCE 29, Appl
SEQUENCE 25, Appl
SEQUENCE 18, Appl
SEQUENCE 49, Appl
SEQUENCE 26, Appl
SEQUENCE 9, Appl
SEQUENCE 94, Appl
SEQUENCE 12, Appl
SEQUENCE 6, Appl
SEQUENCE 6266, Ap
SEQUENCE 2, Appl
SEQUENCE 1479, Ap
SEQUENCE 2948, Ap
SEQUENCE 5004, Ap
SEQUENCE 8534, Ap
SEQUENCE 28, Appl
SEQUENCE 3, Appl
SEQUENCE 3, Appl
SEQUENCE 64, Appl
SEQUENCE 4242, Ap
SEQUENCE 4, Appl
SEQUENCE 975, App
SEQUENCE 9, Appl
SEQUENCE 200, App
SEQUENCE 2, Appl
SEQUENCE 18, Appl
SEQUENCE 252, App
SEQUENCE 4, Appl
SEQUENCE 4, Appl
SEQUENCE 45, Appl
SEQUENCE 5, Appl
SEQUENCE 29, Appl
SEQUENCE 14, Appl
SEQUENCE 1704, Ap
SEQUENCE 28, Appl
SEQUENCE 372, App
SEQUENCE 9186, Ap
SEQUENCE 5448, Ap
SEQUENCE 772, App
SEQUENCE 200, App
SEQUENCE 5366, Ap
SEQUENCE 3962, Ap
SEQUENCE 3376, Ap
SEQUENCE 137, App
SEQUENCE 1708, Ap
SEQUENCE 2074, Ap
SEQUENCE 2512, Ap
SEQUENCE 50, Appl
SEQUENCE 1586, Ap
SEQUENCE 1018, Ap
SEQUENCE 2102, Ap
SEQUENCE 300, App
SEQUENCE 10, Appl
SEQUENCE 10, Appl
SEQUENCE 2282, Ap
SEQUENCE 606, App

; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 4 KLVFFA 9

RESULT 2
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 4 KLVFFA 9

RESULT 3
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
```

ALIGNMENTS

```
RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
```

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 16 KLVFFA 21
|:|||||

RESULT 4
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTO-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 16 KLVFFA 21
|:|||||

RESULT 5
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 16 KLVFFA 21
|:|||||

RESULT 6
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 16 KLVFFA 21
|:|||||

RESULT 7
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 8

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 9

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 10

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 11

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US2005024890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (INAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; US-10-982-545-15

Query Match 93.1%; Score 27; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 687 KLVFFA 692

RESULT 12

US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saidanna, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-789-273-38

Query Match 93.1%; Score 27; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 687 KLVFFA 692

RESULT 13
US-10-467-657-330
; Sequence 330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 330
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-330

Query Match 86.2%; Score 25; DB 6; Length 269;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|:||||
Db 11 KIVFF 15

RESULT 14
US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P0348005
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match 86.2%; Score 25; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
Db 7 KIVFF 11

RESULT 15
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892

Query Match 82.8%; Score 24; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
Db 33 KIIFP 37

RESULT 16
US-10-467-657-2014
; Sequence 2014, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2014
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2014

Query Match 82.8%; Score 24; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 73 IVFFA 77

RESULT 17
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070

Query Match 82.8%; Score 24; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 264 IVFFA 268

RESULT 18
US-10-467-657-2120
; Sequence 2120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2120
; LENGTH: 426

```
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2120

Query Match      82.8%; Score 24; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
      |||||
Db      414 IVFFA 418

RESULT 19
US-10-689-742-13
; Sequence 13, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaValle, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-13

Query Match      82.8%; Score 24; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
      |||||
Db      404 IVFFA 408

RESULT 20
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-125

Query Match      82.8%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      531 KAVFFA 536

RESULT 21
US-10-131-826A-230
; Sequence 230, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining of Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
```

US-10-131-826A-230

Query Match 82.8%; Score 24; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6

DB 557 IVFFA 561

RESULT 22

US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match 82.8%; Score 24; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6

DB 579 KAVFFA 584

RESULT 23

US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match 79.3%; Score 23; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5

DB 1 KLVFF 5

RESULT 24

US-10-131-826A-410
; Sequence 410, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DePorge, Laura
; APPLICANT: DeNovers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-410

Query Match 79.3%; Score 23; DB 6; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5

DB 118 KIVFF 122

RESULT 25

US-10-793-626-2450
; Sequence 2450, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

```
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2450

Query Match      79.3%; Score 23; DB 6; Length 311;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
      :||||
Db      296 VVFFA 300

RESULT 26
US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-959

Query Match      79.3%; Score 23; DB 6; Length 481;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      :|:|:|
Db      275 KVVFFA 280

RESULT 27
US-11-080-991-104
; Sequence 104, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petteer Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
```

```
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-104

Query Match      79.3%; Score 23; DB 7; Length 522;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
      :|:|:|
Db      260 IIVFA 264

RESULT 28
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match      79.3%; Score 23; DB 6; Length 528;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFF 5
      :|:|:|
Db      477 KLVFF 481

RESULT 29
US-10-467-657-2868
; Sequence 2868, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2868
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2868

Query Match      79.3%; Score 23; DB 6; Length 533;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```


QY 2 IVFFA 6
|:|:|
Db 371 IIFFA 375

RESULT 30
US-10-995-561-593
; Sequence 593, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 593
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-593

Query Match 79.3%; Score 23; DB 6; Length 3623;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 2544 KVIFF 2548

RESULT 31
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match 75.9%; Score 22; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 36 KIVFF 40

RESULT 32
US-10-467-657-4746
; Sequence 4746, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4746
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746

Query Match 75.9%; Score 22; DB 6; Length 98;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 62 KIVFF 66

RESULT 33
US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (98)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18

Query Match

75.9%; Score 22; DB 7; Length 167;

Best Local Similarity 60.0%; Pred. NO. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 2;

Qy 2 IVFFA 6
Db 105 VIFFA 109

RESULT 34

US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 2 IVFFA 6
Db 19 LVFFA 23

RESULT 35

US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match 75.9%; Score 22; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 2.1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 2 IVFFA 6
Db 166 LVFFA 170

RESULT 36

US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 2 IVFFA 6
Db 156 LVFFA 160

RESULT 37

US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFPA 6
Db 156 LVFFPA 160

RESULT 38
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt. Seq_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match 75.9%; Score 22; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFPA 6
Db 166 LVFFPA 170

RESULT 39
US-10-467-657-432
; Sequence 432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 432
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-432

Query Match 75.9%; Score 22; DB 6; Length 239;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 128 KVVFFA 133

RESULT 40
US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500

Query Match 75.9%; Score 22; DB 6; Length 265;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 230 KVVFFA 235

RESULT 41
US-10-793-626-2476
; Sequence 2476, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2476
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2476

Query Match 75.9%; Score 22; DB 6; Length 330;

Best Local Similarity 80.0%; Pred. No. 3.1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 1 KIVFF 5
||:|
Db 3 KIMFF 7

RESULT 42

US-10-793-626-2734
; Sequence 2734, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2734
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2734

Query Match 75.9%; Score 22; DB 6; Length 330;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
||:|
Db 3 KIMFF 7

RESULT 43

US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match 75.9%; Score 22; DB 6; Length 338;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
||:|
Db 76 KLIFP 80

RESULT 44

US-10-131-826A-376
; Sequence 376, Application US/10131826A

; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match 75.9%; Score 22; DB 6; Length 344;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
||:|
Db 279 KLIFP 283

RESULT 45

US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

; FILE REFERENCE: BGI-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-572

Query Match 75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||| ||
Db 61 KIWVFA 66

RESULT 46
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-836

Query Match 75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||| ||
Db 61 KIVVFA 66

RESULT 47
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MEI
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match 75.9%; Score 22; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
||| ||
Db 4 KILFF 8

RESULT 48
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 678
; LENGTH: 449

```

; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-678

Query Match          75.9%; Score 22; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
   ||:|
Db 428 KINFF 432

RESULT 49
US-11-082-389-198
; Sequence 198, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 198
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-198

Query Match          75.9%; Score 22; DB 7; Length 453;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
   :|||
Db 401 LVFFA 405

RESULT 50
US-11-210-316-22
; Sequence 22, Application US/11210316
; Publication No. US2005028278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (102)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-22

Query Match          75.9%; Score 22; DB 7; Length 510;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
   :|||
Db 96 VIFFA 100

RESULT 51
US-11-210-316-26
; Sequence 26, Application US/11210316
; Publication No. US2005028278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-210-316-26

Query Match          75.9%; Score 22; DB 7; Length 539;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
   :|||
Db 121 VIFFA 125

RESULT 52
US-10-467-657-7120
; Sequence 7120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: NASIGNANI Vega
; APPLICANT: MONACI Elisabetta

```

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7120
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7120

Query Match 75.9%; Score 22; DB 6; Length 601;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFP 5
:||||
Db 251 RIVFP 255

RESULT 53
US-10-821-234-1673
; Sequence 1673, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1673
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1673

Query Match 75.9%; Score 22; DB 6; Length 635;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFP 5
:||||
Db 259 KIVFP 263

RESULT 54
US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347

; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-6

Query Match 75.9%; Score 22; DB 6; Length 858;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
:||||
Db 348 LVFFA 352

RESULT 55
US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe PG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2233
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 75.9%; Score 22; DB 6; Length 2233;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
:||||
Db 1895 KVQFFA 1900

RESULT 56
US-10-467-657-7886
; Sequence 7886, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 7886
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7886

Query Match 72.4%; Score 21; DB 6; Length 43;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 14 KVRFFA 19

RESULT 57

US-10-467-657-2216
; Sequence 2216, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2216
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2216

Query Match 72.4%; Score 21; DB 6; Length 52;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 42 RIVWFA 47

RESULT 58

US-10-467-657-5690
; Sequence 5690, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5690
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5690

Query Match 72.4%; Score 21; DB 6; Length 76;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 23 QIVFF 27

RESULT 59

US-10-821-234-1703
; Sequence 1703, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PCT SEQ_genes Version 1.0
; SEQ ID NO 1703
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1703

Query Match 72.4%; Score 21; DB 6; Length 91;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 22 EIVFF 26

RESULT 60

US-10-793-626-430
; Sequence 430, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 430
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-430

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 78 IVFFS 82

RESULT 61

US-10-467-657-5166
; Sequence 5166, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5166
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5166

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 29 ILFFA 33

RESULT 62
US-10-793-626-2374
; Sequence 2374, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2374
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2374

Query Match 72.4%; Score 21; DB 6; Length 134;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFP 5
Db 7 KIIVF 11

RESULT 63
US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420

Query Match 72.4%; Score 21; DB 6; Length 155;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 18 MVFFA 22

RESULT 64
US-10-965-694-23
; Sequence 23, Application US/10965694
; Publication No. US20050271644A1
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Johannes
; APPLICANT: Muller-Reible, Clemens
; APPLICANT: Preglin, Andreas
; APPLICANT: Rost, Simone
; APPLICANT: Strom, Tim
; TITLE OF INVENTION: VITAMIN K EPOXID RECYCLING POLYPEPTIDE VKORC1, A THERAPEUTIC TARGET
; TITLE OF INVENTION: OF COUMARIN AND THEIR DERIVATIVES
; FILE REFERENCE: MBP-025XX
; CURRENT APPLICATION NUMBER: US/10/965,694
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 60/511,041
; PRIOR FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-965-694-23

Query Match 72.4%; Score 21; DB 6; Length 175;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 91 IVFFA 95

RESULT 65
US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2836

```
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2836
```

```
Query Match          72.4%; Score 21; DB 6; Length 182;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:|:|
Db      14 KVTFFS 19
```

```
RESULT 66
US-10-467-657-3510
; Sequence 3510, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3510
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3510
```

```
Query Match          72.4%; Score 21; DB 6; Length 182;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 IVFFA 6
       |:|:|
Db      17 ILFFA 21
```

```
RESULT 67
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436
```

```
Query Match          72.4%; Score 21; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:|:|
Db      46 KTVFFA 51
```

```
RESULT 68
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmanl, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: P1 SEQ_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372
```

```
Query Match          72.4%; Score 21; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:|:|
Db      33 KTVFFA 38
```

```
RESULT 69
US-10-467-657-8102
; Sequence 8102, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8102
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8102
```

```
Query Match          72.4%; Score 21; DB 6; Length 216;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 IVFFA 6
       |:|:|
Db      18 LIFFA 22
```

```
RESULT 70
US-10-467-657-290
; Sequence 290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 290
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-290

Query Match          72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFPA 6
DB      41 LIFFPA 45

RESULT 71
US-10-467-657-5750
; Sequence 5750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5750
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5750

Query Match          72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFPA 6
DB      41 LIFFPA 45

RESULT 72
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
```

```
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match          72.4%; Score 21; DB 6; Length 254;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFPA 6
DB      159 LIFFPA 163

RESULT 73
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match          72.4%; Score 21; DB 6; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFPA 6
DB      211 KLIFFPA 216

RESULT 74
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
```

```
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-46

Query Match      72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFEA 6
      |::||
Db      211 KLMYFA 216

RESULT 75
US-11-073-460-46
; Sequence 46, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-46

Query Match      72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFEA 6
      |::||
Db      211 KLMYFA 216

Search completed: December 29, 2005, 18:50:19
Job time : 4.29032 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-10
Perfect score: 29
Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pep:
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	3	US-09-867-847-11 Sequence 11, Appl
2	29	100.0	6	3	US-09-867-847-19 Sequence 19, Appl
3	29	100.0	6	3	US-09-915-092-1 Sequence 1, Appl
4	29	100.0	6	3	US-09-915-092-9 Sequence 9, Appl
5	29	100.0	6	3	US-09-747-408-1 Sequence 1, Appl
6	29	100.0	6	3	US-09-747-408-10 Sequence 10, Appl
7	29	100.0	6	5	US-10-728-028-1 Sequence 1, Appl
8	29	100.0	6	5	US-10-728-028-9 Sequence 9, Appl
9	29	100.0	6	5	US-10-825-958-9 Sequence 9, Appl
10	29	100.0	6	5	US-10-825-958-17 Sequence 17, Appl
11	29	100.0	58	4	US-10-425-115-280164 Sequence 165325, A
12	29	100.0	90	4	US-10-424-599-165325 Sequence 280164, A
13	29	100.0	93	4	US-10-424-599-240310 Sequence 240310, A
14	29	100.0	99	5	US-10-450-763-56957 Sequence 56957, A
15	28	96.6	6	3	US-09-867-847-18 Sequence 18, Appl
16	28	96.6	6	3	US-09-867-847-26 Sequence 26, Appl
17	28	96.6	6	3	US-09-915-092-8 Sequence 8, Appl
18	28	96.6	6	3	US-09-915-092-16 Sequence 16, Appl
19	28	96.6	6	3	US-09-747-408-9 Sequence 9, Appl
20	28	96.6	6	3	US-09-747-408-17 Sequence 17, Appl
21	28	96.6	6	5	US-10-728-028-8 Sequence 8, Appl
22	28	96.6	6	5	US-10-728-028-16 Sequence 16, Appl
23	28	96.6	6	5	US-10-825-958-16 Sequence 16, Appl
24	28	96.6	6	5	US-10-825-958-24 Sequence 24, Appl
25	28	96.6	37	4	US-10-641-924-7 Sequence 7, Appl
26	28	96.6	37	4	US-10-642-255-7 Sequence 7, Appl
27	28	96.6	60	4	US-10-437-963-173619 Sequence 173619, A

28	28	96.6	87	4	US-10-437-963-133986
29	28	96.6	109	4	US-10-437-963-105773
30	28	96.6	135	4	US-10-437-963-141578
31	28	96.6	175	4	US-10-437-963-122124
32	28	96.6	186	5	US-10-481-032A-214
33	28	96.6	186	5	US-10-481-032A-228
34	28	96.6	188	4	US-10-437-963-172476
35	28	96.6	188	4	US-10-437-963-172452
36	28	96.6	416	6	US-10-055-475-14
37	28	96.6	416	6	US-11-042-922-14
38	28	96.6	514	4	US-10-055-475-13
39	28	96.6	514	6	US-11-042-922-13
40	28	96.6	564	6	US-11-097-143-12723
41	28	96.6	925	4	US-10-408-765A-2031
42	28	96.6	925	4	US-10-755-889-234
43	28	96.6	925	5	US-10-370-715B-8
44	28	96.6	925	5	US-10-631-467-680
45	28	96.6	925	5	US-10-631-467-747
46	28	96.6	1144	3	US-09-870-759-124
47	28	96.6	1144	3	US-09-751-708A-124
48	28	96.6	1144	4	US-10-428-817A-120
49	28	96.6	1144	5	US-10-937-758A-101
50	28	96.6	1144	5	US-10-631-467-1388
51	28	96.6	1144	5	US-10-631-467-1464
52	28	96.6	1443	6	US-11-097-143-32208
53	28	96.6	1640	4	US-10-437-963-109646
54	28	93.1	6	3	US-09-867-847-7
55	27	93.1	6	3	US-09-867-847-20
56	27	93.1	6	3	US-09-972-475-9
57	27	93.1	6	3	US-09-915-092-10
58	27	93.1	6	3	US-09-915-092-28
59	27	93.1	6	3	US-09-956-625-25
60	27	93.1	6	3	US-09-747-408-3
61	27	93.1	6	3	US-09-747-408-11
62	27	93.1	6	4	US-10-463-729-9
63	27	93.1	6	5	US-10-728-028-10
64	27	93.1	6	5	US-10-728-028-27
65	27	93.1	6	5	US-10-728-028-28
66	27	93.1	6	5	US-10-825-958-7
67	27	93.1	6	5	US-10-825-958-18
68	27	93.1	6	5	US-10-666-095-3
69	27	93.1	7	3	US-09-867-847-12
70	27	93.1	7	3	US-09-867-847-27
71	27	93.1	7	3	US-09-867-847-28
72	27	93.1	7	3	US-09-972-475-7
73	27	93.1	7	3	US-09-915-092-2
74	27	93.1	7	3	US-09-915-092-17
75	27	93.1	7	3	US-09-915-092-18
76	27	93.1	7	3	US-09-747-408-2
77	27	93.1	7	3	US-09-747-408-18
78	27	93.1	7	3	US-09-747-408-19
79	27	93.1	7	4	US-10-463-729-7
80	27	93.1	7	5	US-10-728-028-2
81	27	93.1	7	5	US-10-728-028-17
82	27	93.1	7	5	US-10-728-028-18
83	27	93.1	7	5	US-10-825-958-10
84	27	93.1	7	5	US-10-825-958-25
85	27	93.1	7	5	US-10-825-958-26
86	27	93.1	7	5	US-10-810-881A-128
87	27	93.1	7	5	US-10-505-313-269
88	27	93.1	8	3	US-09-850-061A-44
89	27	93.1	8	3	US-09-972-475-5
90	27	93.1	8	4	US-10-235-483-1
91	27	93.1	8	4	US-10-463-729-5
92	27	93.1	8	4	US-10-281-092-42
93	27	93.1	8	4	US-10-721-774-44
94	27	93.1	8	5	US-10-810-881A-125
95	27	93.1	8	5	US-10-817-979-73
96	27	93.1	9	3	US-09-867-847-9
97	27	93.1	9	3	US-09-899-815-2
98	27	93.1	9	3	US-09-747-408-20
99	27	93.1	9	4	US-10-235-483-64
100	27	93.1	9	4	US-10-619-454-3

101	27	93.1	9	4	US-10-619-454-25	Sequence 25, Appl	174	27	93.1	13	4	US-10-281-458-1	Sequence 1, Appl
102	27	93.1	9	4	US-10-619-454-28	Sequence 28, Appl	175	27	93.1	13	5	US-10-625-854-127	Sequence 127, App
103	27	93.1	9	4	US-10-619-454-57	Sequence 57, Appl	176	27	93.1	13	5	US-10-625-854-140	Sequence 140, App
104	27	93.1	9	4	US-10-619-454-157	Sequence 157, Appl	177	27	93.1	14	3	US-09-992-800-5	Sequence 5, Appl
105	27	93.1	10	3	US-09-867-847-29	Sequence 29, Appl	178	27	93.1	14	3	US-09-992-994-5	Sequence 5, Appl
106	27	93.1	10	3	US-09-915-082-19	Sequence 19, Appl	179	27	93.1	14	4	US-10-385-065-5	Sequence 5, Appl
107	27	93.1	10	5	US-10-889-999-20	Sequence 20, Appl	180	27	93.1	14	5	US-10-810-881A-114	Sequence 114, App
108	27	93.1	10	5	US-10-889-999-21	Sequence 21, Appl	181	27	93.1	14	5	US-10-505-313-2	Sequence 2, Appl
109	27	93.1	10	5	US-10-889-999-22	Sequence 22, Appl	182	27	93.1	14	5	US-10-625-854-115	Sequence 115, App
110	27	93.1	10	5	US-10-889-999-23	Sequence 23, Appl	183	27	93.1	14	5	US-10-625-854-128	Sequence 128, App
111	27	93.1	10	5	US-10-889-999-24	Sequence 24, Appl	184	27	93.1	14	5	US-10-625-854-141	Sequence 141, App
112	27	93.1	10	5	US-10-890-070-20	Sequence 20, Appl	185	27	93.1	14	6	US-11-063-350-5	Sequence 5, Appl
113	27	93.1	10	5	US-10-890-070-21	Sequence 21, Appl	186	27	93.1	15	3	US-09-972-475-14	Sequence 14, Appl
114	27	93.1	10	5	US-10-890-070-22	Sequence 22, Appl	187	27	93.1	15	3	US-09-996-357-9	Sequence 9, Appl
115	27	93.1	10	5	US-10-890-070-23	Sequence 23, Appl	188	27	93.1	15	4	US-10-235-483-56	Sequence 56, Appl
116	27	93.1	10	5	US-10-890-070-24	Sequence 24, Appl	189	27	93.1	15	4	US-10-235-483-57	Sequence 57, Appl
117	27	93.1	10	5	US-10-890-000-20	Sequence 20, Appl	190	27	93.1	15	4	US-10-235-483-58	Sequence 58, Appl
118	27	93.1	10	5	US-10-890-000-21	Sequence 21, Appl	191	27	93.1	15	4	US-10-235-483-60	Sequence 60, Appl
119	27	93.1	10	5	US-10-890-000-22	Sequence 22, Appl	192	27	93.1	15	4	US-10-235-483-61	Sequence 61, Appl
120	27	93.1	10	5	US-10-890-000-23	Sequence 23, Appl	193	27	93.1	15	4	US-10-235-483-63	Sequence 63, Appl
121	27	93.1	10	5	US-10-890-000-24	Sequence 24, Appl	194	27	93.1	15	4	US-10-235-483-65	Sequence 65, Appl
122	27	93.1	10	5	US-10-823-463-20	Sequence 20, Appl	195	27	93.1	15	4	US-10-463-729-14	Sequence 14, Appl
123	27	93.1	10	5	US-10-823-463-21	Sequence 21, Appl	196	27	93.1	15	5	US-10-625-854-103	Sequence 103, App
124	27	93.1	10	5	US-10-823-463-22	Sequence 22, Appl	197	27	93.1	15	5	US-10-625-854-116	Sequence 116, App
125	27	93.1	10	5	US-10-823-463-23	Sequence 23, Appl	198	27	93.1	15	5	US-10-625-854-129	Sequence 129, App
126	27	93.1	10	5	US-10-823-463-24	Sequence 24, Appl	199	27	93.1	15	5	US-10-625-854-142	Sequence 142, App
127	27	93.1	10	5	US-10-728-028-19	Sequence 19, Appl	200	27	93.1	16	5	US-10-625-854-91	Sequence 91, Appl
128	27	93.1	10	5	US-10-822-968-20	Sequence 20, Appl	201	27	93.1	16	5	US-10-625-854-104	Sequence 104, App
129	27	93.1	10	5	US-10-822-968-21	Sequence 21, Appl	202	27	93.1	16	5	US-10-625-854-117	Sequence 117, App
130	27	93.1	10	5	US-10-822-968-22	Sequence 22, Appl	203	27	93.1	16	5	US-10-625-854-130	Sequence 130, App
131	27	93.1	10	5	US-10-822-968-23	Sequence 23, Appl	204	27	93.1	16	5	US-10-625-854-143	Sequence 143, App
132	27	93.1	10	5	US-10-822-968-24	Sequence 24, Appl	205	27	93.1	17	3	US-09-992-800-3	Sequence 3, Appl
133	27	93.1	10	5	US-10-777-792-20	Sequence 20, Appl	206	27	93.1	17	3	US-09-992-994-3	Sequence 3, Appl
134	27	93.1	10	5	US-10-777-792-21	Sequence 21, Appl	207	27	93.1	17	3	US-09-998-491-8	Sequence 8, Appl
135	27	93.1	10	5	US-10-777-792-22	Sequence 22, Appl	208	27	93.1	17	4	US-10-385-065-3	Sequence 3, Appl
136	27	93.1	10	5	US-10-777-792-23	Sequence 23, Appl	209	27	93.1	17	4	US-10-451-367-26	Sequence 26, Appl
137	27	93.1	10	5	US-10-777-792-24	Sequence 24, Appl	210	27	93.1	17	4	US-10-475-281-8	Sequence 8, Appl
138	27	93.1	10	5	US-10-825-958-27	Sequence 27, Appl	211	27	93.1	17	4	US-10-810-919-3	Sequence 3, Appl
139	27	93.1	10	5	US-10-890-071-20	Sequence 20, Appl	212	27	93.1	17	5	US-10-684-346-24	Sequence 24, Appl
140	27	93.1	10	5	US-10-890-071-21	Sequence 21, Appl	213	27	93.1	17	5	US-10-997-078-46	Sequence 46, Appl
141	27	93.1	10	5	US-10-890-071-22	Sequence 22, Appl	214	27	93.1	17	5	US-10-997-700-19	Sequence 19, Appl
142	27	93.1	10	5	US-10-890-071-23	Sequence 23, Appl	215	27	93.1	17	6	US-11-063-350-3	Sequence 3, Appl
143	27	93.1	10	5	US-10-890-071-24	Sequence 24, Appl	216	27	93.1	17	6	US-11-066-697-950	Sequence 950, App
144	27	93.1	10	5	US-10-890-024-20	Sequence 20, Appl	217	27	93.1	17	6	US-11-066-697-983	Sequence 983, App
145	27	93.1	10	5	US-10-890-024-21	Sequence 21, Appl	218	27	93.1	19	3	US-09-825-242-5	Sequence 5, Appl
146	27	93.1	10	5	US-10-890-024-22	Sequence 22, Appl	219	27	93.1	19	4	US-10-429-216-5	Sequence 5, Appl
147	27	93.1	10	5	US-10-890-024-23	Sequence 23, Appl	220	27	93.1	19	4	US-10-816-022-5	Sequence 5, Appl
148	27	93.1	10	5	US-10-890-024-24	Sequence 24, Appl	221	27	93.1	19	4	US-10-816-529-5	Sequence 5, Appl
149	27	93.1	10	5	US-10-928-926-20	Sequence 20, Appl	222	27	93.1	19	4	US-10-815-353-5	Sequence 5, Appl
150	27	93.1	10	5	US-10-928-926-21	Sequence 21, Appl	223	27	93.1	19	4	US-10-815-391-5	Sequence 5, Appl
151	27	93.1	10	5	US-10-928-926-22	Sequence 22, Appl	224	27	93.1	19	5	US-10-828-548-5	Sequence 5, Appl
152	27	93.1	10	5	US-10-928-926-23	Sequence 23, Appl	225	27	93.1	19	5	US-10-816-380-5	Sequence 5, Appl
153	27	93.1	10	5	US-10-928-926-24	Sequence 24, Appl	226	27	93.1	19	5	US-10-889-399-75	Sequence 75, Appl
154	27	93.1	10	6	US-11-058-757-20	Sequence 20, Appl	227	27	93.1	19	5	US-10-890-070-75	Sequence 75, Appl
155	27	93.1	10	6	US-11-058-757-21	Sequence 21, Appl	228	27	93.1	19	5	US-10-890-000-75	Sequence 75, Appl
156	27	93.1	10	6	US-11-058-757-22	Sequence 22, Appl	229	27	93.1	19	5	US-10-788-666-5	Sequence 5, Appl
157	27	93.1	10	6	US-11-058-757-23	Sequence 23, Appl	230	27	93.1	19	5	US-10-923-471-5	Sequence 5, Appl
158	27	93.1	10	6	US-11-058-757-24	Sequence 24, Appl	231	27	93.1	19	5	US-10-823-463-75	Sequence 75, Appl
159	27	93.1	11	3	US-09-988-842-9	Sequence 9, Appl	232	27	93.1	19	5	US-10-923-469-5	Sequence 5, Appl
160	27	93.1	11	3	US-09-988-842-25	Sequence 25, Appl	233	27	93.1	19	5	US-10-933-559-5	Sequence 5, Appl
161	27	93.1	11	4	US-10-235-483-14	Sequence 14, Appl	234	27	93.1	19	5	US-10-815-404-5	Sequence 5, Appl
162	27	93.1	11	4	US-10-050-200-33	Sequence 33, Appl	235	27	93.1	19	5	US-10-934-609-5	Sequence 5, Appl
163	27	93.1	11	4	US-10-237-673-20	Sequence 20, Appl	236	27	93.1	19	5	US-10-923-474-5	Sequence 5, Appl
164	27	93.1	11	5	US-10-464-117-13	Sequence 13, Appl	237	27	93.1	19	5	US-10-884-892-5	Sequence 5, Appl
165	27	93.1	11	5	US-10-772-230-9	Sequence 9, Appl	238	27	93.1	19	5	US-10-822-968-75	Sequence 75, Appl
166	27	93.1	11	5	US-10-772-230-25	Sequence 25, Appl	239	27	93.1	19	5	US-10-777-792-75	Sequence 75, Appl
167	27	93.1	12	3	US-09-867-847-8	Sequence 8, Appl	240	27	93.1	19	5	US-10-890-071-75	Sequence 75, Appl
168	27	93.1	12	5	US-10-810-881A-115	Sequence 115, App	241	27	93.1	19	5	US-10-890-024-75	Sequence 75, Appl
169	27	93.1	12	5	US-10-810-881A-117	Sequence 117, App	242	27	93.1	19	5	US-10-934-819-5	Sequence 5, Appl
170	27	93.1	12	5	US-10-508-586-2	Sequence 2, Appl	243	27	93.1	19	5	US-10-923-267-5	Sequence 5, Appl
171	27	93.1	12	5	US-10-508-586-3	Sequence 3, Appl	244	27	93.1	19	5	US-10-928-526-75	Sequence 75, Appl
172	27	93.1	12	5	US-10-625-854-139	Sequence 139, App	245	27	93.1	19	6	US-11-058-757-75	Sequence 75, Appl
173	27	93.1	12	6	US-11-012-797A-33	Sequence 33, Appl	246	27	93.1	19	6	US-11-108-102-5	Sequence 5, Appl

```

247 27 93.1 20 3 US-09-908-943A-25
248 27 93.1 20 5 US-10-801-487-25
249 27 93.1 20 5 US-10-801-938-25
250 27 93.1 20 5 US-10-801-509-25
251 27 93.1 20 5 US-10-801-486-25
252 27 93.1 20 5 US-10-801-493-25
253 27 93.1 24 5 US-10-728-246-5
254 27 93.1 24 5 US-10-728-246-6
255 27 93.1 26 3 US-09-792-079-11
256 27 93.1 26 4 US-10-159-279-11
257 27 93.1 28 3 US-09-867-847-4
258 27 93.1 28 3 US-09-865-294-66
259 27 93.1 28 3 US-09-792-079-5
260 27 93.1 28 4 US-10-159-279-5
261 27 93.1 28 4 US-10-363-082-2
262 27 93.1 28 4 US-10-433-385-7
263 27 93.1 28 4 US-10-390-472-4
264 27 93.1 28 4 US-10-741-205-36
265 27 93.1 28 4 US-10-416-262B-7
266 27 93.1 28 4 US-10-478-308-4
267 27 93.1 28 4 US-10-478-307-4
268 27 93.1 28 5 US-10-861-614-66
269 27 93.1 28 5 US-10-825-958-4
270 27 93.1 28 6 US-11-091-309-3
271 27 93.1 28 6 US-11-066-697-959
272 27 93.1 28 6 US-11-066-697-965
273 27 93.1 28 6 US-11-066-697-976
274 27 93.1 28 6 US-11-066-697-992
275 27 93.1 28 6 US-11-066-697-1003
276 27 93.1 30 3 US-09-861-847-1
277 27 93.1 30 4 US-10-301-488A-1
278 27 93.1 30 4 US-10-666-423-1
279 27 93.1 30 4 US-10-617-876-9
280 27 93.1 30 4 US-10-619-454-24
281 27 93.1 30 4 US-10-301-448-1
282 27 93.1 30 5 US-10-775-562-5
283 27 93.1 32 4 US-10-732-862A-99
284 27 93.1 33 3 US-09-930-915A-295
285 27 93.1 33 4 US-10-082-014-84
286 27 93.1 33 4 US-10-372-076-85
287 27 93.1 33 4 US-10-732-862A-98
288 27 93.1 33 4 US-10-806-006-295
289 27 93.1 33 4 US-10-677-074-85
290 27 93.1 33 4 US-10-805-913-295
291 27 93.1 35 3 US-09-867-847-3
292 27 93.1 35 3 US-09-972-475-16
293 27 93.1 35 4 US-10-463-729-16
294 27 93.1 35 5 US-10-825-958-3
295 27 93.1 35 6 US-11-066-697-979
296 27 93.1 35 6 US-11-066-697-1006
297 27 93.1 36 3 US-09-861-847-6
298 27 93.1 36 3 US-09-861-847-11
299 27 93.1 36 4 US-10-301-488A-6
300 27 93.1 36 4 US-10-301-488A-11

```

ALIGNMENTS

```

RESULT 1
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

```

```

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

```

```

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KIVFFA 6
Db 1 KIVFFA 6

```

```

RESULT 2
US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

```

```

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KIVFFA 6
Db 1 KIVFFA 6

```

```

RESULT 3
US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert

```

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 4
US-09-915-092-9
; Sequence 9, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 5
US-09-747-408-1
; Sequence 1, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-747-408-1

; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 6
US-09-747-408-10
; Sequence 10, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 7
US-10-728-028-1
; Sequence 1, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 03/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-728-028-1
```



```
;
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 8
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 9
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-9

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 10
US-10-825-958-17
; Sequence 17, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-17

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 11
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```

; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
US-10-425-115-280164

Query Match 100.0%; Score 29; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 28 KIVFFA 33

RESULT 12

US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
US-10-424-599-165325

Query Match 100.0%; Score 29; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 21 KIVFFA 26

RESULT 13

US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
US-10-424-599-240310

Query Match 100.0%; Score 29; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 34 KIVFFA 39

RESULT 14

US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)-(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM013542, p-values=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56957

Query Match 100.0%; Score 29; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 63 KIVFFA 68

RESULT 15

US-09-867-847-18
; Sequence 18, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
       |:||||
DB      1 KVVFFA 6

RESULT 16
US-09-867-847-26
; Sequence 26, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-26

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
       |:||||
DB      1 KVVFFA 6

RESULT 17
US-09-915-092-8
; Sequence 8, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
```

```
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
       |:||||
DB      1 KVVFFA 6

RESULT 18
US-09-915-092-16
; Sequence 16, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
       |:||||
DB      1 KVVFFA 6

RESULT 19
US-09-747-408-9
; Sequence 9, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9
```

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 20
US-09-747-408-17
; Sequence 17, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 21
US-10-728-028-8
; Sequence 8, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 22
US-10-728-028-16
; Sequence 16, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 23
US-10-825-958-16
; Sequence 16, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-16

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 24
US-10-825-958-24
; Sequence 7, Application US/10825958
; Publication No. US2005090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 25
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 53035AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 18 KVVFFA 23

RESULT 26
US-10-642-255-7
; Sequence 7, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyl, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: eNOS
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 18 KVVFFA 23

RESULT 27
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pap
US-10-437-963-173619

Query Match 96.6%; Score 28; DB 4; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 28

US-10-437-963-133986
; Sequence 133986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pep
US-10-437-963-133986

Query Match 96.6%; Score 28; DB 4; Length 87;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 6 KVVFFA 11

RESULT 29

US-10-437-963-105773
; Sequence 105773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pep
US-10-437-963-105773

Query Match 96.6%; Score 28; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 30

US-10-437-963-141578
; Sequence 141578, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141578
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pep
US-10-437-963-141578

Query Match 96.6%; Score 28; DB 4; Length 135;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 31

US-10-437-963-122124
; Sequence 122124, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122124
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(175)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pep
US-10-437-963-122124

Query Match 96.6%; Score 28; DB 4; Length 175;

Best Local Similarity 83.3%; Pred. No. 3.3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 32

US-10-481-032A-214
; Sequence 214, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: Patentin Ver. 2.2
; SEQ ID NO 214
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 5; Length 186;

Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 33

US-10-481-032A-228
; Sequence 228, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: Patentin Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228

Query Match 96.6%; Score 28; DB 5; Length 186;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 34

US-10-437-963-172476
; Sequence 172476, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pap
US-10-437-963-172476

Query Match 96.6%; Score 28; DB 4; Length 188;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 35

US-10-437-963-172452
; Sequence 172452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pap
US-10-437-963-172452
```

```
Query Match          96.6%; Score 28; DB 4; Length 198;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
         |:||||
Db      4 KVVFFA 9
```

```
RESULT 36
US-10-055-475-14
; Sequence 14, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-055-475-14
```

```
Query Match          96.6%; Score 28; DB 4; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
         |:||||
Db      57 KVVFFA 62
```

```
RESULT 37
US-11-042-922-14
; Sequence 14, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
```

```
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-042-922-14
```

```
Query Match          96.6%; Score 28; DB 6; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
         |:||||
Db      57 KVVFFA 62
```

```
RESULT 38
US-10-055-475-13
; Sequence 13, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-055-475-13
```

```
Query Match          96.6%; Score 28; DB 4; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
         |:||||
Db      57 KVVFFA 62
```

```
RESULT 39
US-11-042-922-13
; Sequence 13, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
```


FILE REFERENCE: A34614-A-PCT-USA-A-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-11-042-922-13

Query Match 96.6%; Score 28; DB 6; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 40

US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match 96.6%; Score 28; DB 6; Length 564;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 53 KIVFFA 58

RESULT 41

US-10-408-765A-2031
; Sequence 2031, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibeon, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2031
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2031

Query Match 96.6%; Score 28; DB 4; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 42

US-10-755-889-234
; Sequence 234, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-234

Query Match 96.6%; Score 28; DB 4; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 43

US-10-370-715B-8
; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY

```
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match          96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      292 KVVFFA 297

RESULT 44
US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match          96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      292 KVVFFA 297

RESULT 45
US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
```

```
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match          96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      292 KVVFFA 297

RESULT 46
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match          96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 47
US-09-751-708A-124
; Sequence 124, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-124

Query Match          96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      514 KVVFFA 519
```

Db 514 KVVFFA 519

RESULT 48

US-10-428-817A-120
; Sequence 120, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-428-817A-120

Query Match 96.6%; Score 28; DB 4; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 49

US-10-937-758A-101
; Sequence 101, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-758A-101

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 50

US-10-631-467-1388
; Sequence 1388, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1388
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1388

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 51

US-10-631-467-1464
; Sequence 1464, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive i
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 52

US-11-097-143-32208
; Sequence 32208, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

```

; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32208

Query Match          96.6%; Score 28; DB 6; Length 1443;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1204 KIIFFA 1209

RESULT 53
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match          96.6%; Score 28; DB 4; Length 1640;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1596 KVVFFA 1601

; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1 KLVFFA 6

RESULT 54
US-09-867-847-7
; Sequence 7, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-20

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1 KLVFFA 6

RESULT 55
US-09-867-847-20
; Sequence 20, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-20

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 56
US-09-972-475-9
; Sequence 9, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-9
Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 57
US-09-915-092-10
; Sequence 10, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 58
US-09-915-092-28
; Sequence 28, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: D-amino acids
US-09-915-092-28
Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 59
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
```

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
```

```
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-10
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 64
US-10-728-028-27
; Sequence 27, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-27
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 65
US-10-728-028-28
; Sequence 28, Application US/10728028
```

```
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-28
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 66
US-10-825-958-7
; Sequence 7, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D. peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-7
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

RESULT 67
US-10-825-958-18
; Sequence 18, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-18

Query Match 93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 68
US-10-666-095-3
; Sequence 3, Application US/10666095
; Publication No. US20050119187A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Robert P.
; APPLICANT: Fu, Yanwen
; APPLICANT: Aucoin, Jed P.
; APPLICANT: Miller, Tod J.
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: McCarley, Robin L.
; TITLE OF INVENTION: Anti-Fibril Peptides
; FILE REFERENCE: 0212.1 Hammer
; CURRENT APPLICATION NUMBER: US/10/666,095
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,081
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-095-3

Query Match 93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 1 KLVFFA 6
|:||||

RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||

Db 1 KLVFFA 6

RESULT 71
US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||

Db 1 KLVFFA 6

RESULT 72
US-09-972-475-7
; Sequence 7, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267

FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-972-475-7

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||

Db 2 KLVFFA 7

RESULT 73
US-09-915-092-2
; Sequence 2, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-2

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||

Db 2 KLVFFA 7

RESULT 74
US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND

```
; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-17

Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 75
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT:  Gervais, Francine
; APPLICANT:  Kong, Xianqi
; APPLICANT:  Chalifour, Robert
; APPLICANT:  Migneault, David
; TITLE OF INVENTION:  AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-18

Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6

Search completed:  December 29, 2005, 18:49:45
Job time : 66.2903 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-10

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
 - 2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
 - 3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
 - 4: /cgn2_6/prodata/1/iaa/PCUS COMB.pep.*
 - 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
 - 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-1
2	29	100.0	6	2	US-09-747-408-10
3	28	96.6	6	2	US-09-747-408-9
4	28	96.6	6	2	US-09-747-408-17
5	28	96.6	77	2	US-09-513-999C-6921
6	28	96.6	1144	1	US-08-147-812-5
7	28	96.6	1144	1	US-08-319-866-12
8	28	96.6	1144	2	US-09-123-708-2
9	28	96.6	1144	2	US-09-123-624-2
10	28	96.6	1144	2	US-09-661-258-5
11	28	96.6	1144	2	US-08-809-917-12
12	28	96.6	1144	2	US-09-419-371-12
13	27	93.1	6	1	US-08-612-785B-9
14	27	93.1	6	2	US-08-703-675C-32
15	27	93.1	6	2	US-08-617-267C-9
16	27	93.1	6	2	US-09-747-408-3
17	27	93.1	6	2	US-09-747-408-11
18	27	93.1	7	1	US-08-127-904-14
19	27	93.1	7	1	US-08-612-785B-7
20	27	93.1	7	2	US-08-703-675C-30
21	27	93.1	7	2	US-08-617-267C-7
22	27	93.1	7	2	US-09-264-709A-13
23	27	93.1	7	2	US-09-747-408-2
24	27	93.1	7	2	US-09-747-408-18
25	27	93.1	7	2	US-09-747-408-19
26	27	93.1	7	4	PCT-US94-10475-14
27	27	93.1	8	1	US-08-612-785B-5

28	27	93.1	8	1	US-08-630-645-1	Sequence 1, Appli
29	27	93.1	8	2	US-08-703-675C-28	Sequence 28, Appl
30	27	93.1	8	2	US-08-617-267C-5	Sequence 5, Appli
31	27	93.1	8	2	US-09-095-106A-44	Sequence 44, Appl
32	27	93.1	8	2	US-08-766-596A-1	Sequence 1, Appli
33	27	93.1	8	2	US-09-668-314C-73	Sequence 73, Appl
34	27	93.1	8	4	PCT-US96-10220-1	Sequence 1, Appli
35	27	93.1	9	2	US-08-766-596A-64	Sequence 64, Appl
36	27	93.1	9	2	US-09-747-408-20	Sequence 20, Appl
37	27	93.1	10	2	US-08-970-833-3	Sequence 3, Appli
38	27	93.1	10	2	US-09-724-961-20	Sequence 20, Appl
39	27	93.1	10	2	US-09-724-961-21	Sequence 21, Appl
40	27	93.1	10	2	US-09-724-961-22	Sequence 22, Appl
41	27	93.1	10	2	US-09-724-961-23	Sequence 23, Appl
42	27	93.1	10	2	US-09-724-961-24	Sequence 24, Appl
43	27	93.1	10	2	US-09-580-018-20	Sequence 20, Appl
44	27	93.1	10	2	US-09-580-018-21	Sequence 21, Appl
45	27	93.1	10	2	US-09-580-018-22	Sequence 22, Appl
46	27	93.1	10	2	US-09-580-018-23	Sequence 23, Appl
47	27	93.1	10	2	US-09-580-018-24	Sequence 24, Appl
48	27	93.1	10	2	US-09-724-551-20	Sequence 20, Appl
49	27	93.1	10	2	US-09-724-551-21	Sequence 21, Appl
50	27	93.1	10	2	US-09-724-551-22	Sequence 22, Appl
51	27	93.1	10	2	US-09-724-551-23	Sequence 23, Appl
52	27	93.1	10	2	US-09-724-551-24	Sequence 24, Appl
53	27	93.1	10	2	US-09-724-940-20	Sequence 20, Appl
54	27	93.1	10	2	US-09-724-940-21	Sequence 21, Appl
55	27	93.1	10	2	US-09-724-940-22	Sequence 22, Appl
56	27	93.1	10	2	US-09-724-940-23	Sequence 23, Appl
57	27	93.1	10	2	US-09-724-940-24	Sequence 24, Appl
58	27	93.1	11	1	US-08-630-645-14	Sequence 14, Appl
59	27	93.1	11	1	US-08-766-596A-4	Sequence 4, Appli
60	27	93.1	11	2	US-09-988-842-9	Sequence 9, Appli
61	27	93.1	11	2	US-09-988-842-25	Sequence 25, Appl
62	27	93.1	11	4	PCT-US96-10220-14	Sequence 14, Appl
63	27	93.1	14	2	US-09-594-366-5	Sequence 5, Appli
64	27	93.1	14	2	US-09-992-800-5	Sequence 5, Appli
65	27	93.1	15	1	US-08-612-785B-14	Sequence 14, Appl
66	27	93.1	15	1	US-08-612-785B-37	Sequence 37, Appl
67	27	93.1	15	2	US-08-617-267C-17	Sequence 17, Appl
68	27	93.1	15	2	US-08-766-596A-56	Sequence 56, Appl
69	27	93.1	15	2	US-08-766-596A-57	Sequence 57, Appl
70	27	93.1	15	2	US-08-766-596A-58	Sequence 58, Appl
71	27	93.1	15	2	US-08-766-596A-60	Sequence 60, Appl
72	27	93.1	15	2	US-08-766-596A-61	Sequence 61, Appl
73	27	93.1	15	2	US-08-766-596A-63	Sequence 63, Appl
74	27	93.1	15	2	US-08-766-596A-65	Sequence 65, Appl
75	27	93.1	17	2	US-09-264-709A-2	Sequence 2, Appli
76	27	93.1	17	2	US-09-594-366-3	Sequence 3, Appli
77	27	93.1	17	2	US-09-623-548A-950	Sequence 950, App
78	27	93.1	17	2	US-09-623-548A-983	Sequence 983, App
79	27	93.1	17	2	US-09-992-800-3	Sequence 3, Appli
80	27	93.1	17	2	US-09-657-276-950	Sequence 950, App
81	27	93.1	17	2	US-09-657-276-983	Sequence 983, App
82	27	93.1	19	2	US-08-970-833-11	Sequence 11, Appl
83	27	93.1	19	2	US-09-723-384-5	Sequence 5, Appli
84	27	93.1	19	2	US-09-724-961-75	Sequence 75, Appl
85	27	93.1	19	2	US-09-724-552-5	Sequence 5, Appli
86	27	93.1	19	2	US-09-580-018-75	Sequence 75, Appl
87	27	93.1	19	2	US-09-723-927-5	Sequence 5, Appli
88	27	93.1	19	2	US-09-724-489-5	Sequence 5, Appli
89	27	93.1	19	2	US-09-723-477-5	Sequence 5, Appli
90	27	93.1	19	2	US-09-723-762-5	Sequence 5, Appli
91	27	93.1	19	2	US-09-201-430-5	Sequence 5, Appli
92	27	93.1	19	2	US-09-724-551-75	Sequence 75, Appl
93	27	93.1	19	2	US-10-815-353-5	Sequence 5, Appli
94	27	93.1	19	2	US-10-816-529-5	Sequence 5, Appli
95	27	93.1	19	2	US-10-815-391-5	Sequence 5, Appli
96	27	93.1	19	2	US-10-816-022-5	Sequence 5, Appli
97	27	93.1	19	2	US-09-724-940-75	Sequence 75, Appl
98	27	93.1	19	2	US-10-934-609-5	Sequence 5, Appli
99	27	93.1	19	2	US-10-884-892-5	Sequence 5, Appli
100	27	93.1	20	2	US-08-970-833-10	Sequence 10, Appl

101	27	93.1	20	2	US-09-724-953-33	Sequence 33, Appl	174	27	93.1	38	2	US-09-657-276-1002	Sequence 1002, Ap
102	27	93.1	20	2	US-09-724-567-33	Sequence 33, Appl	175	27	93.1	39	1	US-08-304-585-5	Sequence 5, Appl
103	27	93.1	20	2	US-09-979-952-33	Sequence 33, Appl	176	27	93.1	39	1	US-08-302-808-2	Sequence 2, Appl
104	27	93.1	20	2	US-09-585-817-33	Sequence 33, Appl	177	27	93.1	39	1	US-08-609-090-7	Sequence 7, Appl
105	27	93.1	26	1	US-08-304-585-7	Sequence 7, Appl	178	27	93.1	39	1	US-08-682-245A-1	Sequence 1, Appl
106	27	93.1	28	1	US-08-346-849-4	Sequence 4, Appl	179	27	93.1	39	1	US-08-986-948-2	Sequence 2, Appl
107	27	93.1	28	1	US-08-303-808-7	Sequence 7, Appl	180	27	93.1	40	1	US-07-744-767A-1	Sequence 1, Appl
108	27	93.1	28	1	US-08-609-090-2	Sequence 2, Appl	181	27	93.1	40	1	US-08-235-400-2	Sequence 2, Appl
109	27	93.1	28	1	US-08-986-948-7	Sequence 7, Appl	182	27	93.1	40	1	US-08-476-464A-2	Sequence 2, Appl
110	27	93.1	28	1	US-08-293-284A-4	Sequence 4, Appl	183	27	93.1	40	1	US-08-304-585-1	Sequence 1, Appl
111	27	93.1	28	1	US-08-461-216-2	Sequence 2, Appl	184	27	93.1	40	1	US-08-304-585-8	Sequence 8, Appl
112	27	93.1	28	2	US-09-388-890-2	Sequence 2, Appl	185	27	93.1	40	1	US-08-302-808-3	Sequence 3, Appl
113	27	93.1	28	2	US-09-388-890-3	Sequence 3, Appl	186	27	93.1	40	1	US-08-433-734-1	Sequence 1, Appl
114	27	93.1	28	2	US-09-388-890-4	Sequence 4, Appl	187	27	93.1	40	1	US-08-609-090-8	Sequence 8, Appl
115	27	93.1	28	2	US-09-388-890-5	Sequence 5, Appl	188	27	93.1	40	1	US-07-737-371B-69	Sequence 69, Appl
116	27	93.1	28	2	US-09-388-890-6	Sequence 6, Appl	189	27	93.1	40	1	US-08-682-245A-2	Sequence 2, Appl
117	27	93.1	28	2	US-09-388-890-7	Sequence 7, Appl	190	27	93.1	40	1	US-08-986-948-3	Sequence 3, Appl
118	27	93.1	28	2	US-09-388-890-8	Sequence 8, Appl	191	27	93.1	40	1	US-08-461-216-1	Sequence 1, Appl
119	27	93.1	28	2	US-09-388-890-9	Sequence 9, Appl	192	27	93.1	40	2	US-08-959-148-1	Sequence 1, Appl
120	27	93.1	28	2	US-09-388-890-10	Sequence 10, Appl	193	27	93.1	40	2	US-09-242-724-22	Sequence 22, Appl
121	27	93.1	28	2	US-09-388-890-12	Sequence 12, Appl	194	27	93.1	40	2	US-08-723-661B-1	Sequence 1, Appl
122	27	93.1	28	2	US-09-388-890-13	Sequence 13, Appl	195	27	93.1	40	2	US-09-062-365-3	Sequence 3, Appl
123	27	93.1	28	2	US-09-388-890-14	Sequence 14, Appl	196	27	93.1	40	2	US-09-133-866-1	Sequence 1, Appl
124	27	93.1	28	2	US-09-264-709A-1	Sequence 1, Appl	197	27	93.1	40	2	US-09-861-847A-7	Sequence 7, Appl
125	27	93.1	28	2	US-08-723-661B-2	Sequence 2, Appl	198	27	93.1	40	2	US-09-861-847A-8	Sequence 8, Appl
126	27	93.1	28	2	US-09-660-954-2	Sequence 2, Appl	199	27	93.1	40	2	US-09-988-842-3	Sequence 3, Appl
127	27	93.1	28	2	US-09-660-954-3	Sequence 3, Appl	200	27	93.1	40	2	US-10-455-218-1	Sequence 1, Appl
128	27	93.1	28	2	US-09-660-954-4	Sequence 4, Appl	201	27	93.1	40	2	US-10-151-614-1	Sequence 1, Appl
129	27	93.1	28	2	US-09-660-954-5	Sequence 5, Appl	202	27	93.1	40	2	US-09-623-548A-956	Sequence 956, App
130	27	93.1	28	2	US-09-660-954-6	Sequence 6, Appl	203	27	93.1	40	2	US-09-623-548A-962	Sequence 962, App
131	27	93.1	28	2	US-09-660-954-7	Sequence 7, Appl	204	27	93.1	40	2	US-09-623-548A-968	Sequence 968, App
132	27	93.1	28	2	US-09-660-954-8	Sequence 8, Appl	205	27	93.1	40	2	US-09-623-548A-978	Sequence 978, App
133	27	93.1	28	2	US-09-660-954-9	Sequence 9, Appl	206	27	93.1	40	2	US-09-623-548A-989	Sequence 989, App
134	27	93.1	28	2	US-09-660-954-10	Sequence 10, Appl	207	27	93.1	40	2	US-09-623-548A-995	Sequence 995, App
135	27	93.1	28	2	US-09-660-954-12	Sequence 12, Appl	208	27	93.1	40	2	US-09-623-548A-1005	Sequence 1005, Ap
136	27	93.1	28	2	US-09-660-954-13	Sequence 13, Appl	209	27	93.1	40	2	US-09-657-276-956	Sequence 956, App
137	27	93.1	28	2	US-09-660-954-14	Sequence 14, Appl	210	27	93.1	40	2	US-09-657-276-962	Sequence 962, App
138	27	93.1	28	2	US-08-898-300-4	Sequence 4, Appl	211	27	93.1	40	2	US-09-657-276-968	Sequence 968, App
139	27	93.1	28	2	US-08-824-513-4	Sequence 4, Appl	212	27	93.1	40	2	US-09-657-276-978	Sequence 978, App
140	27	93.1	28	2	US-09-623-548A-959	Sequence 959, App	213	27	93.1	40	2	US-09-657-276-989	Sequence 989, App
141	27	93.1	28	2	US-09-623-548A-965	Sequence 965, App	214	27	93.1	40	2	US-09-657-276-995	Sequence 995, App
142	27	93.1	28	2	US-09-623-548A-966	Sequence 966, App	215	27	93.1	40	2	US-09-657-276-1005	Sequence 1005, Ap
143	27	93.1	28	2	US-09-623-548A-972	Sequence 972, App	216	27	93.1	40	2	US-09-962-955D-36	Sequence 36, Appl
144	27	93.1	28	2	US-09-623-548A-992	Sequence 1003, Ap	217	27	93.1	40	4	PCT-US92-06700-1	Sequence 1, Appl
145	27	93.1	28	2	US-09-623-548A-1003	Sequence 959, App	218	27	93.1	41	1	US-07-819-361-1	Sequence 1, Appl
146	27	93.1	28	2	US-09-657-276-959	Sequence 965, App	219	27	93.1	41	1	US-08-302-808-4	Sequence 4, Appl
147	27	93.1	28	2	US-09-657-276-965	Sequence 976, App	220	27	93.1	41	1	US-08-682-245A-3	Sequence 3, Appl
148	27	93.1	28	2	US-09-657-276-976	Sequence 976, App	221	27	93.1	41	1	US-08-986-948-4	Sequence 4, Appl
149	27	93.1	28	2	US-09-657-276-992	Sequence 992, App	222	27	93.1	42	1	US-08-179-574-1	Sequence 1, Appl
150	27	93.1	28	2	US-09-657-276-1003	Sequence 1003, Ap	223	27	93.1	42	1	US-08-179-574-2	Sequence 2, Appl
151	27	93.1	30	1	US-09-861-847A-66	Sequence 66, Appl	224	27	93.1	42	1	US-08-271-162-5	Sequence 5, Appl
152	27	93.1	30	2	US-09-861-847A-1	Sequence 3, Appl	225	27	93.1	42	1	US-08-347-144-1	Sequence 1, Appl
153	27	93.1	33	1	US-08-609-090-4	Sequence 1, Appl	226	27	93.1	42	1	US-08-462-859A-19	Sequence 19, Appl
154	27	93.1	34	1	US-08-475-579A-4	Sequence 4, Appl	227	27	93.1	42	1	US-08-123-659A-19	Sequence 19, Appl
155	27	93.1	35	1	US-08-304-585-6	Sequence 6, Appl	228	27	93.1	42	1	US-08-464-247A-19	Sequence 19, Appl
156	27	93.1	35	1	US-08-612-785B-16	Sequence 16, Appl	229	27	93.1	42	1	US-08-464-248A-19	Sequence 19, Appl
157	27	93.1	35	1	US-08-612-785B-36	Sequence 36, Appl	230	27	93.1	42	1	US-08-476-464A-1	Sequence 1, Appl
158	27	93.1	35	1	US-08-612-785B-38	Sequence 38, Appl	231	27	93.1	42	1	US-08-304-585-2	Sequence 2, Appl
159	27	93.1	35	1	US-08-612-785B-40	Sequence 40, Appl	232	27	93.1	42	1	US-08-302-808-5	Sequence 5, Appl
160	27	93.1	35	2	US-08-612-785B-46	Sequence 16, Appl	233	27	93.1	42	1	US-08-268-348A-1	Sequence 1, Appl
161	27	93.1	35	2	US-08-612-785B-16	Sequence 979, App	234	27	93.1	42	1	US-08-268-348A-3	Sequence 3, Appl
162	27	93.1	35	2	US-09-623-548A-979	Sequence 1006, Ap	235	27	93.1	42	1	US-08-268-348A-3	Sequence 4, Appl
163	27	93.1	35	2	US-09-623-548A-1006	Sequence 979, App	236	27	93.1	42	1	US-08-268-348A-4	Sequence 5, Appl
164	27	93.1	35	2	US-09-657-276-979	Sequence 1006, Ap	237	27	93.1	42	1	US-08-268-348A-5	Sequence 6, Appl
165	27	93.1	36	1	US-08-609-090-6	Sequence 6, Appl	238	27	93.1	42	1	US-08-268-348A-6	Sequence 9, Appl
166	27	93.1	36	2	US-09-861-847A-6	Sequence 6, Appl	239	27	93.1	42	1	US-08-433-734-2	Sequence 2, Appl
167	27	93.1	36	2	US-09-861-847A-11	Sequence 11, Appl	240	27	93.1	42	1	US-08-609-090-9	Sequence 9, Appl
168	27	93.1	38	1	US-08-302-808-1	Sequence 1, Appl	241	27	93.1	42	1	US-07-737-371E-72	Sequence 72, Appl
169	27	93.1	38	1	US-07-737-371E-68	Sequence 68, Appl	242	27	93.1	42	1	US-08-422-333-4	Sequence 4, Appl
170	27	93.1	38	1	US-08-986-948-1	Sequence 1, Appl	243	27	93.1	42	1	US-08-682-245A-4	Sequence 4, Appl
171	27	93.1	38	2	US-09-623-548A-975	Sequence 975, App	244	27	93.1	42	1	US-08-986-948-5	Sequence 5, Appl
172	27	93.1	38	2	US-09-623-548A-1002	Sequence 1002, Ap	245	27	93.1	42	2	US-08-717-551A-2	Sequence 2, Appl
173	27	93.1	38	2	US-09-657-276-975	Sequence 975, App	246	27	93.1	42	2	US-09-388-890-1	Sequence 1, Appl

```
247 27 93.1 42 2 US-09-005-215-20
248 27 93.1 42 2 US-09-242-724-23
249 27 93.1 42 2 US-08-922-930-2
250 27 93.1 42 2 US-09-660-954-1
251 27 93.1 42 2 US-08-923-055-2
252 27 93.1 42 2 US-08-922-889-2
253 27 93.1 42 2 US-09-731-460-1
254 27 93.1 42 2 US-09-133-866-2
255 27 93.1 42 2 US-09-723-384-1
256 27 93.1 42 2 US-09-724-961-42
257 27 93.1 42 2 US-09-724-552-1
258 27 93.1 42 2 US-09-580-018-42
259 27 93.1 42 2 US-10-455-218-2
260 27 93.1 42 2 US-09-723-927-1
261 27 93.1 42 2 US-09-724-489-1
262 27 93.1 42 2 US-09-724-477-1
263 27 93.1 42 2 US-09-723-762-1
264 27 93.1 42 2 US-09-201-430-1
265 27 93.1 42 2 US-09-724-551-42
266 27 93.1 42 2 US-10-815-353-1
267 27 93.1 42 2 US-10-278-181-1
268 27 93.1 42 2 US-10-816-529-1
269 27 93.1 42 2 US-09-623-548A-955
270 27 93.1 42 2 US-09-623-548A-961
271 27 93.1 42 2 US-09-623-548A-967
272 27 93.1 42 2 US-09-623-548A-988
273 27 93.1 42 2 US-09-623-548A-994
274 27 93.1 42 2 US-10-815-391-1
275 27 93.1 42 2 US-10-816-022-1
276 27 93.1 42 2 US-09-724-953-34
277 27 93.1 42 2 US-09-657-276-955
278 27 93.1 42 2 US-09-657-276-961
279 27 93.1 42 2 US-09-657-276-967
280 27 93.1 42 2 US-09-657-276-988
281 27 93.1 42 2 US-09-657-276-994
282 27 93.1 42 2 US-09-724-567-34
283 27 93.1 42 2 US-09-724-940-42
284 27 93.1 42 2 US-09-865-294A-65
285 27 93.1 42 2 US-09-979-952-34
286 27 93.1 42 2 US-09-585-817-34
287 27 93.1 42 2 US-09-962-955D-37
288 27 93.1 42 2 US-09-706-574A-20
289 27 93.1 42 2 US-10-934-609-1
290 27 93.1 42 2 US-10-884-892-1
291 27 93.1 42 4 PCT-US92-06700-2
292 27 93.1 42 4 PCT-US93-00325-1
293 27 93.1 42 4 PCT-US95-08302-5
294 27 93.1 42 6 5220013-12
295 27 93.1 42 6 5220013-14
296 27 93.1 42 6 5223482-12
297 27 93.1 43 1 US-08-235-400-1
298 27 93.1 43 1 US-08-437-067-1
299 27 93.1 43 1 US-08-302-808-6
300 27 93.1 43 1 US-08-079-511-1

ALIGNMENTS

RESULT 1
US-09-747-408-1
; Sequence 1, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2
US-09-747-408-10
; Sequence 10, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 4

US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399

; GENERAL INFORMATION:

; APPLICANT: Green, Allan M.

; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: Compounds And Methods For Modulating

; FILE REFERENCE: NBI-088

; CURRENT APPLICATION NUMBER: US/09/747,408

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/171,877

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-747-408-17

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05; Length 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 5

US-09-513-999C-6921

; Sequence 6921, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 6921

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-513-999C-6921

Query Match 96.6%; Score 28; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 38 KVVFFA 43

RESULT 6

US-08-147-812-5

; Sequence 5, Application US/08147812

; Patent No. 5766909

; GENERAL INFORMATION:

; APPLICANT: Xie, Qiao-wen

; APPLICANT: Nathan, Carl F.

; APPLICANT: Mumford, Richard A.

; APPLICANT: Calavcay, Jimmy Ramos

; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merck & Co., Inc.

; STREET: 126 East Lincoln Avenue

; CITY: Rahway

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh Centris650

; OPERATING SYSTEM: Macintosh 7.0.1

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/147,812

; FILING DATE: No. 5766909 Available

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/841,641

; FILING DATE: 02-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Wallen, John W III

; REGISTRATION NUMBER: 35,403

; REFERENCE/DOCKET NUMBER: 186581A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 594-3905

; TELEFAX: (908) 594-4720

; TELEX: 138825

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1144 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-147-812-5

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 7

US-08-319-866-12

; Sequence 12, Application US/08319866

; Patent No. 5929223

; GENERAL INFORMATION:

; APPLICANT: Tully, Timothy P.

; APPLICANT: Yin, Jerry C.

; APPLICANT: Regulski, Michael

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,866
; FILING DATE: 7-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-319-866-12

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 8
US-09-123-708-2
; Sequence 2, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-09-123-708-2

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 9
US-09-123-624-2
; Sequence 2, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

```

```

; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-123-624-2

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 10
US-09-661-258-5
; Sequence 5, Application US/09661258
; Patent No. 6620616
; GENERAL INFORMATION:
; APPLICANT: Stuehr, Dennis J.
; APPLICANT: Adak, Subrata
; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
; FILE REFERENCE: 26473/04028
; CURRENT APPLICATION NUMBER: US/09/661,258
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-661-258-5

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 11
US-08-809-917-12
; Sequence 12, Application US/08809917
; Patent No. 6689557
; GENERAL INFORMATION:
; APPLICANT: APPLICANT
; APPLICANT: APPLICANT
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,917
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13198
FILING DATE:
APPLICATION NUMBER: US 08/361,063
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,866
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-917-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 514 KVVFFA 519

RESULT 12
US-09-419-371-12
Sequence 12, Application US/09419371
Patent No. 6890516
GENERAL INFORMATION:
APPLICANT: Tully, Timothy P.
TITLE OF INVENTION: Cloning and Characterizing of Genes
TITLE OF INVENTION: Associated With Long-Term Memory
FILE REFERENCE: CSHL94-03A32
CURRENT APPLICATION NUMBER: US/09/419,371
CURRENT FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 08/809,917
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: PCT/US95/13198
PRIOR FILING DATE: 1995-10-06
PRIOR APPLICATION NUMBER: 08/361,063
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/319,866
PRIOR FILING DATE: 1994-10-07
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 1144
TYPE: PRT
ORGANISM: mouse
US-09-419-371-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||

Db 514 KVVFFA 519
RESULT 13
US-08-612-785B-9
Sequence 9, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 93.1%; Score 27; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 14
US-08-703-675C-32
Sequence 32, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston

Aggregation Comprising D-


```
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-617-267C-32

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 15
US-08-617-267C-9
; Sequence 9, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Fintelis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
```

```
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Gaudio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-617-267C-9

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 16
US-09-747-408-3
; Sequence 3, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-3

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 17
US-09-747-408-11
; Sequence 11, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
```

; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 18
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951

; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amesic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown

US-08-127-904-14
Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 19
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: AB Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/612,785B
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-7

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 20
US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567

; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

```
;
;
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-703-675C-30

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 21
US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Fintelis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:

;
;
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-617-267C-7

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 22
US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-264-709A-13

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 23
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
```

```
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match          93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 2 KLVFFA 7

RESULT 24
US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match          93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 25
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match          93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 26
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564 or 783-6030
; TELEFAX: (202) 783-6031
; TELEX: None
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
PCT-US94-10475-14

Query Match          93.1%; Score 27; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 27
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
```

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-5

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 28
US-08-630-645-1
Sequence 1, Application US/08630645
Patent No. 5948763
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/630,645
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-630-645-1

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 29
US-08-703-675C-28
Sequence 28, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-28

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 30
US-08-617-267C-5
Sequence 5, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||

Db 3 KLVFFA 8

RESULT 31
US-09-095-106A-44
Sequence 44, Application US/09095106A
Patent No. 6331440
GENERAL INFORMATION:
APPLICANT: NORDSTEDT, Christer
APPLICANT: NASLUND, Jan
APPLICANT: THYBERG, Johan
APPLICANT: TERNBERG, Lars O.
APPLICANT: TERNIUS, Lars
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
FILE REFERENCE: 000500-124
CURRENT APPLICATION NUMBER: US/09/095,106A
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/009,386
PRIOR FILING DATE: 1995-12-29
PRIOR APPLICATION NUMBER: PCT/SE96/01621
PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 8
TYPE: PPT
ORGANISM: Amyloidosis
US-09-095-106A-44

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 32
US-08-766-596A-1
Sequence 1, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-1

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||
Db 1 KLVFFA 6

RESULT 33
US-09-668-314C-73
Sequence 73, Application US/09668314C
Patent No. 6844148
GENERAL INFORMATION:
APPLICANT: Gurney, et al
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280NCP
CURRENT APPLICATION NUMBER: US/09/668,314C
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/169,232
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-668-314C-73

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||
Db 1 KLVFFA 6

RESULT 34
PCT-US96-10220-1
Sequence 1, Application PC/TUS9610220
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEROF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10220
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-10220-1
Query Match 93.1%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||
Db 1 KLVFFA 6

RESULT 35
US-08-766-596A-64
Sequence 64, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-64
```

```
Query Match      93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:||||
Db       2 KLVFFA 7
```

```
RESULT 36
US-09-747-408-20
; Sequence 20, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-20
```

```
Query Match      93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:||||
Db       4 KLVFFA 9
```

```
RESULT 37
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 602859
; GENERAL INFORMATION:
; APPLICANT: Kiessling, Laura L.
```

```
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-970-833-3
```

```
Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 38
US-09-724-961-20
; Sequence 20, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15276J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
```



```
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 39
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 4 KLVFFA 9

RESULT 40
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
;
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 3 KLVFFA 8

RESULT 41
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-23
```

```
Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      2 KLVFFA 7

RESULT 42
US-09-724-961-24
; Sequence 24, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vaquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KLVFFA 6

RESULT 43
US-09-580-018-20
; Sequence 20, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-20

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KLVFFA 6

RESULT 44
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      4 KLVFFA 9

RESULT 45
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-20

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      5 KLVFFA 10

RESULT 44
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      4 KLVFFA 9

RESULT 45
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22
```

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 46

US-09-580-018-23
; Sequence 23, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-23

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 47

US-09-580-018-24
; Sequence 24, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)

US-09-580-018-24

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 48

US-09-724-551-20
; Sequence 20, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-20

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 49

US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)

```
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 4 KLVFFA 9

RESULT 50
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 3 KLVFFA 8

RESULT 51
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 52
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 53
US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905886
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
```

```

; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20

```

```

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta2, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-20

```

RESULT 54
US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686

Query Match	Score 27;	DB 2;	Length 10;
Best Local Similarity	93.1%		
Matches	83.3%		
Conservative	5;	Pred. No. 5.6;	
Mismatches	1;		
Indels	0;		
Gaps	0;		

RESULT 55
US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686

```

1  GENERAL INFORMATION:
2  APPLICANT: Schenk, Dale B.
3  APPLICANT: Bard, Frederique
4  APPLICANT: Vasquez, Nick
5  APPLICANT: Vednock, Ted
6  TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
7  FILE REFERENCE: 15270J-004750UC
8  CURRENT APPLICATION NUMBER: US/09/724,940
9  CURRENT FILING DATE: 2000-11-28
10 PRIOR APPLICATION NUMBER: US/09/580,015
11 PRIOR FILING DATE: 2000-05-26
12 PRIOR APPLICATION NUMBER: US 09/322,289
13 PRIOR FILING DATE: 1999-05-28
14 PRIOR APPLICATION NUMBER: US 09/201,430
15 PRIOR FILING DATE: 1998-11-30
16 PRIOR APPLICATION NUMBER: WO PCT/US00/14810
17 PRIOR FILING DATE: 1998-11-30
18 PRIOR APPLICATION NUMBER: US 60/080,970
19 PRIOR FILING DATE: 1998-04-07
20 PRIOR APPLICATION NUMBER: US 60/067,740
21 PRIOR FILING DATE: 1997-12-02
22 NUMBER OF SEQ ID NOS: 77
23 SOFTWARE: PatentIn Ver. 2.1
24 SEQ ID NO 22
25 LENGTH: 10
26 TYPE: PRT
27 ORGANISM: Artificial Sequence
28 FEATURE:
29 OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
30 OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
31 OTHER INFORMATION: peptide)
32 US-09-724-940-22

```

```

RESULT 56
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
;
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db      2 KLVFFA 7

RESULT 57
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db      1 KLVFFA 6

RESULT 58
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
```

```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-14

Query Match      93.1%; Score 27; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db      2 KLVFFA 7

RESULT 59
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 2 KLVFFA 7

RESULT 60
US-09-988-842-9
;; Sequence 9, Application US/09988842
;; Patent No. 6716589
;; GENERAL INFORMATION:
;; APPLICANT: Johansson, Jan
;; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
;; FILE REFERENCE: 12125-002001
;; CURRENT APPLICATION NUMBER: US/09/988,842
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: US 60/251,662
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: US 60/253,695
;; PRIOR FILING DATE: 2000-11-20
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 2 KLVFFA 7

RESULT 61
US-09-988-842-25
;; Sequence 25, Application US/09988842
;; Patent No. 6716589
;; GENERAL INFORMATION:
;; APPLICANT: Johansson, Jan
;; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
;; FILE REFERENCE: 12125-002001

;; FILE REFERENCE: 12125-002001
;; CURRENT APPLICATION NUMBER: US/09/988,842
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: US 60/251,662
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: US 60/253,695
;; PRIOR FILING DATE: 2000-11-20
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 25
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 2 KLVFFA 7

RESULT 62
PCT-US96-10220-14
;; Sequence 14, Application PC/TUS9610220
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10220
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US96-10220-14

Query Match 93.1%; Score 27; DB 4; Length 11;

Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 63
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 64
US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 65
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:

; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-14

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 66
US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
DB 6 KLVFFA 11

RESULT 67
US-08-617-267C-14
Sequence 14, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Finkelstein, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
DB 1 KLVFFA 6

RESULT 68
US-08-766-596A-56
Sequence 56, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-766-596A-56

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 69

US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 70

US-08-766-596A-58

; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 71

US-08-766-596A-60
; Sequence 60, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-60

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 72
US-08-766-596A-61
; Sequence 61, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 73
US-08-766-596A-63
; Sequence 63, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

```
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 63:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-766-596A-63

Query Match          93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      5 KLVEFA 10

RESULT 74
US-08-766-596A-65
; Sequence 65, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-65

Query Match          93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      5 KLVEFA 10
```

RESULT 75

```
US-09-264-709A-2
; Sequence 2, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-2
```

```
Query Match          93.1%; Score 27; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      5 KLVEFA 10
```

Search completed: December 29, 2005, 17:52:37
Job time : 21.1323 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:33:58 ; Search time 3.58065 Seconds
(without alignments)
18.497 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVPFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 65735 seqs, 11038596 residues

Total number of hits satisfying chosen parameters: 65735

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listings first 300 summaries

Database : Pending Patents AA New.*

1: /cgn2_6/prodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	93.1	7	7	US-11-269-857-6
2	27	93.1	11	7	US-11-291-770-20
3	27	93.1	24	1	PCT-US05-32135-5
4	27	93.1	24	1	PCT-US05-32135-6
5	27	93.1	28	7	US-11-297-316-2
6	27	93.1	39	7	US-11-194-989-19
7	27	93.1	39	7	US-11-195-207-19
8	27	93.1	40	1	PCT-US05-32135-4
9	27	93.1	40	6	US-10-966-919B-2
10	27	93.1	40	7	US-11-194-989-15
11	27	93.1	40	7	US-11-194-989-20
12	27	93.1	40	7	US-11-194-989-21
13	27	93.1	40	7	US-11-194-989-22
14	27	93.1	40	7	US-11-194-989-23
15	27	93.1	40	7	US-11-194-989-24
16	27	93.1	40	7	US-11-194-989-25
17	27	93.1	40	7	US-11-195-207-15
18	27	93.1	40	7	US-11-195-207-20
19	27	93.1	40	7	US-11-195-207-21
20	27	93.1	40	7	US-11-195-207-22
21	27	93.1	40	7	US-11-195-207-23
22	27	93.1	40	7	US-11-195-207-24
23	27	93.1	40	7	US-11-195-207-25
24	27	93.1	40	7	US-11-087-102A-18
25	27	93.1	40	7	US-11-087-102A-19

26	27	93.1	41	7	US-11-194-989-18	Sequence 18, Appl
27	27	93.1	41	7	US-11-195-207-18	Sequence 18, Appl
28	27	93.1	42	6	US-10-966-919B-3	Sequence 3, Appl
29	27	93.1	42	7	US-11-270-774-174	Sequence 174, Appl
30	27	93.1	42	7	US-11-269-857-5	Sequence 5, Appl
31	27	93.1	42	7	US-11-194-989-16	Sequence 16, Appl
32	27	93.1	42	7	US-11-195-207-16	Sequence 16, Appl
33	27	93.1	42	7	US-11-297-316-1	Sequence 1, Appl
34	27	93.1	43	4	US-08-920-162A-1	Sequence 1, Appl
35	27	93.1	43	6	US-10-677-076-1	Sequence 1, Appl
36	27	93.1	43	6	US-10-966-919B-1	Sequence 1, Appl
37	27	93.1	43	6	US-10-250-581-1	Sequence 1, Appl
38	27	93.1	43	7	US-11-194-989-17	Sequence 17, Appl
39	27	93.1	43	7	US-11-195-207-17	Sequence 17, Appl
40	27	93.1	43	7	US-10-721-297-12	Sequence 12, Appl
41	27	93.1	62	6	US-11-270-774-173	Sequence 173, Appl
42	27	93.1	103	4	US-08-920-162A-2	Sequence 2, Appl
43	27	93.1	103	6	US-10-677-076-2	Sequence 2, Appl
44	27	93.1	639	8	US-60-742-871-82	Sequence 82, Appl
45	27	93.1	695	8	US-60-742-871-80	Sequence 80, Appl
46	27	93.1	751	8	US-11-220-372-313	Sequence 313, Appl
47	27	93.1	751	8	US-60-742-871-81	Sequence 81, Appl
48	27	93.1	770	7	US-11-270-774-172	Sequence 172, Appl
49	25	86.2	34	6	US-10-868-184C-4923	Sequence 4923, Ap
50	25	86.2	256	6	US-11-045-004-1961	Sequence 1961, Ap
51	25	86.2	844	6	US-10-018-105A-6	Sequence 6, Appl
52	24	82.8	60	7	US-11-144-947A-659	Sequence 659, Appl
53	24	82.8	234	7	US-11-144-947A-353	Sequence 353, Appl
54	24	82.8	399	6	US-10-868-184C-3591	Sequence 3591, Ap
55	24	82.8	435	7	US-11-045-004-728	Sequence 728, Appl
56	24	82.8	574	7	US-11-045-004-1192	Sequence 1192, Ap
57	24	82.8	660	7	US-11-302-994-113	Sequence 113, Appl
58	24	82.8	677	6	US-10-964-241B-230	Sequence 230, Appl
59	24	82.8	677	6	US-11-290-153-230	Sequence 230, Appl
60	24	82.8	1241	6	US-10-556-060-220	Sequence 220, Appl
61	23	79.3	5	6	US-10-966-919B-4	Sequence 4, Appl
62	23	79.3	5	7	US-11-269-857-7	Sequence 7, Appl
63	23	79.3	20	1	PCT-US05-12482A-5	Sequence 5, Appl
64	23	79.3	29	6	US-10-868-184C-4123	Sequence 4123, Ap
65	23	79.3	49	6	US-10-868-184C-3208	Sequence 3208, Ap
66	23	79.3	77	7	US-11-045-004-2209	Sequence 2209, Ap
67	23	79.3	147	7	US-11-144-947A-503	Sequence 503, Appl
68	23	79.3	166	7	US-11-268-554-406	Sequence 406, Appl
69	23	79.3	166	8	US-60-741-051-80	Sequence 80, Appl
70	23	79.3	183	7	US-11-264-096-399	Sequence 399, Appl
71	23	79.3	183	7	US-11-264-096-1048	Sequence 1048, Ap
72	23	79.3	183	7	US-11-264-096-1048	Sequence 1048, Ap
73	23	79.3	229	6	US-10-964-241B-410	Sequence 410, Appl
74	23	79.3	229	7	US-11-290-153-410	Sequence 410, Appl
75	23	79.3	229	7	US-11-289-102-222	Sequence 222, Appl
76	23	79.3	229	7	US-11-289-102-298	Sequence 298, Appl
77	23	79.3	273	7	US-11-045-004-2163	Sequence 2163, Ap
78	23	79.3	382	7	US-11-045-004-97	Sequence 97, Appl
79	23	79.3	481	7	US-11-197-712-271	Sequence 271, Appl
80	23	79.3	551	8	US-60-732-162-1112	Sequence 1112, Ap
81	23	79.3	609	8	US-60-742-218-316	Sequence 316, Appl
82	23	79.3	747	6	US-10-504-973-1	Sequence 1, Appl
83	22	75.9	5	4	US-08-920-162A-3	Sequence 3, Appl
84	22	75.9	5	4	US-08-920-162A-16	Sequence 16, Appl
85	22	75.9	5	4	US-08-920-162A-33	Sequence 33, Appl
86	22	75.9	5	4	US-08-920-162A-34	Sequence 34, Appl
87	22	75.9	5	6	US-10-677-076-3	Sequence 3, Appl
88	22	75.9	5	6	US-10-677-076-16	Sequence 16, Appl
89	22	75.9	5	6	US-10-677-076-33	Sequence 33, Appl
90	22	75.9	70	8	US-10-558-119-278	Sequence 278, Appl
91	22	75.9	114	8	US-60-742-219-2498	Sequence 2498, Ap
92	22	75.9	215	6	US-10-964-241B-4	Sequence 4, Appl
93	22	75.9	215	6	US-11-290-153-4	Sequence 4, Appl
94	22	75.9	228	6	US-10-206-921A-114	Sequence 114, Appl
95	22	75.9	251	7	US-11-175-121-13	Sequence 13, Appl
96	22	75.9	255	7	US-11-264-096-1036	Sequence 1036, Ap
97	22	75.9	293	6	US-10-703-799B-126	Sequence 126, Appl
98	22	75.9	300	7	US-11-045-004-2750	Sequence 2750, Ap

99	22	75.9	306	7	US-11-045-004-2097	Sequence 2097, Ap	172	20	69.0	99	7	US-11-264-096-1972	Sequence 1972, Ap
100	22	75.9	316	7	US-11-045-004-1254	Sequence 1254, Ap	173	20	69.0	104	6	US-10-395-463A-28	Sequence 28, Appl
101	22	75.9	335	6	US-10-556-060-357	Sequence 357, App	174	20	69.0	109	7	US-11-264-096-1507	Sequence 1507, Ap
102	22	75.9	344	6	US-10-964-241B-376	Sequence 376, App	175	20	69.0	109	7	US-11-264-096-1509	Sequence 1509, Ap
103	22	75.9	344	7	US-11-290-153-376	Sequence 376, App	176	20	69.0	111	6	US-10-031-158B-15	Sequence 15, Appl
104	22	75.9	347	8	US-60-742-219-2754	Sequence 2754, Ap	177	20	69.0	115	8	US-60-742-219-524	Sequence 524, App
105	22	75.9	370	7	US-11-268-745-7	Sequence 7, Appli	178	20	69.0	123	6	US-10-868-184C-2907	Sequence 2907, Ap
106	22	75.9	412	7	US-11-264-096-1676	Sequence 1676, Ap	179	20	69.0	153	6	US-10-206-921A-232	Sequence 232, App
107	22	75.9	463	7	US-11-045-004-1257	Sequence 1257, Ap	180	20	69.0	155	7	US-11-122-396-23	Sequence 23, Appl
108	22	75.9	517	7	US-11-296-657-20	Sequence 20, Appl	181	20	69.0	158	7	US-11-266-446-54	Sequence 54, Appl
109	22	75.9	576	7	US-11-292-951-18	Sequence 18, Appl	182	20	69.0	177	6	US-10-018-470B-65	Sequence 65, Appl
110	22	75.9	589	7	US-11-296-657-40	Sequence 40, Appl	183	20	69.0	184	7	US-11-123-692-109	Sequence 109, App
111	22	75.9	599	7	US-11-302-678-5	Sequence 5, Appli	184	20	69.0	187	6	US-10-018-470B-85	Sequence 85, Appl
112	22	75.9	1475	7	US-11-045-004-1602	Sequence 1602, Ap	185	20	69.0	187	7	US-11-045-004-2114	Sequence 2114, Ap
113	22	75.9	2014	8	US-60-742-219-1856	Sequence 1856, Ap	186	20	69.0	190	6	US-10-395-463A-26	Sequence 26, Appl
114	22	75.9	3906	8	US-60-748-312-1	Sequence 1, Appli	187	20	69.0	214	7	US-11-284-236-213	Sequence 213, App
115	21	72.4	26	7	US-11-264-096-151	Sequence 151, App	188	20	69.0	217	7	US-11-144-347A-570	Sequence 570, App
116	21	72.4	50	6	US-10-868-184C-3203	Sequence 3203, Ap	189	20	69.0	226	7	US-11-045-004-608	Sequence 608, App
117	21	72.4	50	6	US-10-868-184C-3204	Sequence 3204, Ap	190	20	69.0	233	7	US-11-197-712-306	Sequence 306, App
118	21	72.4	57	6	US-10-868-184C-2645	Sequence 2645, Ap	191	20	69.0	236	7	US-11-045-004-1559	Sequence 1559, Ap
119	21	72.4	74	6	US-10-868-184C-4553	Sequence 4553, Ap	192	20	69.0	239	7	US-11-045-004-1828	Sequence 1828, Ap
120	21	72.4	125	7	US-11-045-004-2558	Sequence 2558, Ap	193	20	69.0	248	8	US-60-742-219-2486	Sequence 2486, Ap
121	21	72.4	144	7	US-11-301-554-327	Sequence 327, App	194	20	69.0	252	6	US-10-703-799B-66	Sequence 66, Appl
122	21	72.4	160	7	US-11-197-712-316	Sequence 316, App	195	20	69.0	252	7	US-11-199-489A-142	Sequence 142, App
123	21	72.4	259	7	US-60-742-871-341	Sequence 341, App	196	20	69.0	257	6	US-10-206-921A-304	Sequence 304, App
124	21	72.4	271	8	US-11-045-004-2552	Sequence 2552, Ap	197	20	69.0	257	7	US-11-264-096-198	Sequence 198, App
125	21	72.4	271	8	US-60-732-162-610	Sequence 610, App	198	20	69.0	257	7	US-11-264-096-199	Sequence 199, App
126	21	72.4	275	7	US-11-045-004-2089	Sequence 2089, Ap	199	20	69.0	257	7	US-11-045-004-1339	Sequence 1339, Ap
127	21	72.4	276	7	US-11-045-004-950	Sequence 950, App	200	20	69.0	257	8	US-60-742-219-826	Sequence 826, App
128	21	72.4	277	7	US-11-045-004-2845	Sequence 2845, Ap	201	20	69.0	258	8	US-60-742-219-16	Sequence 16, Appl
129	21	72.4	282	8	US-60-732-162-1078	Sequence 1078, Ap	202	20	69.0	277	7	US-11-264-096-1270	Sequence 1270, Ap
130	21	72.4	348	6	US-10-206-921A-94	Sequence 94, Appl	203	20	69.0	282	1	PCT-US05-40306-72	Sequence 72, Appl
131	21	72.4	348	7	US-11-045-004-602	Sequence 602, App	204	20	69.0	282	1	PCT-US05-40142-46	Sequence 46, Appl
132	21	72.4	350	8	US-60-732-162-612	Sequence 612, App	205	20	69.0	282	1	PCT-US05-40255-85	Sequence 85, Appl
133	21	72.4	388	7	US-11-045-004-36	Sequence 36, Appl	206	20	69.0	282	1	PCT-US05-40256-113	Sequence 113, App
134	21	72.4	398	6	US-10-703-799B-256	Sequence 256, App	207	20	69.0	282	7	US-11-264-737-113	Sequence 113, App
135	21	72.4	415	8	US-60-742-219-196	Sequence 196, App	208	20	69.0	282	7	US-11-265-781-85	Sequence 85, Appl
136	21	72.4	417	5	US-09-155-676C-5	Sequence 5, Appli	209	20	69.0	282	7	US-11-264-784-72	Sequence 72, Appl
137	21	72.4	431	7	US-11-045-004-790	Sequence 790, App	210	20	69.0	286	7	US-11-045-004-2832	Sequence 2832, Ap
138	21	72.4	439	7	US-11-296-657-80	Sequence 80, Appl	211	20	69.0	291	7	US-11-217-995-10	Sequence 10, Appl
139	21	72.4	453	7	US-11-296-657-74	Sequence 74, Appl	212	20	69.0	294	7	US-11-045-004-1428	Sequence 1428, Ap
140	21	72.4	457	7	US-11-045-004-111	Sequence 111, App	213	20	69.0	301	6	US-10-080-960-11	Sequence 11, Appl
141	21	72.4	502	6	US-10-779-251A-13	Sequence 13, Appl	214	20	69.0	301	6	US-10-080-960-11	Sequence 11, Appl
142	21	72.4	525	6	US-10-779-251A-12	Sequence 12, Appl	215	20	69.0	301	8	US-60-732-162-1162	Sequence 1162, Ap
143	21	72.4	544	6	US-10-703-799B-254	Sequence 254, App	216	20	69.0	310	7	US-11-217-995-11	Sequence 11, Appl
144	21	72.4	555	8	US-60-732-162-1330	Sequence 1330, Ap	217	20	69.0	310	7	US-11-045-004-1579	Sequence 1579, Ap
145	21	72.4	584	7	US-11-296-657-131	Sequence 131, App	218	20	69.0	314	7	US-11-045-004-136	Sequence 136, App
146	21	72.4	642	8	US-60-732-162-1414	Sequence 1414, Ap	219	20	69.0	317	7	US-11-217-995-9	Sequence 9, Appli
147	21	72.4	747	7	US-11-077-664-1	Sequence 1, Appli	220	20	69.0	317	7	US-11-217-995-30	Sequence 30, Appl
148	21	72.4	772	6	US-10-556-060-486	Sequence 486, App	221	20	69.0	321	7	US-11-045-004-1924	Sequence 1924, Ap
149	21	72.4	943	8	US-60-732-162-1420	Sequence 1420, Ap	222	20	69.0	321	7	US-11-045-004-1959	Sequence 1959, Ap
150	21	72.4	1077	6	US-10-556-060-265	Sequence 265, App	223	20	69.0	339	7	US-11-264-096-2185	Sequence 2185, Ap
151	21	72.4	1201	7	US-11-045-004-689	Sequence 689, App	224	20	69.0	339	7	US-11-264-096-2186	Sequence 2186, Ap
152	20	69.0	17	6	US-10-868-184C-4095	Sequence 4095, Ap	225	20	69.0	346	7	US-11-045-004-2385	Sequence 2385, Ap
153	20	69.0	24	7	US-11-264-096-403	Sequence 403, App	226	20	69.0	347	7	US-11-045-004-1121	Sequence 1121, Ap
154	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	227	20	69.0	349	7	US-11-264-096-1591	Sequence 1591, Ap
155	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	228	20	69.0	350	6	US-10-511-455-32	Sequence 32, Appl
156	20	69.0	29	6	US-10-868-184C-4775	Sequence 4775, Ap	229	20	69.0	357	7	US-11-045-004-1663	Sequence 1663, Ap
157	20	69.0	36	6	US-10-868-184C-2753	Sequence 2753, Ap	230	20	69.0	361	8	US-60-736-600-10	Sequence 10, Appl
158	20	69.0	36	6	US-10-868-184C-4759	Sequence 4759, Ap	231	20	69.0	370	7	US-11-197-712-456	Sequence 456, App
159	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	232	20	69.0	376	8	US-60-741-048-7	Sequence 7, Appli
160	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	233	20	69.0	376	8	US-60-742-871-202	Sequence 202, App
161	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	234	20	69.0	377	8	US-60-732-162-322	Sequence 322, App
162	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	235	20	69.0	382	6	US-10-206-921A-20	Sequence 20, Appl
163	20	69.0	50	6	US-10-868-184C-4304	Sequence 4304, Ap	236	20	69.0	386	7	US-11-045-004-769	Sequence 769, App
164	20	69.0	56	7	US-11-121-566A-26	Sequence 26, Appl	237	20	69.0	389	7	US-11-197-712-414	Sequence 414, App
165	20	69.0	56	7	US-11-223-699A-26	Sequence 26, Appl	238	20	69.0	389	7	US-11-077-664-2	Sequence 2, Appli
166	20	69.0	75	7	US-11-199-489A-110	Sequence 110, App	239	20	69.0	395	8	US-60-742-219-520	Sequence 520, App
167	20	69.0	88	8	US-60-742-219-1430	Sequence 1430, Ap	240	20	69.0	397	7	US-11-045-004-2019	Sequence 2019, Ap
168	20	69.0	89	7	US-11-264-096-1938	Sequence 1938, Ap	241	20	69.0	399	7	US-11-077-664-3	Sequence 3, Appli
169	20	69.0	89	7	US-11-264-096-1939	Sequence 1939, Ap	242	20	69.0	406	7	US-11-045-004-245	Sequence 245, App
170	20	69.0	97	7	US-11-264-096-2145	Sequence 2145, Ap	243	20	69.0	420	7	US-11-045-004-1329	Sequence 1329, Ap
171	20	69.0	99	7	US-11-264-096-1971	Sequence 1971, Ap	244	20	69.0	429	7	US-11-127-877A-51	Sequence 51, Appl

```
245 20 69.0 432 6 US-10-206-921A-74
246 20 69.0 432 6 US-10-501-841-45
247 20 69.0 436 7 US-11-296-657-68
248 20 69.0 436 7 US-11-296-657-69
249 20 69.0 436 7 US-11-296-657-70
250 20 69.0 442 7 US-11-296-657-67
251 20 69.0 442 7 US-11-296-657-77
252 20 69.0 450 7 US-11-045-004-2808
253 20 69.0 450 7 US-11-296-657-78
254 20 69.0 451 7 US-11-045-004-84
255 20 69.0 453 8 US-60-732-162-656
256 20 69.0 457 1 PCT-US05-43141-19
257 20 69.0 459 7 US-11-045-004-289
258 20 69.0 463 7 US-11-045-004-2865
259 20 69.0 463 8 US-60-741-048-420
260 20 69.0 465 8 US-60-742-219-522
261 20 69.0 466 6 US-10-206-921A-316
262 20 69.0 466 6 US-10-558-119-434
263 20 69.0 466 7 US-11-127-877A-50
264 20 69.0 466 8 US-60-742-872-59
265 20 69.0 466 8 US-60-742-872-60
266 20 69.0 466 8 US-60-742-873-19
267 20 69.0 466 8 US-60-742-873-20
268 20 69.0 470 1 PCT-US05-26647A-141
269 20 69.0 470 8 US-60-732-162-1714
270 20 69.0 472 7 US-11-191-274A-3
271 20 69.0 472 7 US-11-191-274A-5
272 20 69.0 475 6 US-10-206-921A-260
273 20 69.0 475 8 US-60-732-162-1676
274 20 69.0 477 6 US-10-964-241B-452
275 20 69.0 477 7 US-11-290-153-452
276 20 69.0 481 8 US-60-742-219-518
277 20 69.0 482 7 US-11-045-004-2698
278 20 69.0 486 7 US-11-045-004-971
279 20 69.0 493 7 US-11-045-004-828
280 20 69.0 496 6 US-10-503-253A-6
281 20 69.0 497 7 US-11-264-096-1593
282 20 69.0 497 7 US-11-264-096-1594
283 20 69.0 499 8 US-60-741-048-424
284 20 69.0 499 8 US-60-741-048-425
285 20 69.0 501 6 US-10-395-463A-24
286 20 69.0 506 1 PCT-US05-38623-2
287 20 69.0 508 7 US-11-296-657-3
288 20 69.0 509 7 US-11-264-096-2187
289 20 69.0 530 7 US-11-296-657-6
290 20 69.0 530 7 US-11-296-657-11
291 20 69.0 530 7 US-11-296-657-12
292 20 69.0 530 7 US-11-296-657-13
293 20 69.0 539 7 US-11-226-554-126
294 20 69.0 548 7 US-11-045-004-1058
295 20 69.0 562 7 US-11-045-004-2022
296 20 69.0 568 8 US-60-732-162-792
297 20 69.0 574 6 US-10-556-747-18
298 20 69.0 584 7 US-11-292-951-16
299 20 69.0 585 7 US-10-503-836-18
300 20 69.0 585 7 US-11-264-096-18
```

ALIGNMENTS

```
RESULT 1
US-11-269-857-6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)...(2)
; OTHER INFORMATION: methylated leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)...(4)
; OTHER INFORMATION: methylated phenylalanine
; NAME/KEY: MOD_RES
; LOCATION: (6)...(6)
; OTHER INFORMATION: methylated alanine
; FEATURE:
; OTHER INFORMATION: synthetic
US-11-269-857-6
```

```
Query Match 93.1%; Score 27; DB 7; Length 7;
Best Local Similarity 83.3%; Pred. No. 5.4e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
DB 1 KLVFFA 6

RESULT 2
US-11-291-770-20
; Sequence 20, Application US/11291770
; GENERAL INFORMATION:
; APPLICANT: FUJITSU LIMITED
; TITLE OF INVENTION: Method for predicting protein-protein interactions
; FILE REFERENCE: GP01-1001PCT
; CURRENT FILING DATE: 2005-12-02
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US/10/237,673
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: JP P2000-72485
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-291-770-20

Query Match 93.1%; Score 27; DB 7; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
DB 1 KLVFFA 6

RESULT 3
PCT-US05-32135-5
; Sequence 5, Application PC/TUS0532135
; GENERAL INFORMATION:
; APPLICANT: ORSER, CINDY S.
; APPLICANT: PAN, TAO
; TITLE OF INVENTION: IMMOBILIZED PROBES AND METHODS OF DETECTING
; FILE REFERENCE: ADL-102-PCT
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: PCT/US05/32135
; PRIOR FILING DATE: 2004-11-08
```

```
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-32135-5

Query Match          93.1%; Score 27; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
Db 6 KLVFFA 11

RESULT 4
PCT-US05-32135-6
; Sequence 6, Application PC/TUS0532135
; GENERAL INFORMATION:
; APPLICANT: ORSER, CINDY S.
; APPLICANT: PAN, TAO
; TITLE OF INVENTION: IMMOBILIZED PROBES AND METHODS OF DETECTING
; FILE REFERENCE: ADL-102-PCT
; CURRENT APPLICATION NUMBER: PCT/US05/32135
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: 60/608,541
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-32135-6

Query Match          93.1%; Score 27; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
Db 6 KLVFFA 11

RESULT 5
US-11-297-316-2
; Sequence 2, Application US/11297316
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; FILE REFERENCE: 01142-0200-00304
; CURRENT APPLICATION NUMBER: US/11/297,316
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-316-2

Query Match          93.1%; Score 27; DB 7; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
```

```
Db 16 KLVFFA 21

RESULT 6
US-11-194-989-19
; Sequence 19, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-19

Query Match          93.1%; Score 27; DB 7; Length 39;
Best Local Similarity 83.3%; Pred. No. 4.9; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 7
US-11-195-207-19
; Sequence 19, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-195-207-19

Query Match          93.1%; Score 27; DB 7; Length 39;
Best Local Similarity 83.3%; Pred. No. 4.9; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
```



```
Db          16 KLVFFA 21

RESULT 8
PCT-US05-32135-4
; Sequence 4, Application PC/TUS0532135
; GENERAL INFORMATION:
; APPLICANT: ORSER, CINDY S.
; APPLICANT: PAN, TAO
; TITLE OF INVENTION: IMMOBILIZED PROBES AND METHODS OF DETECTING
; FILE OF INVENTION: CONFORMATIONALLY ALTERED PRION PROTEINS
; FILE REFERENCE: ADL-102-PCT
; CURRENT APPLICATION NUMBER: PCT/US05/32135
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: 60/608,541
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-32135-4

Query Match          93.1%; Score 27; DB 1; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 9
US-10-966-919B-2
; Sequence 2, Application US/10966919B
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; APPLICANT: Sundaram, Pazhani
; APPLICANT: Kasinathan, Chinnaswamy
; TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
; FILE REFERENCE: 7628-0001
; CURRENT APPLICATION NUMBER: US/10/966,919B
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,674
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-919B-2

Query Match          93.1%; Score 27; DB 6; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 10
US-11-269-857-3
; Sequence 3, Application US/11269857
; GENERAL INFORMATION:
; APPLICANT: Ponara, Nunzio
; TITLE OF INVENTION: Methods and Compositions for Treatment
; FILE OF INVENTION: and Prevention of Major Depressive Disorder
; FILE REFERENCE: 1049-1-052N
; CURRENT APPLICATION NUMBER: US/11/269,857
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: 60/625,824

; PRIOR FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/676,093
; CURRENT FILING DATE: 2005-08-01
; CURRENT APPLICATION NUMBER: US/11/194,989
; FILE REFERENCE: 514712002300
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; APPLICANT: GRIMM, Jan Markus
; APPLICANT: HO, Wei-Hsien
; APPLICANT: PONS, Jaume
; APPLICANT: ROSENTHAL, Arnon
; GENERAL INFORMATION:
; Sequence 20, Application US/11194989
US-11-194-989-20

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 11
US-11-194-989-15
; Sequence 15, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-15

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 12
US-11-194-989-20
; Sequence 20, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
```

```
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-20
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21
```

```
RESULT 13
US-11-194-989-21
; Sequence 21, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-21
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21
```

```
RESULT 14
US-11-194-989-22
; Sequence 22, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
```

```
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-22
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21
```

```
RESULT 15
US-11-194-989-23
; Sequence 23, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-23
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21
```

```
RESULT 16
US-11-194-989-24
; Sequence 24, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
```

```
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-24
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:|||||
Db      16 KLVFFA 21
```

```
RESULT 17
US-11-194-989-25
; Sequence 25, Application US/11/194,989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-25
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:|||||
Db      16 KLVFFA 21
```

```
RESULT 18
US-11-195-207-15
; Sequence 15, Application US/11/195,207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
```

```
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-195-207-15
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:|||||
Db      16 KLVFFA 21
```

```
RESULT 19
US-11-195-207-20
; Sequence 20, Application US/11/195,207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-20
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:|||||
Db      16 KLVFFA 21
```

```
RESULT 20
US-11-195-207-21
; Sequence 21, Application US/11/195,207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
```

```
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-21

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21

RESULT 21
US-11-195-207-22
; Sequence 22, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-22

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21

RESULT 22
US-11-195-207-23
; Sequence 23, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-23

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21

RESULT 23
US-11-195-207-24
; Sequence 24, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-24

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db     16 KLVFFA 21

RESULT 24
US-11-195-207-25
; Sequence 25, Application US/11195207
```

GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-25

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 25
US-11-087-102A-18
; Sequence 18, Application US/11087102A
; GENERAL INFORMATION:
; APPLICANT: Vereenigde
; APPLICANT: Gebbink, Martijn F. B. G.
; APPLICANT: Bouma, Barend
; APPLICANT: Kranenburg, Onno W.
; APPLICANT: Kroon, Louise M. J.
; TITLE OF INVENTION: Cross-Beta Structure Comprising Amyloid Binding Proteins and Meth
; TITLE OF INVENTION: for Detection of the Cross-Beta Structure, for Modulating Cross-
; TITLE OF INVENTION: Structures Fibril Formation and for Modulating Cross-Beta
; TITLE OF INVENTION: Structure-Mediated Toxicity and Method for Interfering with Bloc
; TITLE OF INVENTION: Coagulation
; FILE REFERENCE: 2183-6874US
; CURRENT APPLICATION NUMBER: US/11/087,102A
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: US 11/033,105
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: PCT/NL03/00501
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: EP 02077797.5
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide A Beta (1-40) from Homo sapiens
US-11-087-102A-18

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||

Db 16 KLVFFA 21
|:||||

RESULT 26
US-11-194-989-18
; Sequence 18, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-18

Query Match 93.1%; Score 27; DB 7; Length 41;
Best Local Similarity 83.3%; Pred. No. 5.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 27
US-11-195-207-18
; Sequence 18, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-195-207-18

Query Match 93.1%; Score 27; DB 7; Length 41;
Best Local Similarity 83.3%; Pred. No. 5.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||

```
Db          16 KLVFFA 21

RESULT 28
US-10-966-919B-3
; Sequence 3, Application US/10966919B
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; APPLICANT: Sundaram, Pazhani
; APPLICANT: Kasinathan, Chinnaswamy
; TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
; FILE REFERENCE: 7628-0001
; CURRENT APPLICATION NUMBER: US/10/966,919B
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,674
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-919B-3

Query Match          93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 29
US-11-270-774-174
; Sequence 174, Application US/11270774
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/11/270,774
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/09/848,616
; PRIOR FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 174
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amyloid Beta Peptide
US-11-270-774-174

Query Match          93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 30
US-11-269-857-5
; Sequence 5, Application US/11269857
; GENERAL INFORMATION:
; APPLICANT: Pomara, Nunzio
; TITLE OF INVENTION: Methods and Compositions for Treatment
; TITLE OF INVENTION: and Prevention of Major Depressive Disorder

; FILE REFERENCE: 1049-1-052N
; CURRENT APPLICATION NUMBER: US/11/269,857
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: 60/625,824
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-269-857-5

Query Match          93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 31
US-11-194-989-16
; Sequence 16, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-16

Query Match          93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 32
US-11-195-207-16
; Sequence 16, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
```

```
;
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-195-207-16
```

```
Query Match 93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFA 6
Db 16 KLVFFA 21
```

```
RESULT 33
US-11-297-316-1
; Sequence 1, Application US/11297316
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; FILE OF INVENTION: particles
; FILE REFERENCE: 01142-0200-00304
; CURRENT APPLICATION NUMBER: US/11/297,316
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-316-1
```

```
Query Match 93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFA 6
Db 16 KLVFFA 21
```

```
RESULT 34
US-08-920-162A-1
; Sequence 1, Application US/08920162A
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid Peptide
; Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: 27-Aug-1997
```

```
;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: <Unknown>
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-920-162A-1
Query Match 93.1%; Score 27; DB 4; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 16 KLVFFA 21
RESULT 35
US-10-677-076-1
; Sequence 1, Application US/10677076
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid
; Peptide
; Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/677,076
; FILING DATE: 30-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162
; FILING DATE: 27-AUG-1997
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: <Unknown>
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-677-076-1

Query Match          93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 36
US-10-966-919B-1
; Sequence 1, Application US/10966919B
; GENERAL INFORMATION:
; APPLICANT: Sundaram, Stanley
; APPLICANT: Stein, Stanley
; APPLICANT: Sundaram, Pazhani
; APPLICANT: Kasinathan, Chinnaswamy
; TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
; FILE REFERENCE: 7628-0001
; CURRENT APPLICATION NUMBER: US/10/966,919B
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,674
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PPT
; ORGANISM: Homo sapiens
US-10-966-919B-1

Query Match          93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 37
US-10-250-581-1
; Sequence 1, Application US/10250581
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PPT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match          93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
```

```
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 38
US-11-194-989-17
; Sequence 17, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 43
; TYPE: PPT
; ORGANISM: Homo sapiens
US-11-194-989-17

Query Match          93.1%; Score 27; DB 7; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 39
US-11-195-207-17
; Sequence 17, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 43
; TYPE: PPT
; ORGANISM: Homo sapiens
US-11-195-207-17

Query Match          93.1%; Score 27; DB 7; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```



```
QY 1 KLVFFA 6
DB 16 KLVFFA 21

RESULT 40
US-10-721-297-12
; Sequence 12, Application US/10721297
; GENERAL INFORMATION:
; APPLICANT: Suchof, Thomas C.
; APPLICANT: Li, Qiming
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND ASSAYS RELATED TO SECRETASE CLEAVAGE
; TITLE OF INVENTION: SPECIFICITY
; FILE REFERENCE: UN1919/4-006US
; CURRENT APPLICATION NUMBER: US/10/721,297
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 12
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-721-297-12

Query Match 93.1%; Score 27; DB 6; Length 62;
Best Local Similarity 83.3%; Pred. No. 7.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 24 KLVFFA 29

RESULT 41
US-11-270-774-173
; Sequence 173, Application US/11270774
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisserot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/11/270,774
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/09/848,616
; PRIOR FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 173
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-270-774-173

Query Match 93.1%; Score 27; DB 7; Length 82;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 33 KLVFFA 38

RESULT 42
US-08-920-162A-2
; Sequence 2, Application US/08920162A
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
Aggregation Comprising D-Amino Acids
```

```
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSES: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/920,162A
FILING DATE: 27-Aug-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
APPLICATION NUMBER: <Unknown>
FILING DATE: 21-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-920-162A-2

Query Match 93.1%; Score 27; DB 4; Length 103;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 20 KLVFFA 25

RESULT 43
US-10-677-076-2
; Sequence 2, Application US/10677076
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSES: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/677,076
; FILING DATE: 30-Sep-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162
; FILING DATE: 27-AUG-1997
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: <Unknown>
; FILING DATE: 21-JUL-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-677-076-2

Query Match 93.1%; Score 27; DB 6; Length 103;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 20 KLVFFA 25

RESULT 44
US-60-742-871-82
; Sequence 82, Application US/60742871
; GENERAL INFORMATION:
; APPLICANT: Steve RUBEN et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001652
; CURRENT APPLICATION NUMBER: US/60/742,871
; CURRENT FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-742-871-82

Query Match 93.1%; Score 27; DB 8; Length 639;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 556 KLVFFA 561

RESULT 45
US-60-742-871-80
; Sequence 80, Application US/60742871
; GENERAL INFORMATION:
; APPLICANT: Steve RUBEN et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001652
; CURRENT APPLICATION NUMBER: US/60/742,871
; CURRENT FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-742-871-80

Query Match 93.1%; Score 27; DB 8; Length 695;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 612 KLVFFA 617

RESULT 46
US-11-220-372-313
; Sequence 313, Application US/11220372
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVALI, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LLOP
; APPLICANT: OLLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN INFECTION
; FILE REFERENCE: INL-084CP
; CURRENT APPLICATION NUMBER: US/11/220,372
; CURRENT FILING DATE: 2005-09-06
; PRIOR APPLICATION NUMBER: PCT/ES05/00355
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US 11/116,144
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/00581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03 380 307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 313
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-220-372-313

Query Match 93.1%; Score 27; DB 7; Length 751;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 668 KLVFFA 673

RESULT 47
US-60-742-871-81
; Sequence 81, Application US/60742871
; GENERAL INFORMATION:
; APPLICANT: Steve RUBEN et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001652
; CURRENT APPLICATION NUMBER: US/60/742,871
; CURRENT FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-742-871-81
```

US-60-742-871-81

Query Match 93.1%; Score 27; DB 8; Length 751;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

|:||||

Db 668 KLVFFA 673

RESULT 48

US-11-270-774-172
; Sequence 172, Application US/11270774

; GENERAL INFORMATION:

; APPLICANT: Sebbel, Peter

; APPLICANT: Dunant, Nicolas

; APPLICANT: Bachmann, Martin

; APPLICANT: Tissot, Alain

; APPLICANT: Lechner, Franziska

; TITLE OF INVENTION: Molecular Antigen Array

; FILE REFERENCE: 1700.0180002

; CURRENT APPLICATION NUMBER: US/11/270,774

; PRIOR FILING DATE: 2005-11-10

; PRIOR APPLICATION NUMBER: US/09/848,616

; PRIOR FILING DATE: 2001-05-05

; NUMBER OF SEQ ID NOS: 186

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 172

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-11-270-774-172

Query Match 93.1%; Score 27; DB 7; Length 770;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

|:||||

Db 687 KLVFFA 692

RESULT 49

US-10-868-184C-4923

; Sequence 4923, Application US/10868184C

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS805

; CURRENT APPLICATION NUMBER: US/10/868,184C

; CURRENT FILING DATE: 2004-06-16

; PRIOR APPLICATION NUMBER: 60/278,650

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 09/833,245

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: PCT/US01/11988

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: PCT/US00/06043

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: PCT/US00/06012

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: PCT/US00/06058

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: PCT/US00/06044

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: PCT/US00/06059

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: PCT/US00/06042

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: PCT/US00/06014

; PRIOR FILING DATE: 2000-03-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4923
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-184C-4923

Query Match 86.2%; Score 25; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5

|:||||

Db 7 KIVFF 11

RESULT 50

US-11-045-004-1961

; Sequence 1961, Application US/11045004

; GENERAL INFORMATION:

; APPLICANT: BUCHRIESER, CARMEN

; APPLICANT: FRANGEUL, LIONEL

; APPLICANT: COUVE, ELISABETH

; APPLICANT: RUSNIOK, CHRISTOPHE

; APPLICANT: PSIH, HAFIDA

; APPLICANT: DEHOUE, PIERRE

; APPLICANT: DUSURGET, OLIVIER

; APPLICANT: CHETOUANI, FARID

; APPLICANT: NEDJARI, HAFED

; APPLICANT: GLASER, PHILIPPE

; APPLICANT: KUNST, FRANCK

; APPLICANT: COSSART, PASCALE

; APPLICANT: DANIELS, JUSTIN

; APPLICANT: GOEBEL, WERNER

; APPLICANT: KREFT, JURGEN

; APPLICANT: KUHN, MICHAEL

; APPLICANT: NG, EVA

; APPLICANT: VAZQUEZ-BOLAND, ANTONIO

; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO

; APPLICANT: GARRIDO-GARCIA, PATRICIA

; APPLICANT: TIERREZ-MARTINEZ, ALBERTO

; APPLICANT: AMEND, ALEXANDRA

; APPLICANT: CHAKRABORTY, TRINAD

; APPLICANT: DOMANN, EUGEN

; APPLICANT: HAIN, THORSTEN

; APPLICANT: BERCHE, PATRICK

; APPLICANT: CHARBIT, ALAIN

; APPLICANT: DURANT, LIONEL

; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO

; APPLICANT: BAQUERO, FERNANDO

; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO

; APPLICANT: GOMEZ-LOPEZ, NURIA

; APPLICANT: MADUENIO, ENCARN

; APPLICANT: PABLOS, BETRIZ DE

; APPLICANT: WEHLAND, JURGEN

; APPLICANT: KARST, UWE

; APPLICANT: ENTIAN, KARL-DIETER

; APPLICANT: HAUF, JORG

; APPLICANT: ROSE, MATTHIAS

; APPLICANT: VOSS, HAMUT

; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES

; FILE REFERENCE: 05394.0018-02

; CURRENT APPLICATION NUMBER: US/11/045,004

; CURRENT FILING DATE: 2005-01-28

; PRIOR APPLICATION NUMBER: 10/637,657

; PRIOR FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: 10/257,023

; PRIOR FILING DATE: 2002-10-08

; PRIOR APPLICATION NUMBER: PCT/FR01/01118

; PRIOR FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: FR 00/04,629

; PRIOR FILING DATE: 2000-04-11

```
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1961
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1961

Query Match      86.2%; Score 25; DB 7; Length 256;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFF 5
Db      3 KIVFF 7

RESULT 51
US-10-018-105A-6
; Sequence 6, Application US/10018105A
; GENERAL INFORMATION:
; APPLICANT: MYCOTA BIOSCIENCES INC.
; APPLICANT: ROEMER, Terry
; APPLICANT: BUSSEY, Howard
; APPLICANT: DAVISON, John
; TITLE OF INVENTION: IDENTIFICATION OF CANDIDA ALBICANS ESSENTIAL FUNGAL
; TITLE OF INVENTION: SPECIFIC GENES AND USE THEREOF IN ANTIFUNGAL DRUG
; FILE REFERENCE: 10182-015-999 (originally 12875.3)
; CURRENT APPLICATION NUMBER: US/10/018,105A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/132,878
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-018-105A-6

Query Match      86.2%; Score 25; DB 6; Length 844;
Best Local Similarity 100.0%; Pred. No. 28+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFF 5
Db      517 KIVFF 521

RESULT 52
US-11-144-947A-659
; Sequence 659, Application US/11144947A
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947A
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 353
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals stop translation
US-11-144-947A-353

Query Match      82.8%; Score 24; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      176 IVFFA 180
```

```
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 659
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-947A-659

Query Match      82.8%; Score 24; DB 7; Length 60;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      56 IVFFA 60

RESULT 53
US-11-144-947A-353
; Sequence 353, Application US/11144947A
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947A
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 353
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals stop translation
US-11-144-947A-353

Query Match      82.8%; Score 24; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      176 IVFFA 180
```

RESULT 54

US-10-868-184C-3591
 ; Sequence 3591, Application US/10868184C
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, et. al
 ; TITLE OF INVENTION: Human Secreted Proteins
 ; FILE REFERENCE: PS805
 ; CURRENT APPLICATION NUMBER: US/10/869,184C
 ; CURRENT FILING DATE: 2004-06-16
 ; PRIOR APPLICATION NUMBER: 60/278,650
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 09/833,245
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: PCT/US01/11988
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: PCT/US00/06043
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06012
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06058
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06044
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06059
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06042
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06014
 ; PRIOR FILING DATE: 2000-03-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 13046
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3591
 ; LENGTH: 399
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-868-184C-3591

Query Match 82.8%; Score 24; DB 6; Length 399;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
 |||||
 Db 279 IVFFA 283

RESULT 55

US-11-045-004-728
 ; Sequence 728, Application US/11045004
 ; GENERAL INFORMATION:
 ; APPLICANT: BUCHRIESEN, CARMEN
 ; APPLICANT: FRANGEUL, LIONEL
 ; APPLICANT: COUVE, ELISABETH
 ; APPLICANT: RUSNIOK, CHRISTOPHE
 ; APPLICANT: FSIHI, HAFIDA
 ; APPLICANT: DEHOUX, PIERRE
 ; APPLICANT: DUSSURGET, OLIVIER
 ; APPLICANT: CHETOUANI, FARID
 ; APPLICANT: NEDJARI, HAFED
 ; APPLICANT: GLASER, PHILIPPE
 ; APPLICANT: KUNST, FRANK
 ; APPLICANT: COSSART, PASCALE
 ; APPLICANT: DANIELS, JUSTIN
 ; APPLICANT: GOEBEL, WERNER
 ; APPLICANT: KREFT, JURGEN
 ; APPLICANT: KUHN, MICHAEL
 ; APPLICANT: NG, EVA
 ; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
 ; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
 ; APPLICANT: GARRIDO-GARCIA, PATRICIA

APPLICANT: TIERREZ-MARTINEZ, ALBERTO
 APPLICANT: AMEND, ALEXANDRA
 APPLICANT: CHAKRABORTY, TRINAD
 APPLICANT: DOMANN, EUGEN
 APPLICANT: HAIN, THORSTEN
 APPLICANT: BERCHE, PATRICK
 APPLICANT: CHARBIT, ALAIN
 APPLICANT: DURANT, LIONEL
 APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
 APPLICANT: BAQUERO, FERNANDO
 APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
 APPLICANT: GOMEZ-LOPEZ, NURIA
 APPLICANT: MADUENIO, ENCARNIA
 APPLICANT: PABLOS, BETRIZ DE
 APPLICANT: WEHLAND, JURGEN
 APPLICANT: KARST, UWE
 APPLICANT: ENTIAN, KARL-DIETER
 APPLICANT: HAUF, JORG
 APPLICANT: ROSE, MATTHIAS
 APPLICANT: VOSS, HAMUT
 ; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
 ; FILE REFERENCE: 05394.0018-02
 ; CURRENT APPLICATION NUMBER: US/11/045,004
 ; CURRENT FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: 10/637,657
 ; PRIOR FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: 10/257,023
 ; PRIOR FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: PCT/FR01/01118
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: FR 00/04,629
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 2854
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 728
 ; LENGTH: 435
 ; TYPE: PRT
 ; ORGANISM: Listeria monocytogenes
 US-11-045-004-728

Query Match 82.8%; Score 24; DB 7; Length 435;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
 |||||
 Db 35 IVFFA 39

RESULT 56

US-11-045-004-1192
 ; Sequence 1192, Application US/11045004
 ; GENERAL INFORMATION:
 ; APPLICANT: BUCHRIESEN, CARMEN
 ; APPLICANT: FRANGEUL, LIONEL
 ; APPLICANT: COUVE, ELISABETH
 ; APPLICANT: RUSNIOK, CHRISTOPHE
 ; APPLICANT: FSIHI, HAFIDA
 ; APPLICANT: DEHOUX, PIERRE
 ; APPLICANT: DUSSURGET, OLIVIER
 ; APPLICANT: CHETOUANI, FARID
 ; APPLICANT: NEDJARI, HAFED
 ; APPLICANT: GLASER, PHILIPPE
 ; APPLICANT: KUNST, FRANK
 ; APPLICANT: COSSART, PASCALE
 ; APPLICANT: DANIELS, JUSTIN
 ; APPLICANT: GOEBEL, WERNER
 ; APPLICANT: KREFT, JURGEN
 ; APPLICANT: KUHN, MICHAEL
 ; APPLICANT: NG, EVA
 ; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
 ; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
 ; APPLICANT: GARRIDO-GARCIA, PATRICIA

; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUP, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1192
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1192

Query Match 82.8%; Score 24; DB 7; Length 574;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 521 RLVFFA 526

RESULT 57
US-11-302-994-13
; Sequence 13, Application US/11302994
; GENERAL INFORMATION:
; APPLICANT: BOGA, RAMESH BABU
; APPLICANT: MALIK, SOHAIL
; APPLICANT: QUIRK, STEPHEN
; TITLE OF INVENTION: MATERIALS FOR INHIBITING COMPLEXATION OF C-REACTIVE
; FILE REFERENCE: KCX-1105
; CURRENT APPLICATION NUMBER: US/11/302,994
; CURRENT FILING DATE: 2005-12-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-302-994-13

Query Match 82.8%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 531 KAVFFA 536

RESULT 58
US-10-964-241B-230
; Sequence 230, Application US/10964241B
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C33
; CURRENT APPLICATION NUMBER: US/10/964,241B
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US/10/123,236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-964-241B-230

Query Match 82.8%; Score 24; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:|||||
Db 557 IVFFA 561

RESULT 59
US-11-290-153-230
; Sequence 230, Application US/11290153
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C321
; CURRENT APPLICATION NUMBER: US/11/290,153
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: US/10/146,728
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-153-230

Query Match      82.8%; Score 24; DB 7; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
        |||||
Db      557 IVFFA 561

RESULT 60
US-10-556-060-220
; Sequence 220, Application US/10556060
; GENERAL INFORMATION:
; APPLICANT: MEINKE, ANDREAS
; APPLICANT: NAGY, ESZTER
; APPLICANT: HANNER, MARKUS
; APPLICANT: HORNY, MARKUS
; APPLICANT: KALLEND, SABINE
; APPLICANT: FRUSTOMERSKY, SONJA
; TITLE OF INVENTION: S. AGALACTIAE ANTIGENS I + II
; FILE REFERENCE: SONN:080US
; CURRENT APPLICATION NUMBER: US/10/556.060
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: PCT/EP2004/004856
```

```
; PRIOR FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 03450112.2
; PRIOR FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: 03450266.6
; PRIOR FILING DATE: 2003-11-28
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 220
; LENGTH: 1241
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-556-060-220

Query Match      82.8%; Score 24; DB 6; Length 1241;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KIVFFA 6
        |||||
Db      80 KVAFPA 85

RESULT 61
US-10-966-919B-4
; Sequence 4, Application US/10966919B
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; APPLICANT: Sundaram, Pazhani
; APPLICANT: Kasinathan, Chinnaswamy
; TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
; FILE REFERENCE: 7628-0001
; CURRENT APPLICATION NUMBER: US/10/966,919B
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,674
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-919B-4

Query Match      79.3%; Score 23; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.4e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFF 5
        |||||
Db      1 KLVFF 5

RESULT 62
US-11-269-857-7
; Sequence 7, Application US/11269857
; GENERAL INFORMATION:
; APPLICANT: Pomara, Nunzio
; TITLE OF INVENTION: Methods and Compositions for Treatment
; TITLE OF INVENTION: and Prevention of Major Depressive Disorder
; FILE REFERENCE: 1049-1-052N
; CURRENT APPLICATION NUMBER: US/11/269,857
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: 60/625,824
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-11-269-857-7
```

```
Query Match          79.3%; Score 23; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.4e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFF 5
Db 1 KLVFF 5

RESULT 63
PCT-US05-12482A-5
; Sequence 5, Application PC/TUS0512482A
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
; APPLICANT: CORNELL RESEARCH FOUNDATION, INC.
; APPLICANT: YAN, SHI DU
; APPLICANT: STERN, DAVID M
; APPLICANT: LUSTBADER, JOYCE W
; APPLICANT: HAO, WU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING ABAD/aa PROTEIN INTERACTI
; FILE REFERENCE: 68545-PCT/JPW/JW
; CURRENT APPLICATION NUMBER: PCT/US05/12482A
; CURRENT FILING DATE: 2005-04-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human
PCT-US05-12482A-5

Query Match          79.3%; Score 23; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFF 5
Db 16 KLVFF 20

RESULT 64
US-10-868-184C-4123
; Sequence 4123, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4123
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-184C-3208

Query Match          79.3%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 43;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFF 5
Db 5 KLVFF 9

RESULT 66
US-11-045-004-2209
; Sequence 2209, Application US/11045004
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
```



```
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCAL
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; APPLICANT: TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; PRIOR FILING DATE: 2005-01-28
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2209
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-2209

Query Match 79.3%; Score 23; DB 7; Length 77;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 63 VVFFA 67

RESULT 67
US-11-144-947A-503
; Sequence 503, Application US/11144947A
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947A
; PRIOR FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
```

```
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 503
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals stop translation
US-11-144-947A-503

Query Match 79.3%; Score 23; DB 7; Length 147;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
Db 34 KVIFP 38

RESULT 68
US-11-268-554-406
; Sequence 406, Application US/11268554
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno et al.
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
; FILE REFERENCE: CL001557
; CURRENT APPLICATION NUMBER: US/11/268,554
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 1004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-268-554-406

Query Match 79.3%; Score 23; DB 7; Length 166;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
Db 130 KVIFP 134

RESULT 69
US-60-741-051-80
; Sequence 80, Application US/60741051
; GENERAL INFORMATION:
; APPLICANT: BIRSE, Charles et al.
; TITLE OF INVENTION: BREAST CANCER SECRETED TARGETS AND USES
; FILE REFERENCE: THEREOF
```

```
; FILE REFERENCE: CL001625
; CURRENT APPLICATION NUMBER: US/60/741,051
; CURRENT FILING DATE: 2005-12-01
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-741-051-80

Query Match          79.3%; Score 23; DB 8; Length 166;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 130 KIVFF 134

RESULT 70
US-11-264-096-399
; Sequence 399, Application US/11264096
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 399
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-399

Query Match          79.3%; Score 23; DB 7; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 6 KISFFA 11

RESULT 71
US-11-264-096-1048
; Sequence 1048, Application US/11264096
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1048
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1048

Query Match          79.3%; Score 23; DB 7; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 6 KISFFA 11

RESULT 72
US-11-264-096-1049
; Sequence 1049, Application US/11264096
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1049
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1049

Query Match          79.3%; Score 23; DB 7; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 6 KISFFA 11

RESULT 73
US-10-964-241B-410
; Sequence 410, Application US/10964241B
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanovers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C33
```

```

; CURRENT APPLICATION NUMBER: US/10/964,241B
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US/10/123,236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-964-241B-410

Query Match          79.3%; Score 23; DB 6; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFF 5
Db      118 KVIFF 122

RESULT 74
US-11-290-153-410
; Sequence 410, Application US/11290153
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: DeNovo, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C321
; CURRENT APPLICATION NUMBER: US/11/290,153
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: US/10/146,728
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17

```

```

; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-290-153-410

Query Match          79.3%; Score 23; DB 7; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFF 5
Db      118 KVIFF 122

RESULT 75
US-11-289-102-222
; Sequence 222, Application US/11289102
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-222

Query Match          79.3%; Score 23; DB 7; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFF 5
Db      118 KVIFF 122

Search completed: December 29, 2005, 18:38:05
Job time : 13.5806 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:19:12 ; Search time 258.871 Seconds
(without alignments)
32.030 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/US060 COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US066 COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US073 COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US074 COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US075 COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US076 COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US077 COMB.pcp.*
8: /cgn2_6/ptodata/1/paa/US078 COMB.pcp.*
9: /cgn2_6/ptodata/1/paa/US079 COMB.pcp.*
10: /cgn2_6/ptodata/1/paa/US080 COMB.pcp.*
11: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
12: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
13: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
14: /cgn2_6/ptodata/1/paa/US084 COMB.pcp.*
15: /cgn2_6/ptodata/1/paa/US085 COMB.pcp.*
16: /cgn2_6/ptodata/1/paa/US086 COMB.pcp.*
17: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
18: /cgn2_6/ptodata/1/paa/US088 COMB.pcp.*
19: /cgn2_6/ptodata/1/paa/US089 COMB.pcp.*
20: /cgn2_6/ptodata/1/paa/US090 COMB.pcp.*
21: /cgn2_6/ptodata/1/paa/US091 COMB.pcp.*
22: /cgn2_6/ptodata/1/paa/US092 COMB.pcp.*
23: /cgn2_6/ptodata/1/paa/US093 COMB.pcp.*
24: /cgn2_6/ptodata/1/paa/US094 COMB.pcp.*
25: /cgn2_6/ptodata/1/paa/US095 COMB.pcp.*
26: /cgn2_6/ptodata/1/paa/US096 COMB.pcp.*
27: /cgn2_6/ptodata/1/paa/US097 COMB.pcp.*
28: /cgn2_6/ptodata/1/paa/US098 COMB.pcp.*
29: /cgn2_6/ptodata/1/paa/US099 COMB.pcp.*
30: /cgn2_6/ptodata/1/paa/US100 COMB.pcp.*
31: /cgn2_6/ptodata/1/paa/US101 COMB.pcp.*
32: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*
33: /cgn2_6/ptodata/1/paa/US103 COMB.pcp.*
34: /cgn2_6/ptodata/1/paa/US104 COMB.pcp.*
35: /cgn2_6/ptodata/1/paa/US105 COMB.pcp.*
36: /cgn2_6/ptodata/1/paa/US106 COMB.pcp.*
37: /cgn2_6/ptodata/1/paa/US107 COMB.pcp.*
38: /cgn2_6/ptodata/1/paa/US108 COMB.pcp.*
39: /cgn2_6/ptodata/1/paa/US109 COMB.pcp.*
40: /cgn2_6/ptodata/1/paa/US110 COMB.pcp.*
41: /cgn2_6/ptodata/1/paa/US111 COMB.pcp.*
42: /cgn2_6/ptodata/1/paa/US112 COMB.pcp.*
43: /cgn2_6/ptodata/1/paa/US114 COMB.pcp.*

44: /cgn2_6/ptodata/1/paa/US600 COMB.pcp.*
45: /cgn2_6/ptodata/1/paa/US601 COMB.pcp.*
46: /cgn2_6/ptodata/1/paa/US602 COMB.pcp.*
47: /cgn2_6/ptodata/1/paa/US603 COMB.pcp.*
48: /cgn2_6/ptodata/1/paa/US604 COMB.pcp.*
49: /cgn2_6/ptodata/1/paa/US605 COMB.pcp.*
50: /cgn2_6/ptodata/1/paa/US606 COMB.pcp.*
51: /cgn2_6/ptodata/1/paa/US607 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	27	US-09-724-842-9
2	29	100.0	6	27	US-09-724-842-17
3	29	100.0	6	27	US-09-724-842A-9
4	29	100.0	6	27	US-09-724-842A-17
5	29	100.0	6	28	US-09-867-847-11
6	29	100.0	6	28	US-09-867-847-19
7	29	100.0	6	28	US-09-867-847A-11
8	29	100.0	6	28	US-09-867-847A-19
9	29	100.0	6	29	US-09-915-092-1
10	29	100.0	6	29	US-09-915-092-9
11	29	100.0	6	30	US-10-009-122-1
12	29	100.0	6	30	US-10-009-122-10
13	29	100.0	6	37	US-10-705-028-1
14	29	100.0	6	37	US-10-705-028-10
15	29	100.0	6	37	US-10-728-028-1
16	29	100.0	6	37	US-10-728-028-9
17	29	100.0	6	38	US-10-825-958-9
18	29	100.0	6	38	US-10-825-958-17
19	29	100.0	58	34	US-10-425-115-280164
20	29	100.0	90	34	US-10-424-599-165325
21	29	100.0	93	34	US-10-424-599-240310
22	29	100.0	99	1	PCT-US01-08631-56957
23	29	100.0	99	34	US-10-450-763-56957
24	29	100.0	690	49	US-60-581-351-2850
25	29	100.0	698	49	US-60-581-351-2835
26	29	96.6	6	27	US-09-724-842-16
27	28	96.6	6	27	US-09-724-842-24
28	28	96.6	6	27	US-09-724-842A-16
29	28	96.6	6	27	US-09-724-842A-24
30	28	96.6	6	28	US-09-867-847-18
31	28	96.6	6	28	US-09-867-847-26
32	28	96.6	6	28	US-09-867-847A-18
33	28	96.6	6	28	US-09-867-847A-26
34	28	96.6	6	29	US-09-915-092-8
35	28	96.6	6	29	US-09-915-092-16
36	28	96.6	6	30	US-10-009-122-9
37	28	96.6	6	30	US-10-009-122-17
38	28	96.6	6	37	US-10-705-028-9
39	28	96.6	6	37	US-10-705-028-17
40	28	96.6	6	37	US-10-728-028-8
41	28	96.6	6	37	US-10-728-028-16
42	28	96.6	6	38	US-10-825-958-16
43	28	96.6	6	38	US-10-825-958-24
44	28	96.6	37	1	PCT-US03-25626-7
45	28	96.6	37	28	US-09-807-877-16
46	28	96.6	37	36	US-10-641-924-7
47	28	96.6	37	36	US-10-642-255-7
48	28	96.6	60	34	US-10-437-963-173619
49	28	96.6	77	37	US-10-793-479-6921
50	28	96.6	87	34	US-10-437-963-133986
51	28	96.6	88	27	US-09-708-427-14352
52	28	96.6	91	27	US-09-708-427-14351
53	28	96.6	109	34	US-10-437-963-105773
54	28	96.6	112	27	US-09-733-089-9030
55	28	96.6	112	28	US-09-816-660-9030

56	28	96.6	135	34	US-10-437-363-141578	Sequence 141578,	129	28	96.6	1144	36	US-10-631-467-1388	Sequence 1388, Ap
57	28	96.6	140	27	US-09-733-089-23062	Sequence 23062, A	130	28	96.6	1144	36	US-10-631-467-1464	Sequence 1464, Ap
58	28	96.6	146	28	US-09-816-660-23062	Sequence 23062, A	131	28	96.6	1144	36	US-10-937-758A-101	Sequence 101, App
59	28	96.6	156	24	US-09-417-507-41853	Sequence 41853, A	132	28	96.6	1196	11	US-08-132-372-5	Sequence 5, Appli
60	28	96.6	158	27	US-09-733-089-23064	Sequence 23064, A	133	28	96.6	1443	26	US-09-614-150-32208	Sequence 32208, A
61	28	96.6	165	27	US-09-733-089-23060	Sequence 23060, A	134	28	96.6	1443	26	US-09-614-150A-32208	Sequence 32208, A
62	28	96.6	165	27	US-09-733-089-23060	Sequence 23060, A	135	28	96.6	1443	40	US-11-097-143-32208	Sequence 32208, A
63	28	96.6	165	28	US-09-816-660-23060	Sequence 23060, A	136	28	96.6	1443	40	US-60-191-637-31780	Sequence 31780, A
64	28	96.6	175	32	US-10-220-366A-25111	Sequence 25111, A	137	28	96.6	1640	34	US-10-437-963-109646	Sequence 109646,
65	28	96.6	175	34	US-10-437-963-122124	Sequence 122124, A	138	28	96.6	1640	34	US-10-438-246-24934	Sequence 24934, A
66	28	96.6	181	27	US-09-733-089-23063	Sequence 23063, A	139	28	96.6	1764	31	US-10-155-881-25401	Sequence 25401, A
67	28	96.6	181	28	US-09-816-660-23063	Sequence 23063, A	140	28	96.6	1764	31	US-10-155-881-28754	Sequence 28754, A
68	28	96.6	186	34	US-10-481-032A-214	Sequence 214, App	141	28	96.6	1764	31	US-10-438-246-17664	Sequence 17664, A
69	28	96.6	186	34	US-10-481-032A-228	Sequence 228, App	142	28	93.1	6	15	US-08-548-998A-8	Sequence 8, Appli
70	28	96.6	188	34	US-10-437-963-172476	Sequence 172476,	143	27	93.1	6	15	US-08-548-998A-8	Sequence 8, Appli
71	28	96.6	190	1	PCT-US01-01354-11385	Sequence 11385, A	144	27	93.1	6	16	US-08-612-785-9	Sequence 9, Appli
72	28	96.6	190	27	US-09-764-905-11385	Sequence 11385, A	145	27	93.1	6	16	US-08-616-081-9	Sequence 9, Appli
73	28	96.6	190	30	US-10-092-399-11385	Sequence 11385, A	146	27	93.1	6	16	US-08-616-081A-9	Sequence 9, Appli
74	28	96.6	198	34	US-10-437-963-172452	Sequence 172452, A	147	27	93.1	6	27	US-09-724-842-7	Sequence 7, Appli
75	28	96.6	199	27	US-09-733-089-23065	Sequence 23065, A	148	27	93.1	6	27	US-09-724-842-18	Sequence 18, Appl
76	28	96.6	199	28	US-09-816-660-23065	Sequence 23065, A	149	27	93.1	6	27	US-09-724-842A-7	Sequence 7, Appli
77	28	96.6	214	50	US-60-655-875-150287	Sequence 150287,	150	27	93.1	6	27	US-09-724-842A-18	Sequence 18, Appl
78	28	96.6	268	50	US-60-655-875-151925	Sequence 151925,	151	27	93.1	6	28	US-09-867-847-7	Sequence 7, Appli
79	28	96.6	416	30	US-10-055-475-14	Sequence 14, Appl	152	27	93.1	6	28	US-09-867-847-20	Sequence 20, Appl
80	28	96.6	416	40	US-11-042-922-14	Sequence 14, Appl	153	27	93.1	6	28	US-09-867-847A-7	Sequence 7, Appli
81	28	96.6	514	30	US-10-055-475-13	Sequence 13, Appl	154	27	93.1	6	28	US-09-867-847A-20	Sequence 20, Appl
82	28	96.6	514	40	US-11-042-922-13	Sequence 13, Appl	155	27	93.1	6	29	US-09-915-092-10	Sequence 10, Appl
83	28	96.6	564	26	US-09-614-150-12723	Sequence 12723, A	156	27	93.1	6	29	US-09-915-092-28	Sequence 28, Appl
84	28	96.6	564	26	US-09-614-150A-12723	Sequence 12723, A	157	27	93.1	6	29	US-09-956-625-25	Sequence 25, Appl
85	28	96.6	564	40	US-11-097-143-12723	Sequence 12723, A	158	27	93.1	6	29	US-09-972-475A-9	Sequence 9, Appli
86	28	96.6	564	45	US-60-167-217-12757	Sequence 12757, A	159	27	93.1	6	29	US-09-972-475A-9	Sequence 9, Appli
87	28	96.6	564	45	US-60-173-464-10379	Sequence 10379, A	160	27	93.1	6	30	US-10-009-122-3	Sequence 3, Appli
88	28	96.6	564	45	US-60-191-637-12761	Sequence 12761, A	161	27	93.1	6	30	US-10-009-122-11	Sequence 11, Appl
89	28	96.6	564	45	US-60-191-681-10037	Sequence 10037, A	162	27	93.1	6	34	US-10-463-729-9	Sequence 9, Appli
90	28	96.6	647	27	US-09-724-676-88682	Sequence 88682, A	163	27	93.1	6	34	US-10-666-095-3	Sequence 3, Appli
91	28	96.6	647	27	US-09-724-676A-88682	Sequence 88682, A	164	27	93.1	6	36	US-10-666-095-3	Sequence 3, Appli
92	28	96.6	666	40	US-11-087-099-8103	Sequence 8103, Ap	165	27	93.1	6	37	US-10-705-028-3	Sequence 3, Appli
93	28	96.6	666	41	US-11-188-298-7496	Sequence 7496, Ap	166	27	93.1	6	37	US-10-705-028-11	Sequence 11, Appl
94	28	96.6	666	49	US-60-556-841-8103	Sequence 8103, Ap	167	27	93.1	6	37	US-10-728-028-10	Sequence 10, Appl
95	28	96.6	666	49	US-60-592-978-7496	Sequence 7496, Ap	168	27	93.1	6	37	US-10-728-028-27	Sequence 27, Appl
96	28	96.6	854	37	US-10-760-320A-3865	Sequence 3865, Ap	169	27	93.1	6	38	US-10-728-028-28	Sequence 28, Appl
97	28	96.6	854	37	US-10-760-320A-3865	Sequence 3865, Ap	170	27	93.1	6	38	US-10-825-958-7	Sequence 7, Appli
98	28	96.6	922	1	PCT-US03-28227-3501	Sequence 3501, Ap	171	27	93.1	7	1	US-10-825-958-18	Sequence 18, Appl
99	28	96.6	925	1	PCT-US03-10870-2031	Sequence 2031, Ap	172	27	93.1	7	1	PCT-US02-08803-3	Sequence 3, Appli
100	28	96.6	925	31	US-10-170-205E-28729	Sequence 28729, A	173	27	93.1	7	11	PCT-US94-10083-13	Sequence 13, Appl
101	28	96.6	925	33	US-10-370-715B-8	Sequence 8, Appli	174	27	93.1	7	11	US-08-117-927A-13	Sequence 13, Appl
102	28	96.6	925	34	US-10-408-765-2031	Sequence 2031, Ap	175	27	93.1	7	15	US-08-117-927B-13	Sequence 6, Appli
103	28	96.6	925	34	US-10-408-765A-2031	Sequence 2031, Ap	176	27	93.1	7	15	US-08-548-998-6	Sequence 6, Appli
104	28	96.6	925	36	US-10-631-467-680	Sequence 680, App	177	27	93.1	7	15	US-08-548-998A-6	Sequence 6, Appli
105	28	96.6	925	36	US-10-631-467-747	Sequence 747, App	178	27	93.1	7	16	US-08-612-785-7	Sequence 7, Appli
106	28	96.6	925	37	US-10-755-889-234	Sequence 234, App	179	27	93.1	7	16	US-08-612-785-7	Sequence 7, Appli
107	28	96.6	925	39	US-10-990-328-9394	Sequence 9394, Ap	180	27	93.1	7	17	US-08-797-782-13	Sequence 13, Appl
108	28	96.6	925	39	US-10-990-328A-9394	Sequence 9394, Ap	181	27	93.1	7	17	US-08-797-782-13	Sequence 13, Appl
109	28	96.6	925	47	US-60-389-987-2031	Sequence 2031, Ap	182	27	93.1	7	27	US-09-724-842-10	Sequence 10, Appl
110	28	96.6	925	48	US-60-412-418-2031	Sequence 2031, Ap	183	27	93.1	7	27	US-09-724-842-25	Sequence 25, Appl
111	28	96.6	925	48	US-60-440-068-234	Sequence 234, App	184	27	93.1	7	27	US-09-724-842A-10	Sequence 10, Appl
112	28	96.6	925	48	US-60-452-680-17249	Sequence 17249, A	185	27	93.1	7	27	US-09-724-842A-25	Sequence 25, Appl
113	28	96.6	925	48	US-60-469-757-234	Sequence 234, App	186	27	93.1	7	27	US-09-724-842A-26	Sequence 26, Appl
114	28	96.6	925	48	US-60-470-166-915	Sequence 915, App	187	27	93.1	7	28	US-09-867-847-12	Sequence 12, Appl
115	28	96.6	1143	27	US-09-791-537-141966	Sequence 141966,	188	27	93.1	7	28	US-09-867-847-27	Sequence 27, Appl
116	28	96.6	1144	8	US-07-841-641A-5	Sequence 5, Appli	189	27	93.1	7	28	US-09-867-847-28	Sequence 28, Appl
117	28	96.6	1144	9	US-07-921-798-1	Sequence 1, Appli	190	27	93.1	7	28	US-09-867-847A-12	Sequence 12, Appl
118	28	96.6	1144	9	US-07-921-798A-2	Sequence 2, Appli	191	27	93.1	7	28	US-09-867-847A-27	Sequence 27, Appl
119	28	96.6	1144	13	US-08-361-063-12	Sequence 12, Appl	192	27	93.1	7	28	US-09-867-847A-28	Sequence 28, Appl
120	28	96.6	1144	15	US-08-553-503-2	Sequence 2, Appli	193	27	93.1	7	29	US-09-915-092-2	Sequence 2, Appli
121	28	96.6	1144	27	US-09-751-708A-124	Sequence 124, App	194	27	93.1	7	29	US-09-915-092-17	Sequence 17, Appl
122	28	96.6	1144	27	US-09-791-537-141967	Sequence 141967,	195	27	93.1	7	29	US-09-915-092-18	Sequence 18, Appl
123	28	96.6	1144	27	US-09-791-537-141969	Sequence 141969,	196	27	93.1	7	29	US-09-972-475A-7	Sequence 7, Appli
124	28	96.6	1144	27	US-09-791-537-141970	Sequence 141970,	197	27	93.1	7	29	US-09-972-475A-7	Sequence 7, Appli
125	28	96.6	1144	27	US-09-791-537-141971	Sequence 141971,	198	27	93.1	7	30	US-10-009-122-2	Sequence 2, Appli
126	28	96.6	1144	27	US-09-791-537-141973	Sequence 141973,	199	27	93.1	7	30	US-10-009-122-18	Sequence 18, Appl
127	28	96.6	1144	28	US-09-870-759-124	Sequence 124, App	200	27	93.1	7	30	US-10-009-122-19	Sequence 19, Appl
128	28	96.6	1144	34	US-10-428-817A-120	Sequence 120, App	201	27	93.1	7	30	US-10-030-137-3	Sequence 3, Appli

202	27	93.1	7	30	US-10-030-137A-3	Sequence 3, Appli	275	27	93.1	10	27	US-09-723-544-23	Sequence 23, Appl
203	27	93.1	7	30	US-10-030-137A-5	Sequence 5, Appli	276	27	93.1	10	27	US-09-723-544-24	Sequence 24, Appl
204	27	93.1	7	30	US-10-030-138A-4	Sequence 4, Appli	277	27	93.1	10	27	US-09-723-544-25	Sequence 25, Appl
205	27	93.1	7	30	US-10-030-138A-5	Sequence 5, Appli	278	27	93.1	10	27	US-09-723-544-26	Sequence 26, Appl
206	27	93.1	7	34	US-10-463-729-7	Sequence 7, Appli	279	27	93.1	10	27	US-09-723-544-27	Sequence 27, Appl
207	27	93.1	7	35	US-10-505-313-269	Sequence 269, App	280	27	93.1	10	27	US-09-723-544-28	Sequence 28, Appl
208	27	93.1	7	37	US-10-705-028-2	Sequence 2, Appli	281	27	93.1	10	27	US-09-723-544-29	Sequence 29, Appl
209	27	93.1	7	37	US-10-705-028-18	Sequence 18, Appl	282	27	93.1	10	27	US-09-724-888-20	Sequence 20, Appl
210	27	93.1	7	37	US-10-705-028-19	Sequence 19, Appl	283	27	93.1	10	27	US-09-724-888-21	Sequence 21, Appl
211	27	93.1	7	37	US-10-728-028-2	Sequence 2, Appli	284	27	93.1	10	27	US-09-724-888-22	Sequence 22, Appl
212	27	93.1	7	37	US-10-728-028-17	Sequence 17, Appl	285	27	93.1	10	27	US-09-724-888-23	Sequence 23, Appl
213	27	93.1	7	37	US-10-728-028-18	Sequence 18, Appl	286	27	93.1	10	27	US-09-724-888-24	Sequence 24, Appl
214	27	93.1	7	38	US-10-810-881A-128	Sequence 128, App	287	27	93.1	10	27	US-09-724-888-25	Sequence 25, Appl
215	27	93.1	7	38	US-10-825-958-10	Sequence 10, Appl	288	27	93.1	10	27	US-09-724-888-26	Sequence 26, Appl
216	27	93.1	7	38	US-10-825-958-25	Sequence 25, Appl	289	27	93.1	10	28	US-09-867-847A-29	Sequence 29, Appl
217	27	93.1	7	38	US-10-825-958-26	Sequence 26, Appl	290	27	93.1	10	28	US-09-867-847A-29	Sequence 29, Appl
218	27	93.1	8	1	PCT-US04-42701-51	Sequence 51, Appl	291	27	93.1	10	29	US-09-915-092-19	Sequence 19, Appl
219	27	93.1	8	1	PCT-US04-42701-54	Sequence 54, Appl	292	27	93.1	10	29	US-09-979-701-20	Sequence 20, Appl
220	27	93.1	8	1	PCT-US04-44093-51	Sequence 51, Appl	293	27	93.1	10	29	US-09-979-701-21	Sequence 21, Appl
221	27	93.1	8	1	PCT-US04-44093-54	Sequence 54, Appl	294	27	93.1	10	29	US-09-979-701-22	Sequence 22, Appl
222	27	93.1	8	14	US-08-478-326A-1	Sequence 1, Appli	295	27	93.1	10	29	US-09-979-701-23	Sequence 23, Appl
223	27	93.1	8	15	US-08-548-998A-4	Sequence 4, Appli	296	27	93.1	10	29	US-09-979-701-24	Sequence 24, Appl
224	27	93.1	8	15	US-08-548-998A-4	Sequence 4, Appli	297	27	93.1	10	37	US-10-728-028-19	Sequence 19, Appl
225	27	93.1	8	16	US-08-612-785-5	Sequence 5, Appli	298	27	93.1	10	37	US-10-777-792-20	Sequence 20, Appl
226	27	93.1	8	16	US-08-612-785-5	Sequence 5, Appli	299	27	93.1	10	37	US-10-777-792-21	Sequence 21, Appl
227	27	93.1	8	16	US-08-616-081-5	Sequence 5, Appli	300	27	93.1	10	37	US-10-777-792-22	Sequence 22, Appl
228	27	93.1	8	16	US-08-616-081A-5	Sequence 5, Appli							
229	27	93.1	8	28	US-09-850-061A-44	Sequence 44, Appl							
230	27	93.1	8	29	US-09-972-475-5	Sequence 5, Appli							
231	27	93.1	8	29	US-09-972-475A-5	Sequence 5, Appli							
232	27	93.1	8	32	US-10-235-483-1	Sequence 1, Appli							
233	27	93.1	8	32	US-10-281-092-42	Sequence 42, Appl							
234	27	93.1	8	34	US-10-463-729-5	Sequence 5, Appli							
235	27	93.1	8	37	US-10-721-774-44	Sequence 44, Appl							
236	27	93.1	8	38	US-10-810-881A-125	Sequence 125, App							
237	27	93.1	8	38	US-10-817-979-73	Sequence 73, Appl							
238	27	93.1	9	1	PCT-US04-42701-45	Sequence 45, Appl							
239	27	93.1	9	1	PCT-US04-42701-48	Sequence 48, Appl							
240	27	93.1	9	1	PCT-US04-44093-45	Sequence 45, Appl							
241	27	93.1	9	1	PCT-US04-44093-48	Sequence 48, Appl							
242	27	93.1	9	8	US-07-877-675A-23	Sequence 23, Appl							
243	27	93.1	9	8	US-07-877-675A-25	Sequence 25, Appl							
244	27	93.1	9	28	US-09-867-847-9	Sequence 9, Appli							
245	27	93.1	9	28	US-09-867-847A-9	Sequence 9, Appli							
246	27	93.1	9	28	US-09-899-815-2	Sequence 2, Appli							
247	27	93.1	9	30	US-10-009-122-20	Sequence 20, Appl							
248	27	93.1	9	32	US-10-235-483-64	Sequence 64, Appl							
249	27	93.1	9	36	US-10-619-454-3	Sequence 3, Appli							
250	27	93.1	9	36	US-10-619-454-25	Sequence 25, Appl							
251	27	93.1	9	36	US-10-619-454-28	Sequence 28, Appl							
252	27	93.1	9	36	US-10-619-454-57	Sequence 57, Appl							
253	27	93.1	9	36	US-10-619-454-157	Sequence 157, App							
254	27	93.1	9	37	US-10-705-028-20	Sequence 20, Appl							
255	27	93.1	10	1	PCT-US05-39497-1	Sequence 1, Appli							
256	27	93.1	10	1	PCT-US05-38125-194	Sequence 194, App							
257	27	93.1	10	1	PCT-US05-38125-195	Sequence 195, App							
258	27	93.1	10	1	PCT-US05-38125-196	Sequence 196, App							
259	27	93.1	10	1	PCT-US05-38125-197	Sequence 197, App							
260	27	93.1	10	1	PCT-US05-38125-198	Sequence 198, App							
261	27	93.1	10	23	US-09-395-234-3	Sequence 3, Appli							
262	27	93.1	10	25	US-09-580-015-20	Sequence 20, Appl							
263	27	93.1	10	25	US-09-580-015-21	Sequence 21, Appl							
264	27	93.1	10	25	US-09-580-015-22	Sequence 22, Appl							
265	27	93.1	10	25	US-09-580-015-23	Sequence 23, Appl							
266	27	93.1	10	25	US-09-580-015-24	Sequence 24, Appl							
267	27	93.1	10	25	US-09-580-019-20	Sequence 20, Appl							
268	27	93.1	10	25	US-09-580-019-21	Sequence 21, Appl							
269	27	93.1	10	25	US-09-580-019-22	Sequence 22, Appl							
270	27	93.1	10	25	US-09-580-019-23	Sequence 23, Appl							
271	27	93.1	10	25	US-09-580-019-24	Sequence 24, Appl							
272	27	93.1	10	26	US-09-652-559B-3	Sequence 3, Appli							
273	27	93.1	10	27	US-09-723-544-20	Sequence 20, Appl							
274	27	93.1	10	27	US-09-723-544-21	Sequence 21, Appl							
					US-09-723-544-22	Sequence 22, Appl							

Sequence 23, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl

US-09-724-842-9
; Sequence 9, Application US/09724842
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiang
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09724, 842
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics

US-09-724-842-9
; Sequence 9, Application US/09724842
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiang
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09724, 842
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics

Best Match
Best Local Similarity 100.0%; Score 29; DB 27; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2
US-09-724-842-17
; Sequence 17, Application US/09724842
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiang

; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842-17

Query Match 100.0%; Score 29; DB 27; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-724-842A-9
; Sequence 9, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-724-842A-9

Query Match 100.0%; Score 29; DB 27; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 4
US-09-724-842A-17
; Sequence 17, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi

; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842A-17

Query Match 100.0%; Score 29; DB 27; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 5
US-09-867-847-11
; Sequence 11, Application US/09867847
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 6
US-09-867-847-19
; Sequence 19, Application US/09867847
; GENERAL INFORMATION:

; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)_
; OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
US-09-867-847-19

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 7

US-09-867-847A-11
; Sequence 11, Application US/09867847A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Vaccine for the Prevention and Treatment
; TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
; FILE REFERENCE: 50291/005001
; CURRENT APPLICATION NUMBER: US/09/867,847A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
US-09-867-847A-11

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 8

US-09-867-847A-19
; Sequence 19, Application US/09867847A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Vaccine for the Prevention and Treatment
; TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
; FILE REFERENCE: 50291/005001
; CURRENT APPLICATION NUMBER: US/09/867,847A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: 6
; OTHER INFORMATION: Amidation
US-09-867-847A-19

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 9

US-09-915-092-1
; Sequence 1, Application US/09915092
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

Query Match 100.0%; Score 29; DB 29; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 10
US-09-915-092-9

```

; Sequence 9, Application US/09915092
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NEI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; TYPE: PRT
; LENGTH: 6
; ORGANISM: Homo sapiens
US-09-915-092-9

Query Match      100.0%; Score 29; DB 29; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 11
US-10-009-122-1
; Sequence 1, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: Gervais, Francine
; APPLICANT: GUPTA, Ajay
; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide having antifibrillogenic activity and/or
; OTHER INFORMATION: neuroprotection
US-10-009-122-1

Query Match      100.0%; Score 29; DB 30; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 12
US-10-009-122-10
; Sequence 10, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: Gervais, Francine
; APPLICANT: GUPTA, Ajay

```

```

; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; TITLE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS THEREOF
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide having antifibrillogenic activity and/or
; OTHER INFORMATION: neuroprotection
; NAME/KEY: AMIDATION
; LOCATION: (6)...(6)
US-10-009-122-10

Query Match      100.0%; Score 29; DB 30; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 13
US-10-705-028-1
; Sequence 1, Application US/10705028
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NEI-088CN
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-028-1

Query Match      100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 14
US-10-705-028-10
; Sequence 10, Application US/10705028
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NEI-088CN
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408

```

; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-028-10

Query Match 100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 15

US-10-728-028-1
; Sequence 1, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match 100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 16

US-10-728-028-9
; Sequence 9, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match 100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 17

US-10-825-958-9
; Sequence 9, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-9

Query Match 100.0%; Score 29; DB 38; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 18

US-10-825-958-17
; Sequence 17, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16

; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)-
; OTHER INFORMATION: AMIDATION
US-10-825-958-17

Query Match 100.0%; Score 29; DB 38; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 1 KIVFFA 6

RESULT 19
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
US-10-425-115-280164

Query Match 100.0%; Score 29; DB 34; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 28 KIVFFA 33

RESULT 20
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
US-10-424-599-165325

Query Match 100.0%; Score 29; DB 34; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 21 KIVFFA 26

RESULT 21
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
US-10-424-599-240310

Query Match 100.0%; Score 29; DB 34; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 34 KIVFFA 39

RESULT 22
PCT-US01-08631-56957
; Sequence 56957, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORE2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-56957

Query Match      100.0%; Score 29; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      63 KIVFFA 68

RESULT 23
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56957

Query Match      100.0%; Score 29; DB 34; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      63 KIVFFA 68

RESULT 24
US-60-581-351-2850
; Sequence 2850, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2850
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Tropheryma whipplei TW08/27

US-60-581-351-2850
Query Match      100.0%; Score 29; DB 49; Length 690;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      526 KIVFFA 531

RESULT 25
US-60-581-351-2835
; Sequence 2835, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2835
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Tropheryma whipplei str. Twist
US-60-581-351-2835

Query Match      100.0%; Score 29; DB 49; Length 698;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      534 KIVFFA 539

RESULT 26
US-09-724-842-16
; Sequence 16, Application US/09724842
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lisa
; APPLICANT: Kong, Xiang
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-724-842-16

Query Match      96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6
```

RESULT 27
US-09-724-842-24
; Sequence 24, Application US/09724842
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842-24

Query Match 96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 28
US-09-724-842A-16
; Sequence 16, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-724-842A-16

Query Match 96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 29
US-09-724-842A-24
; Sequence 24, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842A-24

Query Match 96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 30
US-09-867-847-18
; Sequence 18, Application US/09867847
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match 96.6%; Score 28; DB 28; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

```
Db          |:|||||
            1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 31
US-09-867-847-26
; Sequence 26, Application US/09867847
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-26

Query Match      96.6%;  Score 28;  DB 28;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 KVVFFA 6
            |:|||||
            1 KVVFFA 6

Db          1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 32
US-09-867-847A-18
; Sequence 18, Application US/09867847A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Vaccine for the Prevention and Treatment
; TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
; FILE REFERENCE: 50291/005001
; CURRENT APPLICATION NUMBER: US/09/867,847A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
US-09-867-847A-18

Query Match      96.6%;  Score 28;  DB 28;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

US-09-867-847-26
; Sequence 26, Application US/09867847
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Vaccine for the Prevention and Treatment
; TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
; FILE REFERENCE: 50291/005001
; CURRENT APPLICATION NUMBER: US/09/867,847A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
US-09-867-847A-26

Query Match      96.6%;  Score 28;  DB 28;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 KVVFFA 6
            |:|||||
            1 KVVFFA 6

Db          1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 33
US-09-867-847A-26
; Sequence 26, Application US/09867847A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Vaccine for the Prevention and Treatment
; TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
; FILE REFERENCE: 50291/005001
; CURRENT APPLICATION NUMBER: US/09/867,847A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
US-09-867-847A-26

Query Match      96.6%;  Score 28;  DB 28;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 KVVFFA 6
            |:|||||
            1 KVVFFA 6

Db          1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 34
US-09-915-092-8
; Sequence 8, Application US/09915092
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match      96.6%;  Score 28;  DB 29;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 35
US-09-915-092-16
; Sequence 16, Application US/09915092
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match 96.6%; Score 28; DB 29; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 36
US-10-009-122-9
; Sequence 9, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: GERVAIS, Francine
; APPLICANT: GUPTA, Ajay
; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; FILE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS THEREOF
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide having antifibrillogenetic activity and/or
; OTHER INFORMATION: neuroprotection
US-10-009-122-9

Query Match 96.6%; Score 28; DB 30; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 37
US-10-009-122-17
; Sequence 17, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: GERVAIS, Francine
; APPLICANT: GUPTA, Ajay
; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; FILE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS THEREOF
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide having antifibrillogenetic activity and/or
; OTHER INFORMATION: neuroprotection
US-10-009-122-17

Query Match 96.6%; Score 28; DB 30; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 38
US-10-705-028-9
; Sequence 9, Application US/10705028
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088CN
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-028-9

Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 39
US-10-705-028-17
; Sequence 17, Application US/10705028
; GENERAL INFORMATION:
```



```
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088CN
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-028-17
```

```
Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 40
US-10-728-028-8
; Sequence 8, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-8
```

```
Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 41
US-10-728-028-16
; Sequence 16, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
```

```
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-16
```

```
Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 42
US-10-825-958-16
; Sequence 16, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; US-10-825-958-16
```

```
Query Match 96.6%; Score 28; DB 38; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 43
US-10-825-958-24
; Sequence 24, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
```

```
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match          96.6%; Score 28; DB 38; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KVVFFA 6

RESULT 44
PCT-US03-25626-7
; Sequence 7, Application PC/TUS0325626
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: eNOS
; FILE REFERENCE: 52339AOWM1
; CURRENT APPLICATION NUMBER: PCT/US03/25626
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-25626-7

Query Match          96.6%; Score 28; DB 1; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      18 KVVFFA 23

RESULT 45
US-09-807-877-16
; Sequence 16, Application US/09807877
; GENERAL INFORMATION:
; APPLICANT: STAPLETON, DAVID IAN
```

```
; APPLICANT: CHEN, ZHIPING
; APPLICANT: MICHELL, BELINDA JOYCE
; APPLICANT: KEMP, BRUCE ERNEST
; APPLICANT: MITCHELL, KENNETH IAN
; TITLE OF INVENTION: REGULATION OF NITRIC OXIDE SYNTHASE ACTIVITY
; FILE REFERENCE: 4050.000900
; CURRENT APPLICATION NUMBER: US/09/807,877
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: PCT/AU99/00968
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PFe976
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 37
; TYPE: PRT
; ORGANISM: mus musculus
US-09-807-877-16

Query Match          96.6%; Score 28; DB 28; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      18 KVVFFA 23

RESULT 46
US-10-641-924-7
; Sequence 7, Application US/10641924
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 5303SAUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match          96.6%; Score 28; DB 36; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      18 KVVFFA 23

RESULT 47
US-10-642-255-7
; Sequence 7, Application US/10642255
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: eNOS
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
```

; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match 96.6%; Score 28; DB 36; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 18 KVVFFA 23

RESULT 48
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pap
US-10-437-963-173619

Query Match 96.6%; Score 28; DB 34; Length 60;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 4 KVVFFA 9

RESULT 49
US-10-793-479-6921
; Sequence 6921, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-793-479-6921

Query Match 96.6%; Score 28; DB 37; Length 77;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 38 KVVFFA 43

RESULT 50
US-10-437-963-133986
; Sequence 133986, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pap
US-10-437-963-133986

Query Match 96.6%; Score 28; DB 34; Length 87;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 6 KVVFFA 11

RESULT 51
US-09-708-427-14352
; Sequence 14352, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14352
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..85
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: 1..88
; OTHER INFORMATION: Ceres Seq. ID 1827650
US-09-708-427-14352

Query Match 96.6%; Score 28; DB 27; Length 88;

```
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 35 KIIFFA 40

RESULT 52
US-09-708-427-14351
; Sequence 14351, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14351
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..91
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..91
; OTHER INFORMATION: Ceres Seq. ID 1827649
US-09-708-427-14351

Query Match 96.6%; Score 28; DB 27; Length 91;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 38 KIIFFA 43

RESULT 53
US-10-437-963-105773
; Sequence 105773, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pep
US-10-437-963-105773

Query Match 96.6%; Score 28; DB 34; Length 109;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
```

```
Db 4 KIVFFA 9

RESULT 54
US-09-733-089-9030
; Sequence 9030, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 9030
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(112)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-733-089-9030

Query Match 96.6%; Score 28; DB 27; Length 112;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 21 KIVFFA 26

RESULT 55
US-09-816-660-9030
; Sequence 9030, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: )
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 9030
; LENGTH: 112
```

; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(112)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-816-660-9030

Query Match 96.6%; Score 28; DB 28; Length 112;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 21 KVVFFA 26

RESULT 56
US-10-437-963-141578
; Sequence 141578, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141578
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pap
US-10-437-963-141578

Query Match 96.6%; Score 28; DB 34; Length 135;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 4 KVVFFA 9

RESULT 57
US-09-733-089-23062
; Sequence 23062, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23062
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-733-089-23062

Query Match 96.6%; Score 28; DB 27; Length 140;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 96 KVVFFA 101

RESULT 58
US-09-816-660-23062
; Sequence 23062, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER:) US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23062
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-816-660-23062

Query Match 96.6%; Score 28; DB 28; Length 140;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 96 KVVFFA 101

RESULT 59
US-09-417-507-41853
; Sequence 41853, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 41853
; LENGTH: 156
; TYPE: PRT
; ORGANISM: A. fumigatus
US-09-417-507-41853

```
Query Match      96.6%; Score 28; DB 24; Length 156;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      93 KLIFFA 98

RESULT 60
US-09-733-089-23064
; Sequence 23064, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23064
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-733-089-23064

Query Match      96.6%; Score 28; DB 27; Length 158;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      114 KWFFFA 119

RESULT 61
US-09-816-660-23064
; Sequence 23064, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: )
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
```

```
; SEQ ID NO 23064
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-816-660-23064

Query Match      96.6%; Score 28; DB 28; Length 158;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      114 KWFFFA 119

RESULT 62
US-09-733-089-23060
; Sequence 23060, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23060
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(165)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-733-089-23060

Query Match      96.6%; Score 28; DB 27; Length 165;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      121 KWFFFA 126

RESULT 63
US-09-816-660-23060
; Sequence 23060, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
```

; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER:) US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23060
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(165)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-816-660-23060

Query Match 96.6%; Score 28; DB 28; Length 165;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 121 KVVFFA 126

RESULT 64
US-10-220-366A-25111
; Sequence 25111, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 25111
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(175)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-25111

Query Match 96.6%; Score 28; DB 32; Length 175;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 128 KVVFFA 133

RESULT 65
US-10-437-963-122124
; Sequence 122124, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122124
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(175)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pep
US-10-437-963-122124

Query Match 96.6%; Score 28; DB 34; Length 175;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 66
US-09-733-089-23063
; Sequence 23063, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyva, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23063
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(181)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-733-089-23063

Query Match 96.6%; Score 28; DB 27; Length 181;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 137 KVVFFA 142

RESULT 67
US-09-816-660-23063
; Sequence 23063, Application US/09816660
; GENERAL INFORMATION:

```
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US 09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: ) US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23063
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(181)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-816-660-23063

Query Match 96.6%; Score 28; DB 28; Length 181;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 137 KVVFFA 142

RESULT 68
US-10-481-032A-214
; Sequence 214, Application US/10481032A
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US 60/300,112
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 34; Length 186;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 70
US-10-437-963-172476
; Sequence 172476, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

```
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 34; Length 186;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 69
US-10-481-032A-228
; Sequence 228, Application US/10481032A
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228

Query Match 96.6%; Score 28; DB 34; Length 186;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 70
US-10-437-963-172476
; Sequence 172476, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```



```
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pap
US-10-437-963-172476

Query Match          96.6%; Score 28; DB 34; Length 188;
Best Local Similarity 83.3%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |:||||
Db      4 KVVFFA 9

RESULT 71
PCT-US01-01354-11385
; Sequence 11385, Application PC/TUS0101354
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01354
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 42506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11385
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-01354-11385

Query Match          96.6%; Score 28; DB 1; Length 190;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |:||||
Db      14 KVVFFA 19

RESULT 72
US-09-764-905-11385
; Sequence 11385, Application US/09764905
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004
; CURRENT APPLICATION NUMBER: US/09/764,905
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
```

```
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
```

```
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,398
```

```
Query Match 96.6%; Score 28; DB 27; Length 190;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 1 KIVEFFA 6
|:|:|
Db 14 KIVEFFA 19
```

RESULT 73

```
US-10-092-399-11385
; Sequence 11385, Application US/10092399
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004C1
; CURRENT APPLICATION NUMBER: US/10/092,399
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 42506
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11385
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc feature
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-399-11385
```

```
Query Match      96.6%; Score 28; DB 30; Length 190;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      14 KVVFFA 19

RESULT 74
US-10-437-963-172452
; Sequence 172452, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pep
US-10-437-963-172452

Query Match      96.6%; Score 28; DB 34; Length 198;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      4 KVVFFA 9

RESULT 75
US-09-733-089-23065
; Sequence 23065, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyeva, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23065
; LENGTH: 199
; TYPE: PRT
```

```
; ORGANISM: Oryza sativa
US-09-733-089-23065

Query Match      96.6%; Score 28; DB 27; Length 199;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      155 KVVFFA 160

Search completed: December 29, 2005, 18:37:16
Job time : 263.871 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-10
Perfect score: 29
Sequence: 1 KIVPFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	4	AAB48483
2	29	100.0	6	4	AAB48474
3	29	100.0	6	4	AAB82623
4	29	100.0	6	4	AAB82631
5	29	100.0	6	5	AAB96819
6	29	100.0	6	5	AAB96811
7	29	100.0	6	5	AAB11657
8	29	100.0	6	5	AAB11648
9	29	100.0	6	6	AAB35446
10	29	100.0	6	6	AAB35438
11	29	100.0	6	8	ADQ37322
12	29	100.0	6	8	ADQ37270
13	29	100.0	6	8	ADQ37313
14	29	100.0	6	8	ADQ37262
15	29	100.0	6	9	ADY37921
16	29	100.0	6	9	ADY37929
17	29	100.0	99	4	ABG26598
18	28	96.6	6	4	AAB48482
19	28	96.6	6	4	AAB48490
20	28	96.6	6	4	AAB82630
21	28	96.6	6	4	AAB82638
22	28	96.6	6	5	AAB96818
23	28	96.6	6	5	AAB96826
24	28	96.6	6	5	AAB11664

25	28	96.6	6	5	AAU11656
26	28	96.6	6	6	AAE35452
27	28	96.6	6	8	ADQ37277
28	28	96.6	6	8	ADQ37321
29	28	96.6	6	8	ADQ37329
30	28	96.6	6	9	ADY37928
31	28	96.6	6	9	ADY37936
32	28	96.6	22	8	ADQ09761
33	28	96.6	23	8	ADY37984
34	28	96.6	37	3	ABO5910
35	28	96.6	37	3	ADK34080
36	28	96.6	37	3	ADL70727
37	28	96.6	77	3	AG02840
38	28	96.6	175	4	AO11219
39	28	96.6	186	7	ADCO7962
40	28	96.6	186	7	ADCO7948
41	28	96.6	190	4	AAH83792
42	28	96.6	564	4	ABE61977
43	28	96.6	854	8	ADQ66704
44	28	96.6	922	8	ABM83252
45	28	96.6	925	7	ADF76335
46	28	96.6	925	7	ADJ70225
47	28	96.6	925	8	ADJ75428
48	28	96.6	925	8	ADJ75495
49	28	96.6	925	8	ADN04860
50	28	96.6	925	8	ADR14233
51	28	96.6	925	8	ADR25011
52	28	96.6	925	8	ADR97294
53	28	96.6	925	9	AEA21516
54	28	96.6	925	9	AEA23525
55	28	96.6	1144	2	AAW77360
56	28	96.6	1144	2	AAW51246
57	28	96.6	1144	2	AAW64500
58	28	96.6	1144	6	ABU79138
59	28	96.6	1144	7	ADF43404
60	28	96.6	1144	7	ADJ77432
61	28	96.6	1144	8	ADJ76212
62	28	96.6	1144	8	ADJ76136
63	28	96.6	1144	9	AEA03075
64	28	96.6	1443	4	ABE68472
65	27	93.1	6	2	AAW02314
66	27	93.1	6	2	AAW89378
67	27	93.1	6	4	AB48484
68	27	93.1	6	4	AB48476
69	27	93.1	6	4	AB82632
70	27	93.1	6	5	ABG71009
71	27	93.1	6	5	ABU96820
72	27	93.1	6	5	ABU96820
73	27	93.1	6	5	AB883305
74	27	93.1	6	5	AAU11658
75	27	93.1	6	5	AAU11650
76	27	93.1	6	6	AAE35445
77	27	93.1	6	6	AAE35434
78	27	93.1	6	6	ADJ64060
79	27	93.1	6	8	ADQ37271
80	27	93.1	6	8	ADQ37315
81	27	93.1	6	8	ADQ37368
82	27	93.1	6	8	ADQ37269
83	27	93.1	6	8	ADQ37292
84	27	93.1	6	8	ADQ37258
85	27	93.1	6	8	ADQ37353
86	27	93.1	6	8	ADQ37323
87	27	93.1	6	9	ADY37930
88	27	93.1	6	9	ADY37948
89	27	93.1	6	9	ADY37947
90	27	93.1	6	9	AEA23039
91	27	93.1	7	2	AAH88300
92	27	93.1	7	2	AAH87921
93	27	93.1	7	2	AAW02312
94	27	93.1	7	2	AAW89376
95	27	93.1	7	4	AAW67281
96	27	93.1	7	4	AB48475
97	27	93.1	7	4	AB48492

AAU11656	Peptide #
AAE35452	Abeta pep
ADQ37277	Vaccine a
ADQ37321	Antifibri
ADQ37329	Antifibri
ADY37928	Amyloid-t
ADY37936	Amyloid-t
ADQ09761	Rice 26kd
ADY37984	Rice 26 k
ADT93984	Mouse ind
ABO5910	Human nno
ADK34080	Human ino
ADL70727	Human sec
AG02840	Human pol
AO11219	Human prot
ADCO7962	Rice prot
ADCO7948	Rice prot
AAH83792	Human imm
ABE61977	Drosophila
ADQ66704	Novel hum
ABM83252	Human dia
ADF76335	Novel hum
ADJ70225	Human hea
ADJ75428	Marker ge
ADJ75495	Marker ge
ADN04860	Antipsori
ADR14233	Human NF-
ADR25011	PRO polyp
ADR97294	Human RIG
AEA21516	PRO polyp
AEA23525	Human PRO
AAW77360	Inducible
AAW51246	Inducible
AAW64500	Mouse ind
ABU79138	Inducible
ADF43404	INOS poly
ADJ77432	Mouse ind
ADJ76212	Marker ge
ADJ76136	Marker ge
AEA03075	VEGF amin
ABE68472	Drosophila
AAW02314	Beta-amyl
AAW89378	Beta-amyl
AB48484	Antifibri
AB48476	Antifibri
AB82632	All-D pep
ABG71009	Long form
ABU96820	Beta amyl
ABU96820	Amyloid t
AB883305	Amyloid-b
AAU11658	Peptide #
AAU11650	Peptide #
AAE35445	Abeta pep
AAE35434	Abeta pep
ADJ64060	Human bet
ADQ37271	Vaccine a
ADQ37315	Antifibri
ADQ37368	Beta-amyl
ADQ37269	Vaccine a
ADQ37292	Vaccine a
ADQ37258	Vaccine a
ADQ37353	Beta-amyl
ADQ37323	Antifibri
ADY37930	Amyloid-t
ADY37948	Amyloid-t
ADY37947	Amyloid-t
AEA23039	Human bet
AAH88300	Non-amnes
AAH87921	Test pep
AAW02312	Beta-amyl
AAW89376	Beta-amyl
AAW67281	Residues
AB48475	Antifibri
AB48492	Antifibri

98	27	93.1	7	4	AB48491	Aab48491 Antifibri	171	27	93.1	10	4	AAB46226	Aab46226 Human APP
99	27	93.1	7	4	AB82624	Aab82624 All-D pep	172	27	93.1	10	4	AAB46225	Aab46225 Human APP
100	27	93.1	7	4	AB82640	Aab82640 All-D pep	173	27	93.1	10	4	AAB46228	Aab46228 Human APP
101	27	93.1	7	4	AB82639	Aab82639 All-D pep	174	27	93.1	10	4	AAB46224	Aab46224 Human APP
102	27	93.1	7	5	AB71007	Abg71007 Long form	175	27	93.1	10	4	AB46227	Aab46227 Human APP
103	27	93.1	7	5	AB05155	Ab05155 Beta amyl	176	27	93.1	10	4	AB82641	Aab82641 All-D pep
104	27	93.1	7	5	AAU96827	Aau96827 Amyloid t	177	27	93.1	10	5	AAU96829	Aau96829 Amyloid t
105	27	93.1	7	5	AAU96812	Aau96812 Amyloid t	178	27	93.1	10	6	ABP57511	Abp57511 Different
106	27	93.1	7	5	AAU96828	Aau96828 Amyloid t	179	27	93.1	10	6	AAE35455	Aae35455 Abeta pep
107	27	93.1	7	5	AB04920	Abb04920 Human amy	180	27	93.1	10	8	ADQ37280	Adq37280 Vaccine a
108	27	93.1	7	5	AAU11665	Aau11665 Peptide #	181	27	93.1	10	8	ADQ37371	Adq37371 Amyloid-b
109	27	93.1	7	5	AAU11649	Aau11649 Peptide #	182	27	93.1	10	8	ADQ37374	Adq37374 Amyloid-b
110	27	93.1	7	5	AB82630	Abb82630 Peptide #	183	27	93.1	10	9	ADY37939	Ady37939 Amyloid-t
111	27	93.1	7	6	AB82630	Abb82630 Peptide #	184	27	93.1	11	2	AAW32560	Aaw32560 Anti-amyl
112	27	93.1	7	6	AB82630	Abb82630 Peptide #	185	27	93.1	11	4	AAW52586	Aaw52586 Peptide #
113	27	93.1	7	6	AB82630	Abb82630 Peptide #	186	27	93.1	11	5	AAU99431	Aau99431 Human amy
114	27	93.1	7	6	AB82630	Abb82630 Peptide #	187	27	93.1	11	5	AAE29504	Aae29504 Amyloid b
115	27	93.1	7	6	AB82630	Abb82630 Peptide #	188	27	93.1	11	5	ABU79013	Abu79013 Amyloidog
116	27	93.1	7	6	AB82630	Abb82630 Peptide #	189	27	93.1	11	6	ABR84683	AbR84683 Aggreca
117	27	93.1	7	7	ADD20746	Add20746 Human bet	190	27	93.1	11	7	ABW00147	Abw00147 Amyloid-b
118	27	93.1	7	7	ADF50855	Adf50855 Human cal	191	27	93.1	12	6	AAE35464	Aae35464 Abeta pep
119	27	93.1	7	7	ADP64058	Adp64058 Human bet	192	27	93.1	12	6	AAE35435	Aae35435 Abeta pep
120	27	93.1	7	8	ADP64922	Adp64922 Beta-amyl	193	27	93.1	12	6	AAE35466	Aae35466 Abeta pep
121	27	93.1	7	8	ADQ37278	Adq37278 Vaccine a	194	27	93.1	12	7	ADD20744	Add20744 Human bet
122	27	93.1	7	8	ADQ37314	Adq37314 Antifibri	195	27	93.1	12	7	ADD20744	Add20744 Human bet
123	27	93.1	7	8	ADQ37263	Adq37263 Vaccine a	196	27	93.1	12	8	ADJ71476	Adj71476 N-termina
124	27	93.1	7	8	ADQ37279	Adq37279 Vaccine a	197	27	93.1	12	8	ADQ37407	Adq37407 Amyloid-b
125	27	93.1	7	8	ADQ37330	Adq37330 Antifibri	198	27	93.1	12	8	ADQ37289	Adq37289 Vaccine a
126	27	93.1	7	8	ADQ37331	Adq37331 Antifibri	199	27	93.1	12	8	ADQ37259	Adq37259 Vaccine a
127	27	93.1	7	8	ADQ37351	Adq37351 Beta-amyl	200	27	93.1	12	9	ADZ08890	Adz08890 Human bet
128	27	93.1	7	9	ADY37922	Ady37922 Amyloid-t	201	27	93.1	12	9	ADZ08892	Adz08892 Human bet
129	27	93.1	7	9	ADY37938	Ady37938 Amyloid-t	202	27	93.1	13	6	AAE35465	Aae35465 Abeta pep
130	27	93.1	7	9	ADY37937	Ady37937 Amyloid-t	203	27	93.1	13	6	AAE35467	Aae35467 Abeta pep
131	27	93.1	7	9	ADZ08903	Adz08903 Human bet	204	27	93.1	13	6	ADA37467	Ada37467 Human amy
132	27	93.1	8	2	AAW02310	Aaw02310 Beta-amyl	205	27	93.1	13	8	ADJ71477	Adj71477 N-termina
133	27	93.1	8	2	AAW45967	Aaw45967 Peptide d	206	27	93.1	13	8	ADJ71464	Adj71464 N-termina
134	27	93.1	8	2	AAW32551	Aaw32551 Amyloidog	207	27	93.1	13	8	ADQ37408	Adq37408 Amyloid-b
135	27	93.1	8	2	AAW89374	Aaw89374 Beta-amyl	208	27	93.1	13	8	ADQ37290	Adq37290 Vaccine a
136	27	93.1	8	2	AAE10663	Aae10663 Human amy	209	27	93.1	14	6	ADA89887	Ada89887 Beta-A4 s
137	27	93.1	8	4	AAE02615	Aae02615 Human amy	210	27	93.1	14	6	ADJ71452	Adj71452 N-termina
138	27	93.1	8	5	ABG71005	Abg71005 Long form	211	27	93.1	14	8	ADJ71465	Adj71465 N-termina
139	27	93.1	8	5	ABG78624	Abg78624 Human alp	212	27	93.1	14	8	ADJ71478	Adj71478 N-termina
140	27	93.1	8	5	ABW05153	Abw05153 Beta amyl	213	27	93.1	14	9	ADZ08889	Adz08889 Human bet
141	27	93.1	8	6	ABU09765	Abu09765 Amyloidog	214	27	93.1	15	2	AAW02334	Aaw02334 Beta-amyl
142	27	93.1	8	6	ABR61959	AbR61959 Human amy	215	27	93.1	15	2	AAW89358	Aaw89358 Beta-amyl
143	27	93.1	8	7	ABW00134	Abw00134 Beta-amyl	216	27	93.1	15	2	AAW89354	Aaw89354 Beta-amyl
144	27	93.1	8	8	ADJ64056	Adj64056 Human bet	217	27	93.1	15	5	ABG71014	Abg71014 Long form
145	27	93.1	8	8	ADQ37385	Adq37385 Antifibri	218	27	93.1	15	5	ABW05162	Abw05162 Beta amyl
146	27	93.1	8	8	ADQ37349	Adq37349 Human bet	219	27	93.1	15	5	AAE26271	Aae26271 Human bet
147	27	93.1	8	9	ADZ08900	Adz08900 Human bet	220	27	93.1	15	6	ABU79057	Abu79057 Aggregati
148	27	93.1	8	9	AEA51423	Aea51423 C-Abeta 1	221	27	93.1	15	6	ABU79064	Abu79064 Aggregati
149	27	93.1	8	9	AEA51420	Aea51420 A 16-22-C	222	27	93.1	15	6	ABU79059	Abu79059 Aggregati
150	27	93.1	8	9	AEA62831	Aea62831 Immunocon	223	27	93.1	15	6	ABU79060	Abu79060 Aggregati
151	27	93.1	8	9	AEA62834	Aea62834 Immunocon	224	27	93.1	15	6	ABU79055	Abu79055 Aggregati
152	27	93.1	9	2	AAW45239	Aaw45239 Mutant am	225	27	93.1	15	6	ABU79056	Abu79056 Aggregati
153	27	93.1	9	4	AB48493	Aab48493 Antifibri	226	27	93.1	15	6	ABU79062	Abu79062 Aggregati
154	27	93.1	9	5	AAU11667	Aau11667 Peptide #	227	27	93.1	15	7	ABW00190	Abw00190 Peptide #
155	27	93.1	9	6	ABP57517	Abp57517 Different	228	27	93.1	15	7	ABW00198	Abw00198 Peptide #
156	27	93.1	9	6	ABU79063	Abu79063 Aggregati	229	27	93.1	15	7	ABW00189	Abw00189 Peptide #
157	27	93.1	9	6	AAE35436	Aae35436 Abeta pep	230	27	93.1	15	7	ABW00193	Abw00193 Peptide #
158	27	93.1	9	7	ABW00197	Abw00197 Peptide #	231	27	93.1	15	7	ABW00191	Abw00191 Peptide #
159	27	93.1	9	8	ADI36003	Adi36003 Amyloid b	232	27	93.1	15	7	ABW00196	Abw00196 Peptide #
160	27	93.1	9	8	ADI35849	Adi35849 Amyloid b	233	27	93.1	15	7	ABW00194	Abw00194 Peptide #
161	27	93.1	9	8	ADI35874	Adi35874 Amyloid b	234	27	93.1	15	7	ADK82695	Adk82695 Beta-amyl
162	27	93.1	9	8	ADI35871	Adi35871 Amyloid b	235	27	93.1	15	7	ADK82697	Adk82697 Beta-amyl
163	27	93.1	9	8	ADI35903	Adi35903 Amyloid b	236	27	93.1	15	7	ADK82700	Adk82700 Beta-amyl
164	27	93.1	9	8	ADQ37260	Adq37260 Vaccine a	237	27	93.1	15	7	ADK82698	Adk82698 Beta-amyl
165	27	93.1	9	8	ADQ37332	Adq37332 Antifibri	238	27	93.1	15	7	ADK82699	Adk82699 Beta-amyl
166	27	93.1	9	9	AEA51414	Aea51414 A 16-23-C	239	27	93.1	15	8	ADJ71466	Adj71466 N-termina
167	27	93.1	9	9	AEA51417	Aea51417 C-A 16-23	240	27	93.1	15	8	ADJ71453	Adj71453 N-termina
168	27	93.1	9	9	AEA62825	Aea62825 Immunocon	241	27	93.1	15	8	ADJ71479	Adj71479 N-termina
169	27	93.1	9	9	AEA62828	Aea62828 Immunocon	242	27	93.1	15	8	ADJ71440	Adj71440 N-termina
170	27	93.1	10	3	AA79938	Aay79938 Beta-amyl	243	27	93.1	15	8	ADJ64065	Adj64065 Human bet

244	27	93.1	16	5	AAB26330	Human bet
245	27	93.1	16	8	ADJ71454	N-termina
246	27	93.1	16	8	ADJ71480	N-termina
247	27	93.1	16	8	ADJ71441	N-termina
248	27	93.1	16	8	ADJ71467	N-termina
249	27	93.1	16	8	ADJ71428	N-termina
250	27	93.1	17	2	AAR54703	Beta-amyl
251	27	93.1	17	2	AAW18880	Beta-amyl
252	27	93.1	17	4	AAW18880	Beta-amyl
253	27	93.1	17	4	AAW18880	Beta-amyl
254	27	93.1	17	4	AAW18880	Beta-amyl
255	27	93.1	17	5	ABO4911	Human amyl
256	27	93.1	17	6	ABO4911	Beta pep
257	27	93.1	17	6	ABO4911	Beta pep
258	27	93.1	17	8	ADG93165	Novel exp
259	27	93.1	17	8	ADG93165	Novel exp
260	27	93.1	17	8	ADG93165	Novel exp
261	27	93.1	17	8	ADG93165	Novel exp
262	27	93.1	17	8	ADG93165	Novel exp
263	27	93.1	17	8	ADG93165	Novel exp
264	27	93.1	17	8	ADG93165	Novel exp
265	27	93.1	17	8	ADG93165	Novel exp
266	27	93.1	17	8	ADG93165	Novel exp
267	27	93.1	17	8	ADG93165	Novel exp
268	27	93.1	17	8	ADG93165	Novel exp
269	27	93.1	17	8	ADG93165	Novel exp
270	27	93.1	17	8	ADG93165	Novel exp
271	27	93.1	17	8	ADG93165	Novel exp
272	27	93.1	17	8	ADG93165	Novel exp
273	27	93.1	17	8	ADG93165	Novel exp
274	27	93.1	17	8	ADG93165	Novel exp
275	27	93.1	17	8	ADG93165	Novel exp
276	27	93.1	17	8	ADG93165	Novel exp
277	27	93.1	17	8	ADG93165	Novel exp
278	27	93.1	17	8	ADG93165	Novel exp
279	27	93.1	17	8	ADG93165	Novel exp
280	27	93.1	17	8	ADG93165	Novel exp
281	27	93.1	17	8	ADG93165	Novel exp
282	27	93.1	17	8	ADG93165	Novel exp
283	27	93.1	17	8	ADG93165	Novel exp
284	27	93.1	17	8	ADG93165	Novel exp
285	27	93.1	17	8	ADG93165	Novel exp
286	27	93.1	17	8	ADG93165	Novel exp
287	27	93.1	17	8	ADG93165	Novel exp
288	27	93.1	17	8	ADG93165	Novel exp
289	27	93.1	17	8	ADG93165	Novel exp
290	27	93.1	17	8	ADG93165	Novel exp
291	27	93.1	17	8	ADG93165	Novel exp
292	27	93.1	17	8	ADG93165	Novel exp
293	27	93.1	17	8	ADG93165	Novel exp
294	27	93.1	17	8	ADG93165	Novel exp
295	27	93.1	17	8	ADG93165	Novel exp
296	27	93.1	17	8	ADG93165	Novel exp
297	27	93.1	17	8	ADG93165	Novel exp
298	27	93.1	17	8	ADG93165	Novel exp
299	27	93.1	17	8	ADG93165	Novel exp
300	27	93.1	17	8	ADG93165	Novel exp

ALIGNMENTS

RESULT 1						
AAB48483						
ID	AAB48483	standard; peptide; 6 AA.				
AC	AAB48483;					
XX						
DT	02-MAR-2001	(first entry)				
XX						
DE	Antifibrillogenetic peptide #10.					
XX						
KW	Nootropic; neuroprotective; antifibrillogenetic; amyloidosis inhibition;					

KW	cytoprotection; amyloid deposit degradation; amyloidosis disorder;					
KW	Alzheimer's disease.					
XX						
OS	Homo sapiens.					
XX						
PH	Key	Location/Qualifiers				
FT	Modified-site	6				
FT		/note= "C-terminal amide"				
XX						
XX	WO200068263-A2.					
XX	16-NOV-2000.					
XX						
PF	04-MAY-2000; 2000WO-CA000515.					
XX						
XX	05-MAY-1999; 99US-0132592P.					
XX	(NEUR-) NEUROCHEM INC.					
PA	Chalifour R, Gervais F, Gupta A;					
PI	WPI; 2001-031852/04.					
XX						
XX	Antifibrillogenetic agent useful for inhibiting amyloidosis and/or for					
PT	cytoprotection for treating amyloidosis disorders, comprises a peptide,					
PT	its isomer or peptidomimetic.					
XX						
XX	Claim 7; Page 25; 46pp; English.					
XX						
CC	Peptides AAB48474-B48496 are antifibrillogenetic agents that can be used					
CC	for inhibiting amyloidosis and/or for cytoprotection. The peptides of					
CC	AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore					
CC	useful for treating amyloidosis disorders such as Alzheimer's disease.					
CC	Peptides AAB48474-B48496 were identified from the glycosaminoglycan					
CC	binding region and the prot-prot interaction region of the human amyloid					
CC	protein					
XX						
SQ	Sequence 6 AA;					
	Query Match	100.0%; Score 29; DB 4; Length 6;				
	Best Local Similarity	100.0%; Pred. No. 2e+06;				
	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 KIVFFA 6					
Db	1 KIVFFA 6					
RESULT 2						
AAB48474						
ID	AAB48474	standard; peptide; 6 AA.				
XX						
AC	AAB48474;					
XX						
DT	02-MAR-2001	(first entry)				
XX						
DE	Antifibrillogenetic peptide #1.					
XX						
KW	Nootropic; neuroprotective; antifibrillogenetic; amyloidosis inhibition;					
KW	cytoprotection; amyloid deposit degradation; amyloidosis disorder;					
KW	Alzheimer's disease.					
XX						
OS	Homo sapiens.					
XX						
PN	WO200068263-A2.					
XX						
PD	16-NOV-2000.					
XX						
PF	04-MAY-2000; 2000WO-CA000515.					
XX						
PR	05-MAY-1999; 99US-0132592P.					
XX						
PA	(NEUR-) NEUROCHEM INC.					

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 1 KIVFFPA 6
 RESULT 3
 ID AAB82623
 AC AAB82623;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1. 6
 FT /note= "all D-form residues"
 FT
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 10; 31pp; English.
 XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 1 KIVFFPA 6
 RESULT 4
 ID AAB82631
 AC AAB82631 standard; peptide; 6 AA.
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1. 6
 FT /note= "all D-form residues"
 FT Modified-site 6
 FT /note= "C-terminal amide"
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 XX associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), Familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |||||
 Db 1 KIVFFPA 6

RESULT 5

AAU96819
 ID AAU96819 standard; peptide; 6 AA.

XX

AC AAU96819;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #9.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

PH Key Difference 1..6 /note= "Preferably D-form residue"

FT Modified-site 6 /note= "Ala is amidated"

FT WO200207781-A2.

XX 31-JAN-2002.

XX

XX

PF 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

PI WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid

XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an

XX amyloid targeting moiety, a linker moiety and a labelling moiety. The

XX agent is of general formula A-t-(A₁n₁k₁)z-A₁l₁a₁b₁ (I) where z = 0 - 1;

XX A₁t = an amyloid targeting moiety; A₁l₁n₁k₁ = a linker moiety; and A₁l₁a₁b₁

XX = a labelling moiety. Also included are imaging amyloid deposition or

XX diagnosing an amyloid-related condition in a patient involving

XX administering (I) to the patient, and ultrasound imaging (I) in the

XX patient to determine the presence of amyloid or amyloid-related condition

XX; and a kit for preparing a radiopharmaceutical preparation comprising

XX (I), a reducing agent, a buffering agent, a transchelating agent, and

XX instructions for the preparation and use of the radiopharmaceutical in

XX the imaging of amyloid or an amyloid-related condition. The agents are

XX used for imaging amyloid deposition and for diagnosing an amyloid related

XX condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible

XX cerebral amyloidosis (transmissible virus dementia), familial CJD,

XX scrapie, transmissible mink encephalopathy, bovine spongiform

XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,

XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible

XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,

XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral

XX amyloid angiopathy. The agents are capable of crossing the blood-brain

XX barrier and are capable of binding specifically to amyloid plaques. The

XX present sequence is a peptide forming the amyloid targeting moiety of the

XX agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |||||

Db 1 KIVFFPA 6

RESULT 6

AAU96811

ID AAU96811 standard; peptide; 6 AA.

XX

AC AAU96811;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #1.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;

XX transmissible cerebral amyloidosis; transmissible virus dementia;

XX scrapie; transmissible mink encephalopathy; BSE; type II diabetes;

XX bovine spongiform encephalopathy; inflammation associated amyloid;

XX primary amyloidosis; feline spongiform encephalopathy;

XX Alzheimer's disease; prion-mediated disease; blood-brain barrier;

XX dialysis-related amyloidosis; light chain-related amyloidosis;

XX cerebral amyloid angiopathy.

XX Synthetic.

```

FH Key                               Location/Qualifiers
FT Misc-difference 1..6
FT                                     /note= "Preferably D-form residue"
XX
XX
XX WO200207781-A2.
XX 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
XX 24-JUL-2001; 2001US-00915032.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A_t-(A_1)_n_k)-z-A_1_a_b (I) where z = 0 - 1;
XX A_t = an amyloid targeting moiety; A_1_n_k) = a linker moiety; and A_1_a_b
XX = a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (I) to the patient, and ultrasound imaging (I) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX; and a kit for preparing a radiopharmaceutical preparation comprising
XX (I), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidosis (transmissible virus dementias), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
XX Sequence 6 AA;
XX
XX Query Match          100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy      1 KIVFFPA 6
XX        |||||
XX Db      1 KIVFFPA 6
XX
XX RESULT 7
XX AAU11657
XX ID AAU11657 standard; peptide; 6 AA.
XX
XX AC AAU11657;
XX
XX 09-APR-2002 (first entry)
XX
XX Peptide #10, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nootropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX Synthetic.
XX
XX WO200185093-A2.
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX
XX Sequence 6 AA;
XX
XX Query Match          100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy      1 KIVFFPA 6
XX        |||||
XX Db      1 KIVFFPA 6
XX
XX RESULT 8
XX AAU11648
XX ID AAU11648 standard; peptide; 6 AA.
XX
XX AC AAU11648;
XX
XX 09-APR-2002 (first entry)
XX
XX Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nootropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX Synthetic.
XX
XX WO200185093-A2.
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.

```

```

XX PA (NEUR-) NEUROCHEM INC.
XX PI Green AM, Gervais F;
XX PT WPI; 2002-075222/10.
XX DR
XX PS Disclosure; Page 10; 68pp; English.
XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX PT inhibitor.
XX PS
XX PT The present invention relates to a new method of inhibiting cerebral
XX PT amyloid angiopathy. The new method of the invention involves contacting a
XX PT blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX PT can be used for treating disease states characterised by cerebral amyloid
XX PT angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX PT haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX PT The present sequence represents one of a group of peptides (AAU11648-
XX PT AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX PT carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX PT was used in the invention to treat a disease state characterised by
XX PT cerebral amyloid angiopathy (CAA)
XX PS
XX PT Sequence 6 AA;
XX SQ
XX Query Match 100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KIVFFA 6
XX Db |||||
XX 1 KIVFFA 6
XX
XX RESULT 9
XX AAE35446
XX ID AAE35446 standard; peptide; 6 AA.
XX AC AAE35446;
XX XX
XX DT 17-JUN-2003 (first entry)
XX DE
XX DE Abeta peptide #17.
XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
XX KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
XX KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
XX KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
XX KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
XX KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
XX KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX OS Unidentified.
XX XX
XX XX Key Location/Qualifiers
XX FH Misc-difference 1..6
XX FT Modified-site 6 /note= "D-form residues"
XX FT /note= "C-terminal amide"
XX FT
XX PN WO200296937-A2.
XX XX
XX PD 05-DEC-2002.
XX XX
XX PF 29-MAY-2002; 2002WO-CA000763.
XX XX
XX PR 29-MAY-2001; 2001US-00867847.
XX XX
XX PA (NEUR-) NEUROCHEM INC.
XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

```

```

XX DR WPI; 2003-201269/19.
XX PT Prevention and/or treatment of an amyloid-related disease e.g.
XX PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
XX PS
XX PS Claim 1; Page 59; 44pp; English.
XX XX
XX CC The invention relates to a method for prevention and/or treatment of an
XX CC amyloid-related disease which comprises administration of an all-D -
XX CC amyloid-beta peptide. The method is used for preventing and/or treating
XX CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
XX CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
XX CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
XX CC the mammal; and reducing or inhibiting the formation of plaques. It is
XX CC also used for treating AA (reactive) amyloid diseases including
XX CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
XX CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
XX CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
XX CC disease. AA deposits are also produced as a result of chronic microbial
XX CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
XX CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
XX CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
XX CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
XX CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
XX CC present sequence is an Abeta peptide used to illustrate the method of the
XX CC invention
XX SQ
XX Sequence 6 AA;
XX Query Match 100.0%; Score 29; DB 6; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KIVFFA 6
XX Db |||||
XX 1 KIVFFA 6
XX
XX RESULT 10
XX AAE35438
XX ID AAE35438 standard; peptide; 6 AA.
XX AC AAE35438;
XX XX
XX DT 17-JUN-2003 (first entry)
XX DE
XX DE Abeta peptide #9.
XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
XX KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
XX KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
XX KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
XX KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
XX KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
XX KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX OS Unidentified.
XX XX
XX XX Key Location/Qualifiers
XX FH Misc-difference 1..6
XX FT /note= "D-form residues"
XX FT
XX PN WO200296937-A2.
XX XX
XX PD 05-DEC-2002.
XX XX
XX PF 29-MAY-2002; 2002WO-CA000763.
XX XX
XX PR 29-MAY-2001; 2001US-00867847.
XX XX
XX PA (NEUR-) NEUROCHEM INC.
XX PI

```

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 58; 44pp; English.
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D-
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Rechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 XX invention
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 1 KIVFFA 6
 RESULT 11
 ADQ37322
 ID ADQ37322 standard; peptide; 6 AA.
 XX AC ADQ37322;
 XX 07-OCT-2004 (first entry)
 XX Antifibrillogenic amyloidosis inhibiting peptide.
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 XX Modified-site 6
 XX /note= "amidated"
 XX WO2004058239-A1.

XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 69; 143pp; English.
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 1 KIVFFA 6
 RESULT 12
 ADQ37270
 ID ADQ37270 standard; peptide; 6 AA.

XX ADQ37270;
 XX 07-OCT-2004 (first entry)
 XX Vaccine antigen amyloid-beta related amino acid sequence.
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..6
 FT /note= "D-form residues"
 FT Modified-site 6
 FT /note= "amidated"
 XX
 XX WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 PS
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic, tranquilliser,
 CC ophthalmological, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 DB 1 KIVFFA 6

RESULT 13
 ADQ37313
 ID ADQ37313 standard; peptide; 6 AA.
 XX AC ADQ37313;
 XX 07-OCT-2004 (first entry)
 XX Antifibrillogenic amyloidosis inhibiting peptide.

amyloid-beta; amyloid-beta related disease;
 amyloid-beta fibril formation; immune response; neurotropic;
 neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 cardiant; antidepressant; endocrine; hypnotic;
 amyloid-beta fibril formation modulator; immune system modulator;
 Alzheimer's disease; mild cognitive impairment;
 mild-to-moderate cognitive impairment; vascular dementia;
 cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 senile dementia; Down's syndrome; inclusion body myositis;
 age-related macular degeneration; hypothyroidism;
 cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 behavioural dysfunction; neurological condition; psychological condition;
 vaccine antigen.

Synthetic.

WO2004058239-A1.

15-JUL-2004.

24-DEC-2003; 2003WO-CA002021.

24-DEC-2002; 2002US-0436379P.

23-JUN-2003; 2003US-0482214P.

(NEUR-) NEUROCHEM INT LTD.

Gervais F, Bellini F;

WPI; 2004-543342/52.

Composition for treating e.g. Alzheimer's disease comprises first agent

PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 69; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a behavioural condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |||||

Db 1 KIVFFA 6

RESULT 14

ADQ37262

ID ADQ37262 standard; peptide; 6 AA.

AC ADQ37262;

DT 07-OCT-2004 (first entry)

XX Vaccine antigen amyloid-beta related amino acid sequence.

DE amyloid-beta; amyloid-beta related disease;

XX amyloid-beta fibril formation; immune response; neurotropic;

KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;

KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

KW cardiac; antidepressant; endocrine; hypnotic;

KW amyloid-beta fibril formation modulator; immune system modulator;

KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 1. .6
 FT /note= "D-form residues"

XX WO2004058239-A1.

XX 15-JUN-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 XX that prevents or treats amyloid-beta related disease and second agent
 XX that is either a peptide or peptidomimetic or an immune system modulator.
 PS Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a behavioural condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfilee1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	2	US-09-747-408-4
2	31	100.0	6	2	US-09-747-408-12
3	30	96.8	1283	2	US-09-248-796A-18091
4	28	90.3	490	2	US-08-888-998-2
5	28	90.3	506	2	US-09-362-633-2
6	28	90.3	506	2	US-09-877-476-2
7	28	90.3	506	2	US-09-877-476-28
8	28	90.3	506	2	US-09-877-476-30
9	28	90.3	506	2	US-09-877-476-36
10	28	90.3	506	2	US-09-830-230A-437
11	28	90.3	508	2	US-09-248-796A-26311
12	27	87.1	67	2	US-09-513-999C-4859
13	27	87.1	82	2	US-09-270-767-40694
14	27	87.1	98	2	US-09-270-767-55910
15	27	87.1	98	2	US-09-823-153-4
16	27	87.1	104	2	US-09-270-767-57813
17	27	87.1	116	2	US-09-902-540-10859
18	27	87.1	238	2	US-09-134-001C-5445
19	27	87.1	240	2	US-09-270-767-42516
20	27	87.1	266	2	US-09-248-796A-19539
21	27	87.1	320	2	US-09-270-767-40453
22	27	87.1	340	2	US-09-270-767-55669
23	27	87.1	340	2	US-09-270-767-45548
24	27	87.1	425	2	US-09-270-767-34763
25	27	87.1	475	2	US-09-270-767-49980
26	27	87.1	525	2	US-08-704-711A-1
27	27	87.1	579	2	US-09-747-408-1

28	87.1	579	2	US-09-521-220-1	Sequence 1, Appli
29	87.1	582	2	US-08-704-711A-2	Sequence 2, Appli
30	87.1	582	2	US-08-448-483-1	Sequence 1, Appli
31	87.1	582	2	US-09-211-704A-9	Sequence 9, Appli
32	87.1	582	2	US-09-521-220-2	Sequence 2, Appli
33	87.1	582	2	US-09-391-104-28	Sequence 28, Appli
34	87.1	582	2	US-09-919-497-84	Sequence 84, Appli
35	87.1	582	2	US-09-689-730-1	Sequence 1, Appli
36	87.1	1024	2	US-10-449-315-2	Sequence 2, Appli
37	87.1	1204	2	US-10-449-315-5	Sequence 5, Appli
38	83.9	45	2	US-09-270-767-37091	Sequence 37091, A
39	83.9	45	2	US-09-270-767-52308	Sequence 52308, A
40	83.9	46	2	US-09-798-635A-41	Sequence 41, Appli
41	83.9	60	2	US-10-125-258-44	Sequence 44, Appli
42	83.9	61	2	US-09-583-110-4885	Sequence 4885, Ap
43	83.9	65	2	US-10-125-258-43	Sequence 43, Appli
44	83.9	84	2	US-09-270-767-60733	Sequence 60733, A
45	83.9	104	2	US-09-621-976-6739	Sequence 6739, Ap
46	83.9	111	2	US-09-205-258-303	Sequence 303, App
47	83.9	111	2	US-10-004-860-303	Sequence 303, App
48	83.9	118	2	US-09-627-376-17	Sequence 17, Appli
49	83.9	118	2	US-10-047-676B-17	Sequence 17, Appli
50	83.9	156	2	US-09-270-767-45241	Sequence 45241, A
51	83.9	177	2	US-09-270-767-35390	Sequence 35390, A
52	83.9	177	2	US-09-270-767-50607	Sequence 50607, A
53	83.9	186	2	US-09-251-645-4	Sequence 4, Appli
54	83.9	201	2	US-09-270-767-33463	Sequence 33463, A
55	83.9	201	2	US-09-270-767-48680	Sequence 48680, A
56	83.9	249	2	US-09-270-767-38186	Sequence 38186, A
57	83.9	249	2	US-09-270-767-53403	Sequence 53403, A
58	83.9	249	2	US-09-248-796A-27128	Sequence 27128, A
59	83.9	310	2	US-09-830-910-2	Sequence 2, Appli
60	83.9	328	2	US-09-248-796A-15301	Sequence 15301, A
61	83.9	394	2	US-09-270-767-41366	Sequence 41366, A
62	83.9	394	2	US-09-270-767-56582	Sequence 56582, A
63	83.9	402	2	US-09-252-991A-25289	Sequence 25289, A
64	83.9	414	2	US-09-902-540-11308	Sequence 11308, A
65	83.9	426	2	US-09-602-787A-424	Sequence 424, App
66	83.9	437	2	US-09-489-039A-8958	Sequence 8958, Ap
67	83.9	446	2	US-09-252-991A-17185	Sequence 17185, A
68	83.9	453	2	US-09-489-039A-8303	Sequence 8303, Ap
69	83.9	493	2	US-09-252-991A-28992	Sequence 28992, A
70	83.9	557	2	US-09-540-236-2206	Sequence 2206, Ap
71	83.9	573	2	US-09-489-039A-11884	Sequence 11884, A
72	83.9	597	2	US-09-252-991A-22560	Sequence 22560, A
73	83.9	745	2	US-09-902-540-10375	Sequence 10275, A
74	83.9	892	2	US-09-540-236-2074	Sequence 2074, Ap
75	80.6	6	1	US-08-612-785B-9	Sequence 9, Appli
76	80.6	6	2	US-08-703-675C-32	Sequence 32, Appli
77	80.6	6	2	US-08-617-267C-9	Sequence 9, Appli
78	80.6	6	2	US-09-747-408-1	Sequence 1, Appli
79	80.6	6	2	US-09-747-408-3	Sequence 3, Appli
80	80.6	6	2	US-09-747-408-10	Sequence 10, Appli
81	80.6	6	2	US-09-747-408-11	Sequence 11, Appli
82	80.6	7	1	US-08-127-904-14	Sequence 14, Appli
83	80.6	7	1	US-08-612-785B-7	Sequence 7, Appli
84	80.6	7	2	US-08-703-675C-30	Sequence 30, Appli
85	80.6	7	2	US-08-617-267C-7	Sequence 7, Appli
86	80.6	7	2	US-09-264-709A-13	Sequence 13, Appli
87	80.6	7	2	US-09-747-408-2	Sequence 2, Appli
88	80.6	7	2	US-09-747-408-18	Sequence 18, Appli
89	80.6	7	2	US-09-747-408-19	Sequence 19, Appli
90	80.6	7	4	PCT-US94-10475-14	Sequence 14, Appli
91	80.6	8	1	US-08-612-785B-5	Sequence 5, Appli
92	80.6	8	1	US-08-630-645-1	Sequence 1, Appli
93	80.6	8	2	US-08-703-675C-28	Sequence 28, Appli
94	80.6	8	2	US-08-617-267C-5	Sequence 5, Appli
95	80.6	8	2	US-09-095-106A-44	Sequence 44, Appli
96	80.6	8	2	US-08-766-596A-1	Sequence 1, Appli
97	80.6	8	4	US-09-668-314C-73	Sequence 73, Appli
98	80.6	8	4	PCT-US96-10220-1	Sequence 1, Appli
99	80.6	9	2	US-08-766-596A-64	Sequence 64, Appli
100	80.6	9	2	US-09-747-408-20	Sequence 20, Appli

101	25	80.6	10	2	US-08-970-833-3	Sequence 3, Appli	174	25	80.6	28	1	US-08-293-284A-4	Sequence 4, Appli
102	25	80.6	10	2	US-09-724-961-20	Sequence 20, Appli	175	25	80.6	28	1	US-08-461-216-2	Sequence 2, Appli
103	25	80.6	10	2	US-09-724-961-21	Sequence 21, Appli	176	25	80.6	28	2	US-09-388-890-2	Sequence 2, Appli
104	25	80.6	10	2	US-09-724-961-22	Sequence 22, Appli	177	25	80.6	28	2	US-09-388-890-3	Sequence 3, Appli
105	25	80.6	10	2	US-09-724-961-23	Sequence 23, Appli	178	25	80.6	28	2	US-09-388-890-4	Sequence 4, Appli
106	25	80.6	10	2	US-09-724-961-24	Sequence 24, Appli	179	25	80.6	28	2	US-09-388-890-5	Sequence 5, Appli
107	25	80.6	10	2	US-09-580-018-20	Sequence 20, Appli	180	25	80.6	28	2	US-09-388-890-6	Sequence 6, Appli
108	25	80.6	10	2	US-09-580-018-21	Sequence 21, Appli	181	25	80.6	28	2	US-09-388-890-7	Sequence 7, Appli
109	25	80.6	10	2	US-09-580-018-22	Sequence 22, Appli	182	25	80.6	28	2	US-09-388-890-8	Sequence 8, Appli
110	25	80.6	10	2	US-09-580-018-23	Sequence 23, Appli	183	25	80.6	28	2	US-09-388-890-9	Sequence 9, Appli
111	25	80.6	10	2	US-09-580-018-24	Sequence 24, Appli	184	25	80.6	28	2	US-09-388-890-10	Sequence 10, Appli
112	25	80.6	10	2	US-09-724-551-20	Sequence 20, Appli	185	25	80.6	28	2	US-09-388-890-12	Sequence 12, Appli
113	25	80.6	10	2	US-09-724-551-21	Sequence 21, Appli	186	25	80.6	28	2	US-09-388-890-13	Sequence 13, Appli
114	25	80.6	10	2	US-09-724-551-22	Sequence 22, Appli	187	25	80.6	28	2	US-09-388-890-14	Sequence 14, Appli
115	25	80.6	10	2	US-09-724-551-23	Sequence 23, Appli	188	25	80.6	28	2	US-09-264-709A-1	Sequence 1, Appli
116	25	80.6	10	2	US-09-724-551-24	Sequence 24, Appli	189	25	80.6	28	2	US-08-723-661B-2	Sequence 2, Appli
117	25	80.6	10	2	US-09-724-940-20	Sequence 20, Appli	190	25	80.6	28	2	US-09-660-954-2	Sequence 2, Appli
118	25	80.6	10	2	US-09-724-940-21	Sequence 21, Appli	191	25	80.6	28	2	US-09-660-954-3	Sequence 3, Appli
119	25	80.6	10	2	US-09-724-940-22	Sequence 22, Appli	192	25	80.6	28	2	US-09-660-954-4	Sequence 4, Appli
120	25	80.6	10	2	US-09-724-940-23	Sequence 23, Appli	193	25	80.6	28	2	US-09-660-954-5	Sequence 5, Appli
121	25	80.6	10	2	US-09-724-940-24	Sequence 24, Appli	194	25	80.6	28	2	US-09-660-954-6	Sequence 6, Appli
122	25	80.6	11	1	US-08-630-645-14	Sequence 14, Appli	195	25	80.6	28	2	US-09-660-954-7	Sequence 7, Appli
123	25	80.6	11	2	US-08-766-596A-14	Sequence 14, Appli	196	25	80.6	28	2	US-09-660-954-8	Sequence 8, Appli
124	25	80.6	11	2	US-09-988-842-9	Sequence 9, Appli	197	25	80.6	28	2	US-09-660-954-9	Sequence 9, Appli
126	25	80.6	11	2	US-09-988-842-25	Sequence 25, Appli	198	25	80.6	28	2	US-09-660-954-10	Sequence 10, Appli
127	25	80.6	11	4	PCT-US96-10220-14	Sequence 14, Appli	199	25	80.6	28	2	US-09-660-954-12	Sequence 12, Appli
128	25	80.6	14	2	US-09-594-366-5	Sequence 5, Appli	200	25	80.6	28	2	US-09-660-954-13	Sequence 13, Appli
129	25	80.6	15	1	US-09-992-800-5	Sequence 5, Appli	201	25	80.6	28	2	US-09-660-954-14	Sequence 14, Appli
130	25	80.6	15	1	US-08-612-785B-14	Sequence 14, Appli	202	25	80.6	28	2	US-08-898-300-4	Sequence 4, Appli
131	25	80.6	15	1	US-08-612-785B-37	Sequence 37, Appli	203	25	80.6	28	2	US-08-824-513-4	Sequence 4, Appli
132	25	80.6	15	2	US-08-617-267C-14	Sequence 14, Appli	204	25	80.6	28	2	US-09-623-548A-959	Sequence 959, App
133	25	80.6	15	2	US-08-766-596A-56	Sequence 56, Appli	205	25	80.6	28	2	US-09-623-548A-965	Sequence 965, App
134	25	80.6	15	2	US-08-766-596A-57	Sequence 57, Appli	206	25	80.6	28	2	US-09-623-548A-976	Sequence 976, App
135	25	80.6	15	2	US-08-766-596A-58	Sequence 58, Appli	207	25	80.6	28	2	US-09-623-548A-992	Sequence 992, App
136	25	80.6	15	2	US-08-766-596A-60	Sequence 60, Appli	208	25	80.6	28	2	US-09-623-548A-1003	Sequence 1003, Ap
137	25	80.6	15	2	US-08-766-596A-61	Sequence 61, Appli	209	25	80.6	28	2	US-09-657-276-959	Sequence 959, App
138	25	80.6	15	2	US-08-766-596A-63	Sequence 63, Appli	210	25	80.6	28	2	US-09-657-276-965	Sequence 965, App
139	25	80.6	15	2	US-08-766-596A-65	Sequence 65, Appli	211	25	80.6	28	2	US-09-657-276-976	Sequence 976, App
140	25	80.6	17	2	US-09-264-709A-2	Sequence 2, Appli	212	25	80.6	28	2	US-09-657-276-992	Sequence 992, App
141	25	80.6	17	2	US-09-594-366-3	Sequence 3, Appli	213	25	80.6	28	2	US-09-657-276-1003	Sequence 1003, Ap
142	25	80.6	17	2	US-09-623-548A-950	Sequence 950, App	214	25	80.6	28	2	US-09-865-294A-66	Sequence 66, Appli
143	25	80.6	17	2	US-09-623-548A-983	Sequence 983, App	215	25	80.6	30	1	US-08-609-090-3	Sequence 3, Appli
144	25	80.6	17	2	US-09-992-800-3	Sequence 3, Appli	216	25	80.6	30	1	US-08-609-090-4	Sequence 4, Appli
145	25	80.6	17	2	US-09-657-276-950	Sequence 950, App	217	25	80.6	33	1	US-08-609-090-4	Sequence 4, Appli
146	25	80.6	19	2	US-09-657-276-983	Sequence 983, App	218	25	80.6	33	1	US-08-475-579A-4	Sequence 4, Appli
147	25	80.6	19	2	US-09-723-384-5	Sequence 11, Appli	219	25	80.6	35	1	US-08-304-585-6	Sequence 6, Appli
148	25	80.6	19	2	US-09-723-384-5	Sequence 5, Appli	220	25	80.6	35	1	US-08-612-785B-16	Sequence 16, Appli
149	25	80.6	19	2	US-09-724-961-75	Sequence 75, Appli	221	25	80.6	35	1	US-08-612-785B-36	Sequence 36, Appli
150	25	80.6	19	2	US-09-724-552-5	Sequence 5, Appli	222	25	80.6	35	1	US-08-612-785B-38	Sequence 38, Appli
151	25	80.6	19	2	US-09-580-018-75	Sequence 75, Appli	223	25	80.6	35	1	US-08-612-785B-40	Sequence 40, Appli
152	25	80.6	19	2	US-09-723-927-5	Sequence 5, Appli	224	25	80.6	35	2	US-08-617-267C-16	Sequence 16, Appli
153	25	80.6	19	2	US-09-724-477-5	Sequence 5, Appli	225	25	80.6	35	2	US-09-623-548A-979	Sequence 979, App
154	25	80.6	19	2	US-09-723-762-5	Sequence 5, Appli	226	25	80.6	35	2	US-09-623-548A-1006	Sequence 1006, Ap
155	25	80.6	19	2	US-09-201-430-5	Sequence 5, Appli	227	25	80.6	35	2	US-09-657-276-979	Sequence 979, App
156	25	80.6	19	2	US-09-724-551-75	Sequence 75, Appli	228	25	80.6	35	2	US-09-657-276-1006	Sequence 1006, Ap
157	25	80.6	19	2	US-10-815-353-5	Sequence 5, Appli	229	25	80.6	36	1	US-08-609-090-6	Sequence 6, Appli
158	25	80.6	19	2	US-10-816-529-5	Sequence 5, Appli	230	25	80.6	36	1	US-09-861-847A-6	Sequence 6, Appli
159	25	80.6	19	2	US-10-815-391-5	Sequence 5, Appli	231	25	80.6	36	2	US-09-861-847A-11	Sequence 11, Appli
160	25	80.6	19	2	US-10-816-022-5	Sequence 5, Appli	232	25	80.6	38	1	US-08-302-808-1	Sequence 1, Appli
161	25	80.6	19	2	US-09-724-940-75	Sequence 75, Appli	233	25	80.6	38	1	US-07-737-371E-68	Sequence 68, Appli
162	25	80.6	19	2	US-10-934-609-5	Sequence 5, Appli	234	25	80.6	38	1	US-08-986-948-1	Sequence 1, Appli
163	25	80.6	19	2	US-08-894-892-5	Sequence 5, Appli	235	25	80.6	38	2	US-09-623-548A-975	Sequence 975, App
164	25	80.6	20	2	US-08-970-833-10	Sequence 10, Appli	236	25	80.6	38	2	US-09-623-548A-1002	Sequence 1002, Ap
165	25	80.6	20	2	US-09-724-953-33	Sequence 33, Appli	237	25	80.6	38	2	US-09-657-276-975	Sequence 975, App
166	25	80.6	20	2	US-09-724-567-33	Sequence 33, Appli	238	25	80.6	38	2	US-09-657-276-1002	Sequence 1002, Ap
167	25	80.6	20	2	US-09-979-952-33	Sequence 33, Appli	239	25	80.6	39	1	US-08-304-585-5	Sequence 5, Appli
168	25	80.6	20	2	US-09-585-817-33	Sequence 33, Appli	240	25	80.6	39	1	US-08-302-808-2	Sequence 2, Appli
169	25	80.6	26	1	US-08-304-585-7	Sequence 7, Appli	241	25	80.6	39	1	US-08-609-090-7	Sequence 7, Appli
170	25	80.6	28	1	US-08-346-849-4	Sequence 4, Appli	242	25	80.6	39	1	US-08-682-245A-1	Sequence 1, Appli
171	25	80.6	28	1	US-08-302-808-7	Sequence 7, Appli	243	25	80.6	39	1	US-08-986-948-2	Sequence 2, Appli
172	25	80.6	28	1	US-08-609-090-2	Sequence 2, Appli	244	25	80.6	40	1	US-07-744-767A-1	Sequence 1, Appli
173	25	80.6	28	1	US-08-586-948-7	Sequence 7, Appli	245	25	80.6	40	1	US-08-235-400-2	Sequence 2, Appli
							246	25	80.6	40	1	US-08-476-464A-2	Sequence 2, Appli


```
247 25 80.6 40 1 US-08-304-585-1 Sequence 1, Appli
248 25 80.6 40 1 US-08-304-585-8 Sequence 8, Appli
249 25 80.6 40 1 US-08-302-808-3 Sequence 3, Appli
250 25 80.6 40 1 US-08-433-734-1 Sequence 1, Appli
251 25 80.6 40 1 US-08-609-090-8 Sequence 8, Appli
252 25 80.6 40 1 US-07-737-371B-69 Sequence 69, Appli
253 25 80.6 40 1 US-08-682-245A-2 Sequence 2, Appli
254 25 80.6 40 1 US-08-986-948-3 Sequence 3, Appli
255 25 80.6 40 1 US-08-461-216-1 Sequence 1, Appli
256 25 80.6 40 2 US-08-959-148-1 Sequence 1, Appli
257 25 80.6 40 2 US-09-242-724-22 Sequence 22, Appli
258 25 80.6 40 2 US-08-723-661B-1 Sequence 1, Appli
259 25 80.6 40 2 US-09-062-365-3 Sequence 3, Appli
260 25 80.6 40 2 US-09-133-866-1 Sequence 1, Appli
261 25 80.6 40 2 US-09-861-847A-7 Sequence 7, Appli
262 25 80.6 40 2 US-09-861-847A-8 Sequence 8, Appli
263 25 80.6 40 2 US-09-988-842-3 Sequence 3, Appli
264 25 80.6 40 2 US-10-455-218-1 Sequence 1, Appli
265 25 80.6 40 2 US-10-151-614-1 Sequence 1, Appli
266 25 80.6 40 2 US-09-623-548A-956 Sequence 956, App
267 25 80.6 40 2 US-09-623-548A-962 Sequence 962, App
268 25 80.6 40 2 US-09-623-548A-968 Sequence 968, App
269 25 80.6 40 2 US-09-623-548A-978 Sequence 978, App
270 25 80.6 40 2 US-09-623-548A-989 Sequence 989, App
271 25 80.6 40 2 US-09-623-548A-995 Sequence 995, App
272 25 80.6 40 2 US-09-623-548A-1005 Sequence 1005, Ap
273 25 80.6 40 2 US-09-657-276-956 Sequence 956, App
274 25 80.6 40 2 US-09-657-276-962 Sequence 962, App
275 25 80.6 40 2 US-09-657-276-968 Sequence 968, App
276 25 80.6 40 2 US-09-657-276-978 Sequence 978, App
277 25 80.6 40 2 US-09-657-276-989 Sequence 989, App
278 25 80.6 40 2 US-09-657-276-995 Sequence 995, App
279 25 80.6 40 2 US-09-657-276-1005 Sequence 1005, App
280 25 80.6 40 4 PCT-US92-06700-1 Sequence 1, Appli
281 25 80.6 41 1 US-07-819-361-1 Sequence 1, Appli
282 25 80.6 41 1 US-08-302-808-4 Sequence 4, Appli
283 25 80.6 41 1 US-08-682-245A-3 Sequence 3, Appli
284 25 80.6 41 1 US-08-986-948-4 Sequence 4, Appli
285 25 80.6 41 1 US-08-986-948-4 Sequence 4, Appli
286 25 80.6 42 1 US-07-744-767A-2 Sequence 2, Appli
287 25 80.6 42 1 US-08-179-574-1 Sequence 1, Appli
288 25 80.6 42 1 US-08-271-162-5 Sequence 5, Appli
289 25 80.6 42 1 US-08-347-144-1 Sequence 1, Appli
290 25 80.6 42 1 US-08-462-859A-19 Sequence 19, Appli
291 25 80.6 42 1 US-08-123-659A-19 Sequence 19, Appli
292 25 80.6 42 1 US-08-464-247A-19 Sequence 19, Appli
293 25 80.6 42 1 US-08-464-248A-19 Sequence 19, Appli
294 25 80.6 42 1 US-08-476-464A-1 Sequence 1, Appli
295 25 80.6 42 1 US-08-304-585-2 Sequence 2, Appli
296 25 80.6 42 1 US-08-302-808-5 Sequence 5, Appli
297 25 80.6 42 1 US-08-268-348A-1 Sequence 1, Appli
298 25 80.6 42 1 US-08-268-348A-2 Sequence 2, Appli
299 25 80.6 42 1 US-08-268-348A-3 Sequence 3, Appli
300 25 80.6 42 1 US-08-268-348A-4 Sequence 4, Appli
```

ALIGNMENTS

```
RESULT 1
US-09-747-408-4
; Sequence 4, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
```

```
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4

Query Match          100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
        |||||
DB      1 KVFVFA 6
```

RESULT 2

```
US-09-747-408-12
; Sequence 12, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12
```

```
Query Match          100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
        |||||
DB      1 KVFVFA 6
```

RESULT 3

```
US-09-248-796A-18091
; Sequence 18091, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18091
; LENGTH: 1283
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18091
```

```
Query Match          96.8%; Score 30; DB 2; Length 1283;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
      ||:||||
Db      259 KFIFFA 264

RESULT 4
US-09-830-230A-438
; Sequence 438, Application US/09830230A
; Patent No. 6902893
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481US
; CURRENT APPLICATION NUMBER: US/09/830,230A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 438
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-230A-438

Query Match      90.3%; Score 28; DB 2; Length 490;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      ||:||||
Db      23 RVVFFA 28

RESULT 5
US-09-888-998-2
; Sequence 2, Application US/08888998
; Patent No. 6124524
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAE1 GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US 08/888,998
; APPLICATION NUMBER: US 08/329,603
; FILING DATE: 26-OCT-1994

QY      1 KVFVFA 6
      ||:||||
Db      356 KFLFFA 361

Query Match      90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      ||:||||
Db      356 KFLFFA 361

RESULT 6
US-09-362-633-2
; Sequence 2, Application US/09362633
; Patent No. 6184355
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAE1 GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,633
; FILING DATE:
; APPLICATION NUMBER: 08/888,998
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
```

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..506

; OTHER INFORMATION: /note= "Amino acid sequence of FAE1

; OTHER INFORMATION: protein."

; US-09-362-633-2

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

||:||||

Db 356 KFLFFA 361

RESULT 7

US-09-877-476-2

; Sequence 2, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; PRIOR FILING DATE: 2000-06-08

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; US-09-877-476-2

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

||:||||

Db 356 KFLFFA 361

RESULT 8

US-09-877-476-28

; Sequence 28, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ

; OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana

; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176

; US-09-877-476-28

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

||:||||

Db 356 KFLFFA 361

RESULT 9

US-09-877-476-30

; Sequence 30, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; PRIOR FILING DATE: 2000-06-08

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 5' 399 amino acids from A. thaliana FAE1 (SEQ ID

; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus

; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399

; NAME/KEY: VARIANT

; LOCATION: (0)...(0)

; OTHER INFORMATION: Xaa = Pro or Gln

; US-09-877-476-30

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

||:||||

Db 356 KFLFFA 361

RESULT 10

US-09-877-476-36

; Sequence 36, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 36

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 506 amino acids from A. thaliana FAE1 (SEQ ID

; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated

; OTHER INFORMATION: At K92R; hypothetical

; US-09-877-476-36

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 6
||:|:|
Db 356 KFLFPA 361

RESULT 11
US-09-830-230A-437
; Sequence 437, Application US/09830230A
; Patent No. 6902893
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481US
; CURRENT APPLICATION NUMBER: US/09/830,230A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 437
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-230A-437

Query Match 90.3%; Score 28; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 6
:|||||
Db 41 REVFPA 46

RESULT 12
US-09-248-796A-26311
; Sequence 26311, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26311
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26311

Query Match 87.1%; Score 27; DB 2; Length 67;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 6
||:|:|
Db 16 KFIYFA 21

RESULT 13
US-09-513-999C-4859
; Sequence 4859, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4859
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4859

Query Match 87.1%; Score 27; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVF 5
|||||
Db 32 KFVF 36

RESULT 14
US-09-270-767-40694
; Sequence 40694, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40694
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40694

Query Match 87.1%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVF 5
|||||
Db 84 KFVF 88

RESULT 15
US-09-270-767-55910
; Sequence 55910, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 55910
LENGTH: 98
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55910

Query Match 87.1%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
DB 84 KVVFF 88

RESULT 16
US-09-823-153-4
Sequence 4; Application US/09823153
Patent No. 6713248
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Roberts, Susan
APPLICANT: Pak, Roger
APPLICANT: Lewis, Martin
APPLICANT: Smith, David
APPLICANT: Hendrick, Joseph
APPLICANT: Vinitesky, Alexander
TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
FILE REFERENCE: D0004
CURRENT APPLICATION NUMBER: US/09/823,153
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 104
TYPE: PRT
ORGANISM: Human Beta App
US-09-823-153-4

Query Match 87.1%; Score 27; DB 2; Length 104;
Best Local Similarity 83.3%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
DB 21 EFVFFA 26

RESULT 17
US-09-270-767-57813
Sequence 57813, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57813
LENGTH: 116
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:

OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57813

Query Match 87.1%; Score 27; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
DB 62 KVVFF 66

RESULT 18
US-09-902-540-10859
Sequence 10859, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10859
LENGTH: 238
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-10859

Query Match 87.1%; Score 27; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
DB 132 KVVFF 136

RESULT 19
US-09-134-001C-5445
Sequence 5445, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5445
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5445

Query Match 87.1%; Score 27; DB 2; Length 240;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 168 QVVFFA 173

```
RESULT 20
US-09-270-767-42516
; Sequence 42516, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42516
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42516
Query Match      87.1%; Score 27; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 62 KPVFF 66

RESULT 21
US-09-248-796A-19539
; Sequence 19539, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19539
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19539
Query Match      87.1%; Score 27; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 23 KPVFF 27

RESULT 22
US-09-270-767-40453
; Sequence 40453, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40453
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40453
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 6
Db 310 KYIFFA 315

RESULT 23
US-09-270-767-55669
; Sequence 55669, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55669
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55669
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 6
Db 310 KYIFFA 315

RESULT 24
US-09-270-767-45548
; Sequence 45548, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45548
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45548
Query Match      87.1%; Score 27; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 49 KPVFF 53
```

```
RESULT 25
US-09-270-767-34763
; Sequence 34763, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34763
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34763

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFFA 6
      |:|:|
Db      446 KYIFFA 451

RESULT 26
US-09-270-767-49980
; Sequence 49980, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49980
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49980

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFFA 6
      |:|:|
Db      446 KYIFFA 451

RESULT 27
US-08-704-711A-1
; Sequence 1, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
```

```
;
;
; CLTY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DB 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DB 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-1

Query Match      87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFF 5
      |:|:|
Db      375 KPVFF 379

RESULT 28
US-09-521-220-1
; Sequence 1, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
```

```

; 21-OCT-1994
; 17-MAR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;
US-09-521-220-1
;
Query Match 87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5
Db 375 KPVFF 379
|||||

RESULT 29
US-08-704-711A-2
; Sequence 2, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683

```



```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,704A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SP0781K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-211-704A-9

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||
Db      378 KVVFF 382

RESULT 32
US-09-521-220-2
; Sequence 2, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,704A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SP0781K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-521-220-2

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||
Db      378 KVVFF 382

RESULT 33
US-09-391-104-28
; Sequence 28, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; FALDUTO, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; PROTEINS ENCODED THEREFROM AND METHODS
; OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-28

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||
Db      378 KVVFF 382

RESULT 34
US-09-919-497-84
; Sequence 84, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 582
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-519-497-84

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
Db 378 KPVFF 382

RESULT 35
US-09-689-730-1
; Sequence 1, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-689-730-1

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
Db 378 KPVFF 382

RESULT 36
US-10-449-315-2
; Sequence 2, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-2

Query Match      87.1%; Score 27; DB 2; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
|||
```

```
Db 198 KPVFF 202

RESULT 37
US-10-449-315-5
; Sequence 5, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-5

Query Match      87.1%; Score 27; DB 2; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
|||
Db 355 KPVFF 359

RESULT 38
US-09-270-767-37091
; Sequence 37091, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37091
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37091

Query Match      83.9%; Score 26; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 FVFFA 6
|||
Db 16 FVFFA 20

RESULT 39
US-09-270-767-52308
; Sequence 52308, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
```

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52308
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52308

Query Match 83.9%; Score 26; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||
Db 16 FVFFA 20

RESULT 40
US-09-798-635A-41
; Sequence 41, Application US/09798635A
; Patent No. 6936432
; GENERAL INFORMATION:
; APPLICANT: Gopalan, Venkat
; APPLICANT: Jovanovic, Milan
; APPLICANT: Eder, Paul S.
; APPLICANT: Giordano, Tony
; APPLICANT: Powers, Gordon D.
; APPLICANT: Xavier, K. Ashish
; TITLE OF INVENTION: No. 6936432el Bacterial RNase P Proteins and
; TITLE OF INVENTION: Their Use in Identifying Antibacterial Compounds
; FILE REFERENCE: 50093/016002
; CURRENT APPLICATION NUMBER: US/09/798, 635A
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/516.061
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-798-635A-41

Query Match 83.9%; Score 26; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||
Db 39 FVFFA 43

RESULT 41
US-10-125-258-44
; Sequence 44, Application US/10125258
; Patent No. 6891085
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnail, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-10-125-258-44

Query Match 83.9%; Score 26; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||
Db 8 FVFFA 12

RESULT 42
US-09-583-110-4885
; Sequence 4885, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4885
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4885

Query Match 83.9%; Score 26; DB 2; Length 61;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
|||
Db 44 KTIFF 48

RESULT 43
US-10-125-258-43
; Sequence 43, Application US/10125258
; Patent No. 6891085
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnail, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis

```
US-10-125-258-43
Query Match      83.9%; Score 26; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 FVFFA 6
    |||||
Db   8 FVFFA 12

RESULT 44
US-09-270-767-60733
; Sequence 60733, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; EARLIER FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60733
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-60733

Query Match      83.9%; Score 26; DB 2; Length 84;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVF 5
    |||||
Db  48 KFIFF 52

RESULT 45
US-09-621-976-6739
; Sequence 6739, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; EARLIER FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6739
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6739

Query Match      83.9%; Score 26; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 FVFFA 6
    |||||
Db  31 FVFFA 35

RESULT 46
US-09-205-258-303
; Sequence 303, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
```

```
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007E1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
```

```
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
        |||||
Db      79 FVFFA 83

RESULT 47
US-10-004-860-303
; Sequence 303, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
        |||||
Db      79 FVFFA 83

RESULT 48
US-09-627-376-17
; Sequence 17, Application US/09627376
; Patent No. 6342385
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376

Query Match      83.9%; Score 26; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
        |||||
```

```
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-627-376-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
        |||||
Db      39 FVFFA 43

RESULT 49
US-10-047-676B-17
; Sequence 17, Application US/10047676B
; Patent No. 6699970
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; APPLICANT: Caulfield, Page W.
; APPLICANT: Chen, Ping
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17403/22
; CURRENT APPLICATION NUMBER: US/10/047,676B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-047-676B-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
        |||||
Db      39 FVFFA 43

RESULT 50
US-09-270-767-45241
; Sequence 45241, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45241
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45241

Query Match      83.9%; Score 26; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
        |||||
```

```
Db      120 KEIFF 124

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CCG1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-4

Query Match      83.9%; Score 26; DB 2; Length 186;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFFA 6
       :|:|
Db      134 QFIFFA 139

RESULT 54
US-09-270-767-33463
; Sequence 33463, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33463
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33463

Query Match      83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
       :|:|
Db      80 FVFFA 84

RESULT 55
US-09-270-767-48680
; Sequence 48680, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48680
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48680

Query Match      83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
       :|:|
Db      80 FVFFA 84

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CCG1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-4

Query Match      83.9%; Score 26; DB 2; Length 186;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFFA 6
       :|:|
Db      134 QFIFFA 139

RESULT 54
US-09-270-767-33463
; Sequence 33463, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33463
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33463

Query Match      83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
       :|:|
Db      122 FVFFA 126

RESULT 52
US-09-270-767-50607
; Sequence 50607, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50607
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50607

Query Match      83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
       :|:|
Db      122 FVFFA 126

RESULT 53
US-09-251-645-4
; Sequence 4, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
```

Db 80 FVFFA 84

RESULT 56
US-09-270-767-38186
; Sequence 38186, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38186
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-38186

Query Match 83.9%; Score 26; DB 2; Length 249;
Best Local Similarity 80.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
||:|

Db 196 KFIFF 200

RESULT 57
US-09-270-767-53403
; Sequence 53403, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 53403
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53403

Query Match 83.9%; Score 26; DB 2; Length 249;
Best Local Similarity 80.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
||:|

Db 196 KFIFF 200

RESULT 58
US-09-248-796A-27128
; Sequence 27128, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27128
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27128

Query Match 83.9%; Score 26; DB 2; Length 249;
Best Local Similarity 80.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
||:|

Db 108 KFIFF 112

RESULT 59
US-09-830-910-2
; Sequence 2, Application US/09830910
; Patent No. 6482807
; GENERAL INFORMATION:
; APPLICANT: Van Der Ley, Peter Andre
; APPLICANT: Hamstra, Hendrik Jan
; APPLICANT: Steeghs, Liانا Juliana Josephine Margriet
; TITLE OF INVENTION: LPS with reduced toxicity from Genetically modified
; FILE REFERENCE: Gram-negative bacteria
; FILE REFERENCE: LPS with reduced toxicity
; CURRENT APPLICATION NUMBER: US/09/830,910
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: PCT/NL98/00633
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-830-910-2

Query Match 83.9%; Score 26; DB 2; Length 310;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
||:|

Db 6 KFIFF 10

RESULT 60
US-09-248-796A-15301
; Sequence 15301, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15301
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE

```
; LOCATION: (4), (5)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-15301

Query Match      83.9%; Score 26; DB 2; Length 328;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||
   6 QFVFA 11

Db

RESULT 61
US-09-270-767-41366
; Sequence 41366, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41366
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41366

Query Match      83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||
   267 KFWFA 272

Db

RESULT 62
US-09-270-767-56582
; Sequence 56582, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56582
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56582

Query Match      83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||
   267 KFWFA 272

Db

RESULT 63
US-09-252-991A-25289
```

```
; Sequence 25289, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25289
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25289

Query Match      83.9%; Score 26; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
   :|||
   309 FVFFA 313

Db

RESULT 64
US-09-902-540-11308
; Sequence 11308, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11308
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11308

Query Match      83.9%; Score 26; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
   :|||
   185 FVFFA 189

Db

RESULT 65
US-09-602-787A-424
; Sequence 424, Application US/09602787A
; Patent No. 6695561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schüder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
```


FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932182.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932190.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932191.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932229.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932927.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940830.0
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940833.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941395.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942077.7
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942078.5
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942079.3
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 678
SEQ ID NO 424
LENGTH: 426
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-602-787A-424
Query Match 83.9%; Score 26; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 120 FVFFA 124
RESULT 66
US-09-489-039A-8958
Sequence 8958, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8958
LENGTH: 437
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8958
Query Match 83.9%; Score 26; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 36 FVFFA 40
RESULT 67
US-09-252-991A-17185
Sequence 17185, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17185
LENGTH: 446
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17185
Query Match 83.9%; Score 26; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 11111

Db 48 FVFFA 52

RESULT 68

US-09-489-039A-8303
; Sequence 8303, Application US/09489039A
; Patent No. 6610836

GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8303

; LENGTH: 453

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (133)

; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.

US-09-489-039A-8303

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 453;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

|||||

Db 266 FVFFA 270

RESULT 69

US-09-252-991A-28992
; Sequence 28992, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 28992

; LENGTH: 493

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28992

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 493;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5

|||||

Db 2 KPIFF 6

RESULT 70

US-09-540-236-2206
; Sequence 2206, Application US/09540236
; Patent No. 6673910

GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 2206

; LENGTH: 557

; TYPE: PRT

; ORGANISM: M.catarrhalis

US-09-540-236-2206

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 557;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

|||||

Db 355 FVFFA 359

RESULT 71

US-09-489-039A-11884
; Sequence 11884, Application US/09489039A
; Patent No. 6610836

GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 11884

; LENGTH: 573

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11884

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 573;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

|||||

Db 511 FVFFA 515

RESULT 72

US-09-252-991A-22560
; Sequence 22560, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 22560

; LENGTH: 597

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22560

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 597;

Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6
|
|
|
|
Db 90 FVFFA 94

RESULT 73

US-09-902-540-10275
; Sequence 10275, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10275
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10275

Query Match 83.9%; Score 26; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6
|
|
|
|
Db 185 FVFFA 189

RESULT 74

US-09-540-236-2074
; Sequence 2074, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2074
; LENGTH: 892
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2074

Query Match 83.9%; Score 26; DB 2; Length 892;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6
|
|
|
|
Db 658 FVFFA 662

RESULT 75

US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid

; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 80.6%; Score 25; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1;

Qy 1 KVFVFA 6
|
|
|
|
Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:52:38
Job time : 21.1323 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-12
Perfect score: 31
Sequence: 1 KRVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	4	AAB48477
2	31	100.0	6	4	AAB48485
3	31	100.0	6	4	AAB82625
4	31	100.0	6	4	AAB82633
5	31	100.0	6	5	AAB96813
6	31	100.0	6	5	AAB96821
7	31	100.0	6	5	AAB11659
8	31	100.0	6	5	AAB11651
9	31	100.0	6	6	AAB35447
10	31	100.0	6	6	AAB35440
11	31	100.0	6	8	ADQ37264
12	31	100.0	6	8	ADQ37316
13	31	100.0	6	8	ADQ37324
14	31	100.0	6	8	ADQ37272
15	31	100.0	6	9	ADY37931
16	31	100.0	6	9	ADY37923
17	31	100.0	336	7	ABM89186
18	30	96.8	202	5	ADK35620
19	28	90.3	75	4	ABBI17989
20	28	90.3	452	8	ADN23626
21	28	90.3	485	8	ADN46740
22	28	90.3	490	2	AAV19993
23	28	90.3	506	2	AAV55594
24	28	90.3	506	5	AAI17850

25	28	90.3	506	5	AAE17622
26	28	90.3	506	5	AAE17625
27	28	90.3	506	5	AAE17621
28	28	90.3	506	5	AAE17608
29	28	90.3	506	9	AEA37517
30	28	90.3	508	2	AAV19992
31	28	90.3	508	6	ABU19128
32	28	90.3	508	6	ABU24005
33	28	90.3	571	6	ADN24005
34	27	87.1	1089	8	ADN19501
35	27	87.1	52	3	AGG61668
36	27	87.1	57	8	ADG67964
37	27	87.1	62	6	ABU12483
38	27	87.1	62	8	ADJ28509
39	27	87.1	82	3	AGG00778
40	27	87.1	82	3	AGG00778
41	27	87.1	91	4	ABG13797
42	27	87.1	99	4	AAO10108
43	27	87.1	104	4	AAE12897
44	27	87.1	114	4	AAE93728
45	27	87.1	115	5	ABP33134
46	27	87.1	126	4	AAO02898
47	27	87.1	132	4	AAO00490
48	27	87.1	144	4	ABG26562
49	27	87.1	146	4	AAO07503
50	27	87.1	148	8	ADQ66558
51	27	87.1	173	4	AAU27710
52	27	87.1	173	5	AAU77842
53	27	87.1	173	7	ADJ69976
54	27	87.1	184	3	AG47987
55	27	87.1	186	9	ABE38594
56	27	87.1	189	5	AAU79255
57	27	87.1	189	5	AAU79257
58	27	87.1	189	5	AAU79258
59	27	87.1	189	5	AAU79256
60	27	87.1	197	7	ABM73888
61	27	87.1	206	4	ABE52559
62	27	87.1	221	4	ABG22983
63	27	87.1	221	4	ABG06994
64	27	87.1	227	8	ADH45453
65	27	87.1	238	9	ABM91660
66	27	87.1	240	5	ABP40600
67	27	87.1	240	8	ADSO7805
68	27	87.1	248	3	AGG10914
69	27	87.1	252	3	AGG10913
70	27	87.1	270	3	AAU80872
71	27	87.1	297	5	ABU81731
72	27	87.1	297	5	ABU81731
73	27	87.1	312	8	ADP47907
74	27	87.1	313	3	AGG33404
75	27	87.1	335	8	ADT58396
76	27	87.1	344	8	AGG28863
77	27	87.1	347	8	ADY78439
78	27	87.1	350	9	ADY15182
79	27	87.1	350	9	ADY15180
80	27	87.1	351	5	AAU74357
81	27	87.1	351	8	ABM80293
82	27	87.1	393	8	ADT55938
83	27	87.1	401	5	ABP52840
84	27	87.1	401	7	ABR84483
85	27	87.1	409	8	ADN74449
86	27	87.1	422	8	ADT58936
87	27	87.1	436	5	ABB91404
88	27	87.1	454	6	ADB08942
89	27	87.1	478	7	ABP73100
90	27	87.1	478	7	ADJ15262
91	27	87.1	498	6	ABP73103
92	27	87.1	504	7	ADP60748
93	27	87.1	549	8	ADP29329
94	27	87.1	579	2	AAE86406
95	27	87.1	581	6	ABU37981
96	27	87.1	581	9	ABE94410
97	27	87.1	582	2	AAE86407

AAE17622	A. thalia
AAE17625	Arabidops
AAE17621	Brassica
AAE17608	Arabidops
AEA37517	Arabidops
AAV19992	B. burgdo
ABU19128	Protein e
ABU24005	Protein e
ADN24005	Bacterial
ADG61668	Arabidops
ADG67964	Plant ful
ABU12483	Human mus
ABU2483	Novel hum
ADJ28509	Human mus
AGG00778	Human sec
AGG00778	Novel hum
ABG13797	Human pol
AAO12276	Human pol
AAO10108	Human pol
AAE12897	Human rec
AAE93728	Human pro
ABP33134	Human iso
AAO02898	Human pol
AAO00490	Human pol
ABG26562	Novel hum
AAO7503	Human pol
ADQ66558	Novel hum
AAU27710	Human ful
AAU77842	Oestrogen
ADJ69976	Human hea
AG47987	Arabidops
ABE38594	L. pneumo
AAU79255	Human mem
AAU79257	Rat membr
AAU79258	Rabbit me
AAU79256	Murine me
ABM73888	DNA clone
ABE52559	Echerich
ABG22983	Novel hum
ABG06994	Novel hum
ADH45453	Human mol
ABM91660	M. xanthu
ABP40600	Staphyloc
ADSO7805	Staphyloc
AGG10914	Arabidops
AGG10913	Arabidops
AAU80872	Human CLA
ABU81731	Human cas
ADP47907	Human CAT
AGG33404	Zea may
ADT58396	Plant pol
AGG28863	Arabidops
ADY78439	Plant ful
ADY15182	PRO polyp
ADY15180	PRO polyp
AAU74357	Human cyc
ABM80293	Tumour-as
ADT55938	Plant pol
ABP52840	Anopheles
ABR84483	Mosquito
ADN74449	Thale cre
ADT58936	Plant pol
ABB91404	Herbicida
ADB08942	Alloioioc
ABP73100	Amino aci
ADJ15262	African m
ABP73103	Amino aci
ADP60748	Termitomy
ADP29329	Human sec
AAE86406	Human mat
ABU37981	Protein e
ABE94410	Human MT1
AAE86407	Human mat

98	27	87.1	582	2	AAR75648	Aar75648 Human pla	171	26	83.9	223	8	ADE75401	Ade75401 Goat alph
99	27	87.1	582	2	AAW52134	Aaw52134 Rabbit me	172	26	83.9	243	8	ADN24282	Adn24282 Bacterial
100	27	87.1	582	4	AAB84616	Aab84616 Amino aci	173	26	83.9	289	3	AAy74724	Aay74724 Neisseria
101	27	87.1	582	4	AAE10423	Aae10423 Human mat	174	26	83.9	289	3	AAy74722	Aay74722 Neisseria
102	27	87.1	582	5	AAU84294	Aau84294 Human end	175	26	83.9	289	3	AAy74723	Aay74723 Neisseria
103	27	87.1	582	5	AAE21037	Aae21037 Human mem	176	26	83.9	291	4	AAB60656	Aab60656 N. mening
104	27	87.1	582	5	AAM50865	Aam50865 Matrix me	177	26	83.9	291	5	AAU85401	Aau85401 Neisseria
105	27	87.1	582	7	ADC15498	Adc15498 Human bas	178	26	83.9	293	3	AAy79683	Aay79683 Neisseria
106	27	87.1	582	7	ADB64179	Adb64179 Human Pro	179	26	83.9	293	3	AAy75339	Aay75339 Neisseria
107	27	87.1	582	7	ADE64177	Ade64177 Rat Prote	180	26	83.9	293	3	AAy75337	Aay75337 Neisseria
108	27	87.1	582	7	ADP13708	Adp13708 Tumor-Asa	181	26	83.9	293	3	AAy75338	Aay75338 Neisseria
109	27	87.1	582	7	ADN95589	Adn95589 Human BEC	182	26	83.9	293	8	ADR31670	Adr31670 N. mening
110	27	87.1	582	8	ADN07703	Adn07703 Human mat	183	26	83.9	295	6	ABU37645	Abu37645 Protein e
111	27	87.1	582	8	ABM81541	Abm81541 Tumor-as	184	26	83.9	299	6	ABP77830	Abp77830 N. gonorr
112	27	87.1	582	8	ADP23426	Adp23426 PRO polytp	185	26	83.9	317	6	ABP78259	Abp78259 N. gonorr
113	27	87.1	582	9	AEb94378	Aeb94378 Human MT1	186	26	83.9	321	7	ADG90764	Adg90764 Hepatic s
114	27	87.1	592	6	ABP79179	Abp79179 N. gonorr	187	26	83.9	321	8	ADP04189	Adp04189 Human col
115	27	87.1	592	6	ABU37131	Abu37131 Protein e	188	26	83.9	322	4	AAU30371	Aau30371 Novel hum
116	27	87.1	626	8	AUS22906	Aus22906 Bacterial	189	26	83.9	330	4	AAU49675	Aau49675 Propionib
117	27	87.1	738	4	AAg67526	Aag67526 Amino aci	190	26	83.9	330	6	ABM46194	Abm46194 Propionib
118	27	87.1	833	8	ADM98835	Adm98835 HMG-CoA r	191	26	83.9	339	4	AAg72670	Aag72670 Murine OR
119	27	87.1	841	4	AAm23595	Aam23595 Murine ES	192	26	83.9	344	7	ADe40136	Ade40136 Human NOV
120	27	87.1	856	8	ADM98920	Adm98920 HMG-CoA r	193	26	83.9	346	7	ADe62833	Ade62833 Rat Prote
121	27	87.1	856	8	ADM98784	Adm98784 HMG-CoA r	194	26	83.9	369	3	AAy75249	Aay75249 Neisseria
122	27	87.1	856	8	ADM98820	Adm98820 HMG-CoA r	195	26	83.9	371	3	AAy75248	Aay75248 Neisseria
123	27	87.1	1024	4	AAU02880	Aau02880 Human cas	196	26	83.9	371	3	AAy75247	Aay75247 Neisseria
124	27	87.1	1024	5	AAU08061	Aau08061 Human CIA	197	26	83.9	384	6	ADb12503	Adb12503 Alloiococ
125	27	87.1	124	5	ABU81720	Abu81720 Human cas	198	26	83.9	390	8	ADn23888	Adn23888 Bacterial
126	27	87.1	1024	6	ABG72211	Abg72211 Human cas	199	26	83.9	393	8	ADS24065	Ads24065 Bacterial
127	27	87.1	1024	6	ABE99643	Abeg99643 Amino aci	200	26	83.9	395	6	ABP77710	Abp77710 N. gonorr
128	27	87.1	1070	4	AAg67527	Aag67527 Amino aci	201	26	83.9	397	5	ABb49314	Abb49314 Listeria
129	27	87.1	1204	6	AAU02881	Aau02881 Human cas	202	26	83.9	400	8	ADT58012	Adt58012 Human GPC
130	27	87.1	1204	6	ABG72212	Abg72212 Protein e	203	26	83.9	407	7	ADc87413	Adc87413 Human GPC
131	27	87.1	2697	6	AAO26550	Aao26550 Cochliobo	204	26	83.9	402	7	ABO76543	AbO76543 Pseudomon
132	26	83.9	45	6	ABU02448	Abu02448 S. pneumo	205	26	83.9	404	8	ADS26059	Ads26059 Bacterial
133	26	83.9	53	8	ADx80309	Adx80309 Plant ful	206	26	83.9	405	6	ABM67471	Abm67471 Photorhab
134	26	83.9	60	6	ABP55940	Abp55940 Ostrinia	207	26	83.9	414	6	ABU20391	Abu20391 Protein e
135	26	83.9	61	8	ADK48370	Adk48370 Streptoco	208	26	83.9	414	8	ADS22533	Ads22533 Bacterial
136	26	83.9	62	1	AAp94262	Aap94262 Antibacte	209	26	83.9	414	9	ABM92109	Abm92109 M. xanthu
137	26	83.9	63	1	AAp90000	Aap90000 Antibacte	210	26	83.9	416	3	AAg41542	Aag41542 Arabidops
138	26	83.9	65	6	AAO13635	Aao13635 Human pol	211	26	83.9	418	6	ABP79629	Abp79629 N. gonorr
139	26	83.9	65	6	ABP55939	Abp55939 Ostrinia	212	26	83.9	426	4	AAg76721	Aag76721 Corynebac
140	26	83.9	69	9	ABE41581	Abe41581 L. pneumo	213	26	83.9	426	4	AAg92282	Aag92282 C. glutami
141	26	83.9	72	4	ABG21901	Abg21901 Novel hum	214	26	83.9	426	7	ADL65521	Adl65521 C. glutam
142	26	83.9	72	5	ADK36142	Adk36142 Novel hum	215	26	83.9	431	7	ADD69592	Add69592 Human REM
143	26	83.9	72	9	AEA20997	Aea20997 Novel hum	216	26	83.9	437	6	ADb11164	Adb11164 Alloiococ
144	26	83.9	74	3	AAg10736	Aag10736 Arabidops	217	26	83.9	437	7	ABO62441	AbO62441 Klebsiell
145	26	83.9	84	3	AAg61260	Aag61260 Arabidops	218	26	83.9	438	6	ADA48730	Ada48730 Rice prot
146	26	83.9	84	3	AAg61260	Aag61260 Arabidops	218	26	83.9	444	8	ADN27113	Adn27113 Bacterial
147	26	83.9	87	9	ABE38299	Abe38299 L. pneumo	219	26	83.9	446	7	ABO68439	AbO68439 Pseudomon
148	26	83.9	90	4	AAU31916	Aau31916 Novel hum	220	26	83.9	448	8	ADG25774	Adg25774 Mycobacte
149	26	83.9	91	3	AAg57206	Aag57206 Arabidops	221	26	83.9	453	7	ABO61786	AbO61786 Klebsiell
150	26	83.9	93	4	AAm92337	Aam92337 Human dig	222	26	83.9	459	8	ADS29238	Ads29238 Bacterial
151	26	83.9	96	3	AAg57205	Aag57205 Arabidops	223	26	83.9	479	3	AAg41541	Aag41541 Arabidops
152	26	83.9	96	3	AAg61259	Aag61259 Arabidops	224	26	83.9	483	8	ADN22834	Adn22834 Bacterial
153	26	83.9	101	8	ADx94447	Adx94447 Plant ful	225	26	83.9	483	8	ADN22833	Adn22833 Pseudomon
154	26	83.9	101	4	ABE50355	AbE50355 Human sec	226	26	83.9	483	7	ABO80246	AbO80246 Pseudomon
155	26	83.9	111	6	ABO44612	AbO44612 Novel hum	227	26	83.9	493	7	ABO80246	AbO80246 Pseudomon
156	26	83.9	111	7	ADP26092	Adp26092 Human pro	228	26	83.9	504	4	ABb64964	Abb64964 Drosophil
157	26	83.9	115	8	ADP84584	Adp84584 Human bre	229	26	83.9	510	8	ADM67214	Adm67214 Murine ad
158	26	83.9	116	6	ABP71848	Abp71848 Human Fur	230	26	83.9	511	6	ABM68291	Abm68291 Photorhab
159	26	83.9	118	5	ABO90650	AbO90650 Amino aci	231	26	83.9	512	3	AAg41540	Aag41540 Arabidops
160	26	83.9	118	6	ABG72548	Abg72548 Streptoco	232	26	83.9	518	5	ABP74027	Abp74027 Candida a
161	26	83.9	118	8	ADU08025	Adu08025 OrfZ, SEQ	233	26	83.9	526	8	ADn21271	Adn21271 Bacterial
162	26	83.9	137	4	AAO05457	Aao05457 Human pol	234	26	83.9	540	7	ABM86731	Abm86731 Rice abio
163	26	83.9	138	4	AAO08691	Aao08691 Human pol	235	26	83.9	548	6	ABU35322	Abu35322 Protein e
164	26	83.9	186	2	AAO37325	Aao37325 Photorhab	236	26	83.9	557	7	ADL04520	Adl04520 M. cattar
165	26	83.9	187	6	ABM69853	Abm69853 Photorhab	237	26	83.9	573	8	ABO65367	AbO65367 Klebsiell
166	26	83.9	188	5	ABE54792	AbE54792 Lactococc	238	26	83.9	581	4	ABB63013	Abb63013 Drosophil
167	26	83.9	191	4	AAg922339	Aag922339 C. glutami	239	26	83.9	597	7	ABO73814	AbO73814 Pseudomon
168	26	83.9	218	5	ABE55107	AbE55107 Lactococc	240	26	83.9	618	4	ABG26117	Abg26117 Novel hum
169	26	83.9	220	6	ABP78312	Abp78312 N. gonorr	241	26	83.9	641	4	ABG25497	Abg25497 Novel hum
170	26	83.9	223	5	AAE17475	Aae17475 Alpha-S2	242	26	83.9	673	6	ABM65701	Abm65701 Propionib
	26	83.9					243	26	83.9	690	8	ADY05578	Ady05578 Plant ful

244 AAW20827 83.9 717 2 AAW20827 H. pylori
 245 AAm91076 83.9 745 9 AAm91076 M. xanthu
 246 ADS43929 83.9 749 8 ADS43929 Bacterial
 247 ABb65665 83.9 754 4 ABb65665 Drosophil
 248 ABm86804 83.9 854 7 ABm86804 Rice abio
 249 ABb64834 83.9 860 4 ABb64834 Drosophil
 250 ABu35124 83.9 888 6 ABu35124 Protein e
 251 ABm88494 83.9 890 7 ABm88494 Rice abio
 252 ABb66627 83.9 891 4 ABb66627 Drosophil
 253 ADl04388 83.9 892 8 ADl04388 M. catarr
 254 ADz75752 83.9 919 9 ADz75752 Xanthomon
 255 ADs34925 83.9 931 8 ADs34925 Human aut
 256 ADs34926 83.9 931 8 ADs34926 Human aut
 257 ADs34924 83.9 931 8 ADs34924 Human aut
 258 ADs34927 83.9 931 8 ADs34927 Human aut
 259 ADr66427 83.9 936 8 ADr66427 Human pro
 260 ADr666085 83.9 936 8 ADr666085 Human pro
 261 ABu21740 83.9 1082 6 ABu21740 Protein e
 262 ADrl2606 83.9 1772 8 ADrl2606 Gene vacc
 263 AAw02314 80.6 6 2 AAw02314 Beta-amyl
 264 AAw93378 80.6 6 2 AAw93378 Beta-amyl
 265 AAb48484 80.6 6 4 AAb48484 Antifibr
 266 AAb48483 80.6 6 4 AAb48483 Antifibr
 267 AAb48474 80.6 6 4 AAb48474 Antifibr
 268 AAb48476 80.6 6 4 AAb48476 Antifibr
 269 AAb82623 80.6 6 4 AAb82623 All-D pep
 270 AAb82631 80.6 6 4 AAb82631 All-D pep
 271 AAb82632 80.6 6 4 AAb82632 All-D pep
 272 ABg71009 80.6 6 5 ABg71009 Long form
 273 ABb05157 80.6 6 5 ABb05157 Beta amyl
 274 AAu96819 80.6 6 5 AAu96819 Amyloid t
 275 AAu96820 80.6 6 5 AAu96820 Amyloid t
 276 AAu96811 80.6 6 5 AAu96811 Amyloid t
 277 AAb83305 80.6 6 5 AAb83305 Amyloid-b
 278 AAu11657 80.6 6 5 AAu11657 Peptide #
 279 AAu11658 80.6 6 5 AAu11658 Peptide #
 280 AAu11648 80.6 6 5 AAu11648 Peptide #
 281 AAu11650 80.6 6 5 AAu11650 Peptide #
 282 AAE35446 80.6 6 6 AAE35446 Abeta pep
 283 AAE35438 80.6 6 6 AAE35438 Abeta pep
 284 AAE35445 80.6 6 6 AAE35445 Abeta pep
 285 AAE35434 80.6 6 6 AAE35434 Abeta pep
 286 ADj64060 80.6 6 8 ADj64060 Human bet
 287 ADq37271 80.6 6 8 ADq37271 Vaccine a
 288 ADq37322 80.6 6 8 ADq37322 Antifibr
 289 ADq37315 80.6 6 8 ADq37315 Antifibr
 290 ADq37368 80.6 6 8 ADq37368 Beta-amyl
 291 ADq37270 80.6 6 8 ADq37270 Vaccine a
 292 ADq37313 80.6 6 8 ADq37313 Antifibr
 293 ADq37269 80.6 6 8 ADq37269 Vaccine a
 294 ADq37292 80.6 6 8 ADq37292 Vaccine a
 295 ADq37258 80.6 6 8 ADq37258 Vaccine a
 296 ADq37262 80.6 6 8 ADq37262 Vaccine a
 297 ADq37353 80.6 6 8 ADq37353 Beta-amyl
 298 ADq37323 80.6 6 8 ADq37323 Antifibr
 299 ADy37930 80.6 6 9 ADy37930 Amyloid-t
 300 ADy37921 80.6 6 9 ADy37921 Amyloid-t

ALIGNMENTS

RESULT 1
 AAB48477
 ID AAB48477 standard; peptide; 6 AA.
 AC
 XX AAB48477;
 XX

02-MAR-2001 (first entry)
 DT
 XX

Antifibrillogenic peptide #4.
 DE
 XX

Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW (NEUR-) NEUROCHEM INC. PA

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 OS
 PN WO200068263-A2.
 XX
 PD 16-NOV-2000.
 XX
 PF 04-MAY-2000; 2000WO-CA000515.
 XX
 PR 05-MAY-1999; 99US-0132592P.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalfour R, Gervais F, Gupta A;
 XX
 DR WPI; 2001-031852/04.
 XX
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 cytoprotection for treating amyloidosis disorders, comprises a peptide,
 its isomer or peptidomimetic.
 XX
 PS Claim 7; Page 25; 46pp; English.
 XX
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;
 QY 1 KEVFFFA 6
 |||||
 Db 1 KEVFFFA 6
 RESULT 2
 AAB48485
 ID AAB48485 standard; peptide; 6 AA.
 XX
 AC AAB48485;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #12.
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PF Key Location/Qualifiers
 Modified-site 6 /note= "C-terminal amide"
 FT
 XX
 PN WO200068263-A2.
 XX
 PD 16-NOV-2000.
 XX
 PF 04-MAY-2000; 2000WO-CA000515.
 XX
 PR 05-MAY-1999; 99US-0132592P.
 XX (NEUR-) NEUROCHEM INC. PA

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 PS
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 1 KVFVFA 6
 RESULT 3
 AAB82625
 ID AAB82625 standard; peptide; 6 AA.
 AC AAB82625;
 XX
 DT 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT
 FT
 PN WO200139796-A2.
 XX
 XX 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-CA001413.
 XX
 PR 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 PI WPI; 2001-441458/47.
 DR
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX
 PS Disclosure; Page 11; 31pp; English.
 XX
 XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis) familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 1 KVFVFA 6
 RESULT 4
 AAB82633
 ID AAB82633 standard; peptide; 6 AA.
 AC AAB82633;
 XX
 DT 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 PN WO200139796-A2.
 XX
 XX 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-CA001413.
 XX
 PR 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 DR WPI; 2001-441458/47.
 XX
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 FT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in
 XX preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesized from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 |||||
 Db 1 KVFVFA 6

RESULT 5
 AAU96813
 ID AAU96813 standard; peptide; 6 AA.

AC AAU96813;

DT 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #3.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

OS Key Location/Qualifiers

XX Key Misc-difference 1..6 /note= "Preferably D-form residue"

FT WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A_t-(A_l)_n_k-z-A_l_a_b (1) where z = 0 - 1;
 CC A_t = an amyloid targeting moiety; A_l)_n_k = a linker moiety; and A_l_a_b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (1) to the patient, and ultrasound imaging (1) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (1), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 |||||
 Db 1 KVFVFA 6

RESULT 6
 AAU96821
 ID AAU96821 standard; peptide; 6 AA.

XX AAU96821;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #11.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6

```

FT Modified-site 6 /note= "Preferably D-form residue"
FT FT /note= "Ala is amidated"
XX
XX
XX Key Location/Qualifiers
XX Modified-site 6
XX FT /note= "C-terminal amide"
XX
XX
XX WO200207781-A2.
XX 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
XX 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A1-L1-K1-A2 where z = 0 - 1;
XX A1 = an amyloid targeting moiety; L1-n1-K1 = a linker moiety; and A1-a1-b1
XX = a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (i) to the patient, and ultrasound imaging (i) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (i), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidosis (transmissible virus dementia), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 31; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVFVFA 6
XX |||||
XX Db 1 KVFVFA 6
XX
XX
XX
XX RESULT 8
XX AAU11651
XX ID AAU11651 standard; peptide; 6 AA.
XX
XX AC AAU11651;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #4, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 22-DEC-2000; 2000WO-IB002078.
XX
XX PR 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 31; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVFVFA 6
XX |||||
XX Db 1 KVFVFA 6
XX
XX
XX
XX RESULT 8
XX AAU11651
XX ID AAU11651 standard; peptide; 6 AA.
XX
XX AC AAU11651;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #4, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 22-DEC-2000; 2000WO-IB002078.
XX
XX PR 23-DEC-1999; 99US-0171877P.
XX
XX Cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

```

XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX DR WPI; 2002-075222/10.
 XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 XX PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 XX PT inhibitor.
 XX PS Disclosure; Page 10; 68pp; English.
 XX CC The present invention relates to a new method of inhibiting cerebral
 XX CC amyloid angiopathy. The new method of the invention involves contacting a
 XX CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 XX CC can be used for treating disease states characterised by cerebral amyloid
 XX CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 XX CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 XX CC The present sequence represents one of a group of peptides (AAU11648;
 XX CC AAU11659, AAU11910 & AAU11911) that were used in the invention as a
 XX CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 XX CC was used in the invention to treat a disease state characterised by
 XX CC cerebral amyloid angiopathy (CAA)
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFFA 6
 Db 1 KPVFFFA 6
 RESULT 9
 AAE35447
 ID AAE35447 standard; peptide; 6 AA.
 XX AC AAE35447;
 DT 17-JUN-2003 (first entry)
 XX ABeta peptide #18.
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; renal carcinoma; carcinomas of gut, lung
 KW ulcer; antiinflammatory; cytotstatic; uropathic; therapy.
 XX Unidentified.
 XX Key Location/Qualifiers
 FH Misc-difference 1. .6
 FT Modified-site 6 /note= "C-terminal amide"
 FT WO200296937-A2.
 XX 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-CA000763.
 XX 29-MAY-2001; 2001US-00867847.
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 59; 44pp; English.
 XX The invention relates to a method for prevention and/or treatment of an
 XX CC amyloid-related disease which comprises administration of an all-D -
 XX CC amyloid-beta peptide. The method is used for preventing and/or treating
 XX CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 XX CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 XX CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 XX CC the mammal; and reducing or inhibiting the formation of plaques. It is
 XX CC also used for treating AA (reactive) amyloid diseases including
 XX CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 XX CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 XX CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 XX CC disease. AA deposits are also produced as a result of chronic microbial
 XX CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 XX CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 XX CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 XX CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 XX CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 XX CC present sequence is an Abeta peptide used to illustrate the method of the
 XX CC invention
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFFA 6
 Db 1 KPVFFFA 6
 RESULT 10
 AAE35440
 ID AAE35440 standard; peptide; 6 AA.
 XX AC AAE35440;
 DT 17-JUN-2003 (first entry)
 XX ABeta peptide #11.
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; renal carcinoma; carcinomas of gut, lung
 KW ulcer; antiinflammatory; cytotstatic; uropathic; therapy.
 XX Unidentified.
 XX Key Location/Qualifiers
 FH Misc-difference 1. .6
 FT Modified-site 6 /note= "D-form residues"
 FT WO200296937-A2.
 XX 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-CA000763.
 XX 29-MAY-2001; 2001US-00867847.
 XX (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 59; 44pp; English.
 XX
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 31; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFFA 6
 Db |||||
 1 KVFVFFA 6
 RESULT 11
 ADQ37264
 ID ADQ37264 standard; peptide; 6 AA.
 AC ADQ37264;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "D-form residues"
 FT
 XX WO2004058239-A1.

15-JUL-2004.
 24-DEC-2003; 2003WO-CA002021.
 24-DEC-2002; 2002US-0436379P.
 23-JUN-2003; 2003US-0482214P.
 (NEUR-) NEUROCHEM INT LTD.
 Gervais F, Bellini F;
 WPI; 2004-543342/52.
 Composition for treating e.g. Alzheimer's disease comprises first agent
 that prevents or treats amyloid-beta related disease and second agent
 that is either a peptide or peptidomimetic or an immune system modulator.
 Disclosure; Page 67; 143pp; English.
 The present invention describes compositions (C) comprising: (a) a first
 agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 a second agent (a2) that is: (i) a peptide or peptidomimetic that
 modulates amyloid-beta fibril formation or induces a prophylactic or
 therapeutic immune response against amyloid-beta fibril formation; or
 (ii) an immune system modulator that prevents or inhibits amyloid-beta
 fibril formation. Also described is a kit comprising (C). (C) have
 neurotropic, neuroprotective, cerebroprotective, haemostatic, tranquiliser,
 ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,
 uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 and can be used as amyloid-beta fibril formation modulators, and as
 immune system modulators. (C) can be used for preventing or treating an
 amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 mild-to-moderate cognitive impairment, vascular dementia, senile dementia,
 amyloid angiopathy, hereditary cerebral haemorrhage, cerebral
 Down's syndrome, inclusion body myositis, age-related dementia,
 degeneration, or a condition associated with Alzheimer's disease
 (including hypothyroidism, cerebrovascular disease, cardiovascular
 disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 aggression, or incontinence), a neurological condition (e.g. Huntington's
 disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 field deficits, incoordination, gait disturbance, transient ischaemic
 attack or stroke, transient alertness, attention deficit, frequent falls,
 syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 damage), or a psychological condition (e.g. depression, delusions,
 illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 excessive guilt)) in a subject e.g. human having a genomic mutation in an
 amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 having amyloid-beta deposits. The present sequence represents a peptide
 that can be used as a vaccine antigen in the exemplification of the
 present invention.
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFFA 6
 Db |||||
 1 KVFVFFA 6
 RESULT 12
 ADQ37316
 ID ADQ37316 standard; peptide; 6 AA.

ADQ37316;
07-OCT-2004 (first entry)
Antifibrillogenic amyloidosis inhibiting peptide.
amyloid-beta; amyloid-beta related disease;
amyloid-beta fibril formation; immune response; neurotropic;
neuroprotective; cerebroprotective; haemostatic; ophthalmological;
antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
cardiant; antidepressant; endocrine; hypnotic;
amyloid-beta fibril formation modulator; immune system modulator;
Alzheimer's disease; mild cognitive impairment; vascular
mild-to-moderate cognitive impairment; vascular dementia;
cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
senile dementia; Down's syndrome; inclusion body myositis;
age-related macular degeneration; hypothyroidism;
cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
behavioural dysfunction; neurological condition; psychological condition;
vaccine antigen.
Synthetic.
WO2004058239-A1.
15-JUL-2004.
24-DEC-2003; 2003WO-CA002021.
24-DEC-2002; 2002US-0436379P.
23-JUN-2003; 2003US-0482214P.
(NEUR-) NEUROCHEM INT LTD.
Gervais F, Bellini F;
WPI; 2004-543342/52.
Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.
Disclosure; Page 69; 143pp; English.
The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have neurotropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
CC damage), or a psychological condition (e.g. depression, delusions,
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
CC having amyloid-beta deposits. The present sequence represents a peptide
CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
CC in the exemplification of the present invention.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 1 KVFVFA 6

RESULT 13

ADQ37324
ID ADQ37324 standard; peptide; 6 AA.

XX AC ADQ37324;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX KW amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; neurotropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "amidated"

XX WO2004058239-A1.

XX PD 15-JUL-2004.

XX PF 24-DEC-2003; 2003WO-CA002021.

XX PR 24-DEC-2002; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Bellini F;

XX DR WPI; 2004-543342/52.

XX PT Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.

XX PS Disclosure; Page 70; 143pp; English.

XX CC The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

XX CC neurotropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

XX CC Sequence 6 AA;

XX SQ Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
|||||

Db 1 KPVFFA 6

RESULT 14

ADQ37272

ID ADQ37272 standard; peptide; 6 AA.

XX ADQ37272;

AC ADQ37272;

XX 07-OCT-2004 (first entry)

XX Vaccine antigen amyloid-beta related amino acid sequence.

XX amyloid-beta; amyloid-beta related disease;

KW amyloid-beta fibril formation; immune response; neurotropic;

KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;

KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

KW cardiant; antidepressant; endocrine; hypnotic;

KW amyloid-beta fibril formation modulator; immune system modulator;

KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;

KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

senile dementia; Down's syndrome; inclusion body myositis; age-related macular degeneration; hypothyroidism; cerebrovascular disease; cardiovascular disease; memory loss; anxiety; behavioural dysfunction; neurological condition; psychological condition; vaccine antigen.

XX Synthetic.

XX OS

XX FH

XX Key Location/Qualifiers

FT Misc-difference 1. 6 /note= "D-form residues"

FT Modified-site 6 /note= "amidated"

FT WO2004058239-A1.

XX 15-JUN-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

XX CC neurotropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

XX CC Sequence 6 AA;

XX SQ Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
|||||

Db 1 KPVFFA 6

RESULT 14

ADQ37272

ID ADQ37272 standard; peptide; 6 AA.

XX ADQ37272;

AC ADQ37272;

XX 07-OCT-2004 (first entry)

XX Vaccine antigen amyloid-beta related amino acid sequence.

XX amyloid-beta; amyloid-beta related disease;

KW amyloid-beta fibril formation; immune response; neurotropic;

KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;

KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

KW cardiant; antidepressant; endocrine; hypnotic;

KW amyloid-beta fibril formation modulator; immune system modulator;

KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;

KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFFA 6
 |||||
 DB 1 KEVFFA 6

RESULT 15
 ADY37931
 ID ADY37931 standard; peptide; 6 AA.
 XX AC ADY37931;
 XX DT 19-MAY-2005 (first entry)
 XX DE Amyloid-targeting peptide, SEQ ID NO:11, for use in imaging agent.
 XX DE Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alzheimer's disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX US2005048000-A1.
 XX 03-MAR-2005.
 XX 03-DEC-2003; 2003US-00728028.
 XX 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 PR 29-JAN-2003; 2003US-0443291P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2005-212201/22.
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX Disclosure; SEQ ID NO 11; 34pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging
 agent comprises an amyloid targeting moiety (such as a peptide) joined to
 a labeling moiety via a linking moiety, and is preferably able to cross
 the blood-brain barrier. The invention also relates to a kit for
 preparing a radiopharmaceutical preparation from the imaging agent of the
 invention, a method for imaging amyloid deposition in a patient and a
 method for diagnosing an amyloid-related condition in a patient. The
 amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 transmissible cerebral amyloidosis (also known as transmissible virus
 dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 mediated diseases, dialysis-related amyloidosis, light chain-related
 amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 patient. The agent does not exhibit excessive toxicity or irritation,
 does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 31; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFFA 6
 |||||
 DB 1 KEVFFA 6

RESULT 16
 ADY37923
 ID ADY37923 standard; peptide; 6 AA.
 XX AC ADY37923;
 XX DT 19-MAY-2005 (first entry)
 XX DE Amyloid-targeting peptide, SEQ ID NO:3, for use in imaging agent.
 XX DE Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alzheimer's disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.
 XX OS Synthetic.
 XX US2005048000-A1.
 XX 03-MAR-2005.
 XX 03-DEC-2003; 2003US-00728028.
 XX 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 PR 29-JAN-2003; 2003US-0443291P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2005-212201/22.
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX Disclosure; SEQ ID NO 3; 34pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging
 agent comprises an amyloid targeting moiety (such as a peptide) joined to
 a labeling moiety via a linking moiety, and is preferably able to cross
 the blood-brain barrier. The invention also relates to a kit for
 preparing a radiopharmaceutical preparation from the imaging agent of the
 invention, a method for imaging amyloid deposition in a patient and a
 method for diagnosing an amyloid-related condition in a patient. The
 amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 transmissible cerebral amyloidosis (also known as transmissible virus
 dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 mediated diseases, dialysis-related amyloidosis, light chain-related
 amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 patient. The agent does not exhibit excessive toxicity or irritation,
 does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 |||||
 Db 1 KVFVFA 6

RESULT 17

ID ABM89186 standard; protein; 336 AA.

AC ABM89186;

DT 02-JUN-2005 (first entry)

DE Rice abiotic stress responsive polypeptide SEQ ID NO:7432.

XX abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.

OS Oryza sativa.

PN WO2003008540-A2.

XX 30-JAN-2003.

XX 21-JUN-2002; 2002WO-US019668.

XX 22-JUN-2001; 2001US-0300112P.

PR 24-AUG-2001; 2001US-0314662P.

PR 26-SEP-2001; 2001US-0325277P.

PR 21-NOV-2001; 2001US-0332132P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;

XX Moughamer T, Provart N, Ricke D, Zhu T;

XX WPI; 2003-248011/24.

XX New stress-responsive nucleic acid, useful for altering the

XX stress, salt stress or osmotic stress.

XX Claim 1; SEQ ID NO 7432; 89pp; English.

CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention

XX Sequence 336 AA;

Query Match 100.0%; Score 31; DB 7; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVFVFA 6
 |||||
 Db 80 KVFVFA 85

RESULT 18

ADK35620
 ID ADK35620 standard; protein; 202 AA.

XX ADK35620;

XX 06-MAY-2004 (first entry)

XX Novel human polypeptide SeqID7702.

XX antiarthritic; antiparkinsonian; neuroprotective; nontropic;
 KW immunosuppressive; cytostatic; antipsoriatic; antiinflammatory;
 KW antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
 KW arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;
 KW psoriasis; inflammatory bowel disease; infection; bacteria; virus;
 KW fungus; parasite; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..202

FT /label= OTHER

FT /note= "OTHER= All Xaa's in this sequence are unknown

XX amino acids or the site of a stop codon within the DNA

XX sequence"

XX WO200216439-A2.

XX 28-FEB-2002.

XX 05-MAR-2001; 2001WO-US004941.

XX 07-MAR-2000; 2000US-00519705.

XX 19-MAY-2000; 2000US-00574454.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2002-280918/32.

XX Isolated polynucleotide encoding bone marrow derived polypeptides useful

XX for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's

XX disease, and inflammatory bowel disease.

XX Claim 20; SEQ ID NO 7702; 504pp; English.

CC This invention relates to a novel isolated polynucleotide comprising a
 CC nucleotide sequence selected from one of 1680 sequences, a mature protein
 CC coding portion of them, an active domain of them and their complementary
 CC sequences. The invention may be useful for the production of compounds
 CC with an antiarthritic, antiparkinsonian, neuroprotective, nontropic,
 CC immunosuppressive, cytostatic, antipsoriatic, antiinflammatory,
 CC antibacterial, antiviral, antifungal or antiparasitic activity. In
 CC addition, the disclosed sequences may be useful for gene therapy. The
 CC polypeptides or their antibodies are useful for treating many diseases
 CC such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
 CC psoriasis, inflammatory bowel disease and infections caused by bacteria,
 CC viruses, fungi or parasites. The present sequence is that of a human
 CC polypeptide of the invention.

XX Sequence 202 AA;

Query Match 96.8%; Score 30; DB 5; Length 202;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 35 KVFVFA 40

RESULT 19
ABBI7989
ID ABB17989 standard; protein; 75 AA.
XX
AC ABB17989;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polypeptide SEQ ID NO 6646.
XX
KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritis; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US0001334.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 01-DEC-2000; 2000US-0251160P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251989P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 FI WPI; 2001-541565/60.
 DR N-PSDB; ABA14315.
 XX
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX
 XX Claim 11; SEQ ID NO 6646; 1701pp + Sequence Listing; English.
 PS
 XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (AB14678-AB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 75 AA;
 SQ
 Query Match 90.3%; Score 28; DB 4; Length 75;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFPA 6
 ||:||||
 Db 5 KFLFPA 10
 RESULT 20
 ADN23626
 ID ADN23626 standard; protein; 452 AA.
 XX
 AC ADN23626;
 XX
 DT 02-DEC-2004 (first entry)
 XX

DE Bacterial polypeptide #6279.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 XX
 XX 18-DEC-2003.
 PD
 PD 20-FEB-2003; 2003US-00369493.
 PP
 PP 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 FI WPI; 2004-061375/06.
 DR
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 6279; 122pp; English.
 PS
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX Sequence 452 AA;
 SQ
 Query Match 90.3%; Score 28; DB 8; Length 452;
 Best Local Similarity 83.3%; Pred. No. 9.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFPA 6
 :|||||
 Db 291 RFVFPA 296
 RESULT 21

RESULT 22
 AAY1993
 ID AAY1993 standard; protein; 490 AA.
 XX
 AC AAY1993;
 XX

```

PF 23-OCT-1995; 95WO-US013918.
XX
XX
PR 26-OCT-1994; 94US-00329603.
XX
XX
PA (DNAP ) DNA PLANT TECHNOLOGY CORP.
XX
PI James DW, Lim E, Keller J, Dooner HK;
XX
XX WPI; 1996-239495/24.
DR N-PSDB; AAT27036.
XX
XX New DNA constructs contg. FAE1 gene sequences - used to produce
PT transgenic plants with modified fatty acid content in plant organs or
PT parts, esp. seeds.
XX
XX Example 1; Page 36; 48pp; English.
XX
XX Arabidopsis fatty acid elongation enzyme FAE1 (AA095594) catalyses the
CC conversion of oleic acid (18:1) to eicosenoic acid (20:1) and of
CC eicosenoic acid to erucic acid (22:1). Its amino acid sequence was
CC deduced from that of a clone (AAT27036) isolated from a cDNA library
CC prepd. from Arabidopsis green siliques. Expression of the FAE1 enzyme in
CC transgenic plants, e.g. Brassica napus, can be used to modulate the fatty
CC acid content of the plant, partic. the seed oil. Use of antisense DNA
CC constructs suppresses the native FAE1 gene, allowing prodn. of edible
CC oils with reduced content of very long chain fatty acids (VLCFA). Use of
CC sense DNA constructs allows prodn. of oils with raised VLCFA content for
CC industrial use. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 506 AA;
SQ

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
DB 356 KFLFFA 361

RESULT 24
AAE17850
ID AAE17850 standard; protein; 506 AA.
XX
XX AAE17850;
XX
XX 29-AUG-2003 (revised)
DT 22-APR-2002 (first entry)
XX
XX Alternative version of At399 protein.
DE
XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAE1 protein; chimeric.
XX
XX Arabidopsis thaliana.
OS Brassica napus.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH Region 1..399
FT /note= "Arabidopsis thaliana elongase KCS protein"
FT Region 400..506
FT /note= "Brassica napus elongase KCS protein"
FT Misc-difference 502
FT /note= "Encoded by CMA"
XX
XX WO200194565-A2.
PN
XX 13-DEC-2001.
PD
XX 08-JUN-2001; 2001WO-US018737.
PF
XX 08-JUN-2000; 2000US-0210326P.
XX
XX
XX
XX

```

```

XX (UYMI-) UNIV MIAMI.
PA
XX Jaworski JG, Blacklock BJ;
XX
XX WPI; 2002-154572/20.
DR N-PSDB; AAD28537.
XX
XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
PT acids encoding the polypeptide, useful for producing very long chain
PT fatty acids.
XX
XX Example 1; Page 114-115; 139pp; English.
XX
XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC (KCS) polypeptides with altered substrate specificity and/or catalytic
CC activity and nucleic acid molecules encoding such polypeptides.
CC Polypeptides of the invention are useful for catalysing the condensation
CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
CC C20 fatty acyl CoA. They are especially useful for producing very long
CC chain fatty acids (VLCFA) and may be used in the development of reagents
CC for various purposes, e.g., immunological reagents to monitor expression
CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
CC inheritance of an elongase KCS gene in plant breeding programs. The
CC present sequence is an alternative version of Arabidopsis thaliana FAE1-
CC Brassica napus elongase KCS chimeric protein designated as At399.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 506 AA;
SQ

Query Match 90.3%; Score 28; DB 5; Length 506;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
DB 356 KFLFFA 361

RESULT 25
AAE17622
ID AAE17622 standard; protein; 506 AA.
XX
XX AAE17622;
XX
XX 29-AUG-2003 (revised)
DT 22-APR-2002 (first entry)
XX
XX A. thaliana FAE1-Brassica napus elongase KCS chimeric protein, At399.
DE
XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAE1 protein; chimeric.
XX
XX Arabidopsis thaliana.
OS Brassica napus.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH Region 1..399
FT /note= "Arabidopsis thaliana elongase KCS protein"
FT Region 400..506
FT /note= "Brassica napus elongase KCS protein"
XX
XX WO200194565-A2.
PN
XX 13-DEC-2001.
PD
XX 08-JUN-2001; 2001WO-US018737.
PF
XX 08-JUN-2000; 2000US-0210326P.
XX
XX (UYMI-) UNIV MIAMI.
XX

```

PI Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28514.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX
 PS Example 1; Fig 1-5; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalyzing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is Arabidopsis thaliana FAE1- Brassica napus elongase
 CC KCS chimeric protein designated as At399. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFPA 6
 DB 356 KPLFFA 361
 ||:||||
 356 KPLFFA 361
 RESULT 26
 AAE17625
 ID AAE17625 standard; protein; 506 AA.
 AC AAE17625;
 DT 22-APR-2002 (first entry)
 XX Arabidopsis thaliana FAE1 protein mutant, At K92R.
 XX
 XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 gene; mutant; mutain.
 XX
 XX Arabidopsis thaliana.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 92
 FT /note= "Wild-type Lys substituted with Arg"
 XX
 XX WO200194565-A2.
 XX
 XX 13-DEC-2001.
 XX
 XX 08-JUN-2001; 2001WO-US018737.
 XX
 XX 08-JUN-2000; 2000US-0210326P.
 XX (UYMI-) UNIV MIAMI.
 XX
 XX Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28517.
 XX
 XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.

XX Claim 7; Fig 1-6; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalyzing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is a mutant of Arabidopsis thaliana elongase KCS
 CC protein/FAE1 protein designated as At K92R
 XX
 SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFPA 6
 DB 356 KPLFFA 361
 ||:||||
 356 KPLFFA 361
 RESULT 27
 AAE17621
 ID AAE17621 standard; protein; 506 AA.
 XX
 AC AAE17621;
 XX
 DT 29-AUG-2003 (revised)
 DT 22-APR-2002 (first entry)
 XX
 DE Brassica napus elongase KCS-A. thaliana FAE1 chimeric protein, Bn176.
 XX
 XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 gene; chimeric.
 XX
 XX Brassica napus.
 OS Arabidopsis thaliana.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Region 1..176
 FT /note= "Brassica napus elongase KCS protein"
 FT Region 177..506
 FT /note= "Arabidopsis thaliana FAE1 protein"
 XX
 XX WO200194565-A2.
 XX
 XX 13-DEC-2001.
 XX
 XX 08-JUN-2001; 2001WO-US018737.
 XX
 XX 08-JUN-2000; 2000US-0210326P.
 XX (UYMI-) UNIV MIAMI.
 XX
 XX Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28513.
 XX
 XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX
 XX Example 1; Fig 1-5; 139pp; English.
 PS
 XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase

CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is *Brassica napus* elongase KCS- Arabidopsis thaliana
 CC FAEI chimeric protein designated as Bn176. (Updated on 25-AUG-2003 to
 CC standardise OS field)
 XX

SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 28
 AAEL17608
 ID AAEL17608 standard; protein; 506 AA.
 XX
 AC AAEL17608;

DT 22-APR-2002 (first entry)

DE Arabidopsis thaliana elongase KCS protein.

KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAEI protein.

OS Arabidopsis thaliana.
 XX
 PN WO200194565-A2.
 XX

PD 13-DEC-2001.

PF 08-JUN-2001; 2001WO-US018737.

PR 08-JUN-2000; 2000US-0210326P.

PA (UYMI-) UNIV MIAMI.

PI Jaworski JG, Blacklock BJ;

XX WPI; 2002-154572/20.

DR N-PSDB; AAD28500.

XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.

PS Example 3; Fig 1-1; 139pp; English.

XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is Arabidopsis thaliana elongase KCS protein encoded by
 CC FAEI gene
 XX

SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 29
 AEA37517
 ID AEA37517 standard; protein; 506 AA.
 XX
 AC AEA37517;

DT 11-AUG-2005 (first entry)

DE Arabidopsis sp. fatty acid elongase 1 (FAEI) protein.

KW vector; transformation; plant; fatty acid elongase 1;

KW 3-ketoacyl-CoA synthase; promoter; gene expression; seed; oil; enzyme.

OS Arabidopsis sp.

PN WO2005052162-A1.

PD 09-JUN-2005.

PF 24-NOV-2004; 2004WO-CA002021.

PR 25-NOV-2003; 2003US-0524645P.

XX (CANA) NAT RES COUNCIL CANADA.

XX Mietkiewska E, Taylor DC, Katavic V;

XX WPI; 2005-418004/42.

DR N-PSDB; AEA37518.

XX New expression vector for transforming a cell comprising a gene coding
 PT for a plant fatty acid elongase, useful for altering erucic acid content
 PT or the very long chain fatty acid content (C20 or greater) in a plant.

PS Disclosure; SEQ ID NO 26; 72pp; English.

XX The invention relates to an expression vector for transforming a cell.
 CC The expression vector comprises a gene coding for a plant fatty acid
 CC elongase (FAE), also designated 3-ketoacyl-CoA synthase (KCS)) in reading
 CC frame alignment with a promoter capable of increasing the expression of
 CC the gene, when the transformed cell is in a seed, sufficient to increase
 CC the proportion of very long chain monounsaturated fatty acid when
 CC compared with a control cell. Also described are: (1) a cell comprising a
 CC heterologous gene coding for a heterologous plant fatty acid elongase or
 CC its allelic variant, the cell being capable of producing an increase in
 CC proportion of a very long chain monounsaturated fatty acid when compared
 CC a control cell lacking the heterologous gene; (2) a seed comprising the
 CC plant cells above; (3) a plant comprising the plant cells; and (4) a
 CC method of altering erucic acid content of a plant-derived oil. The gene
 CC coding for a plant fatty acid elongase is a Nasturtium, Crambe, or
 CC Arabidopsis fatty acid elongase gene. The cell is a fungal cell,
 CC preferably yeast cell, or a plant cell, specifically a plant seed cell.
 CC The plant cell additionally comprises a further heterologous gene coding
 CC for an additional heterologous plant fatty acid elongase or its allelic
 CC variant or a heterologous plant desaturase gene or its allelic variant.
 CC It is capable of producing oil with an increased content of erucic acid
 CC or other very long chain fatty acid (C20 or greater). The heterologous
 CC gene codes for a 3-ketoacyl-CoA synthase. The very long chain
 CC monounsaturated fatty acid comprises erucic acid. The heterologous plant
 CC fatty acid elongase gene is useful for altering erucic acid content in a
 CC plant or the very long chain fatty acid content (C20 or greater) in a
 CC plant. The vector is useful for altering erucic acid content in a plant.

CC This sequence represents a *Arabidopsis* sp. PAE1.

XX Sequence 506 AA;

Query Match 90.3%; Score 28; DB 9; Length 506;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

|||||

Db 356 KFLFFA 361

RESULT 30

AAV19992

ID RAY19992 standard; protein; 508 AA.

XX AC

XX AAY19992;

XX DT 19-JUL-1999 (first entry)

XX DE B. burgdorferi antigenic protein, f752.aa.

XX KW Antigenic protein; vaccine; Lyme disease; infection; detection.

XX OS Borrelia burgdorferi.

XX PN WO9859071-AL.

XX PD 30-DEC-1998.

XX PF 18-JUN-1998; 98WO-US012718.

XX PR 20-JUN-1997; 97US-0050359P.

XX PR 23-JUL-1997; 97US-0053344P.

XX PR 22-JUL-1997; 97US-0053377P.

XX PR 03-SEP-1997; 97US-0057483P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI (MEDI-) MEDIMUNE INC.

XX PI Choi GH, Erwin AL, Hanson MS, Lathigra R;

XX WPI; 1999-189980/16.

XX DR N-PSDB; AAX61689.

XX PT New isolated Borrelia burgdorferi nucleic acids - used to develop

XX PT products for the diagnosis, prevention and treatment of diseases caused

XX PT by Borrelia, particularly Lyme disease.

XX PS Claim 12; Page 153; 275pp; English.

XX CC This sequence represents a Borrelia burgdorferi (Bb) protein of the

XX CC invention, which is suitable for use in a vaccine. The Bb polypeptides

XX CC can be used in vaccines for eliciting protective antibodies to members of

XX CC the Borrelia genus, particularly for the use against Lyme disease in

XX CC humans and animals. They can be used for preventing or attenuating an

XX CC infection caused by a member of the Borrelia genus. The products can also

XX CC be used for detection of members of the Borrelia genus

XX SQ Sequence 508 AA;

Query Match 90.3%; Score 28; DB 2; Length 508;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

|||||

Db 41 RLVFFA 46

RESULT 31

ABU19128

ID ABU19128 standard; protein; 508 AA.

XX AC ABU19128;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #4655.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Borrelia burgdorferi.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX DR N-PSDB; ACA22998.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 47052; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of

XX CC the 6213 antisense sequences given in the specification where expression

XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

XX CC (1) a vector comprising a promoter operably linked to the nucleic acid

XX CC encoding a polypeptide whose expression is inhibited by the antisense

XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX CC polypeptide or its fragment whose expression is inhibited by the

XX CC antisense nucleic acid; (4) an antibody capable of specifically binding

XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX CC proliferation or the activity of a gene in an operon required for

XX CC proliferation; (7) identifying a compound that influences the activity of

XX CC the gene product or that has an activity against a biological pathway

XX CC required for proliferation, or that inhibits cellular proliferation; (8)

XX CC identifying a gene required for cellular proliferation or the biological

XX CC pathway in which a proliferation-required gene or its gene product lies

XX CC or a gene on which the test compound that inhibits proliferation of an

XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX CC compound's activity; (11) a culture comprising strains in which the gene

XX CC product is overexpressed or underexpressed; (12) determining the extent

XX CC to which each of the strains is present in a culture or collection of

XX CC strains; or (13) identifying the target of a compound that inhibits the

XX CC proliferation of an organism. The antisense nucleic acids are useful for

XX CC identifying proteins or screening for homologous nucleic acids required

XX CC for cellular proliferation to isolate candidate molecules for rational

XX CC drug discovery programs, or for screening homologous nucleic acids

XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

XX CC the target prokaryotic essential genes. Note: The sequence data for this

XX CC patent did not form part of the printed specification, but was obtained

XX CC in electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 508 AA;

Query Match 90.3%; Score 28; DB 6; Length 508;

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1089 AA;

Query Match 90.3%; Score 28; DB 8; Length 1089;
 Best Local Similarity 83.3%; Pred. No. 2.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFPA 6
 |||||:
 Db 13 KPVFFS 18

RESULT 34

AAAG61668
 ID AAG61668 standard; protein; 52 AA.

XX AC AAG61668;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 80017.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123380P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 08-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132407P.

PR 05-MAY-1999; 99US-0132484P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 15-JUL-1999; 99US-0143624P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144884P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 22-JUL-1999; 99US-0145085P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.

PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.

PR 26-JUL-1999; 99US-0145276P.

PR 27-JUL-1999; 99US-0145513P.

```
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156450P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0158293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160981P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.

PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      87.1%; Score 27; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFP 5
Db 31 KFVFP 35
|||||
RESULT 35
ADX67964
ID ADX67964 standard; protein; 57 AA.
XX
AC ADX67964;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 38807.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
XX US2004034888-A1.
PN
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 38807; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
```

CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 57 AA;

Query Match 87.1%; Score 27; DB 8; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2.1e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 Db 29 KPVFF 33

RESULT 36

ABB03189
 ID ABB03189 standard; protein; 62 AA.

XX ABB03189;

DT 08-JAN-2002 (first entry)

DE Human musculoskeletal system related polypeptide SEQ ID NO 1136.

XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatocytic; antidiabetic; anti-inflammatory; antiulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system.

OS Homo sapiens.

PN WO200155367-A1.

XX
 PD 02-AUG-2001.

XX
 PF 17-JAN-2001; 2001WO-US001338.

XX
 PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 28-JUN-2000; 2000US-0209467P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-451937/48.
XX N-PSDB; AAL34771.
XX
XX Isolated polypeptide for treating, preventing and/ or prognosing
XX disorders related to the musculoskeletal system including musculoskeletal
XX cancers and also for testing and detection e.g. diagnosis.
XX
XX Claim 11; SEQ ID NO 1136; 781pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
XX (ABB03087-ABB04109) associated with the musculoskeletal system useful for
XX preventing, treating or ameliorating medical conditions e.g. by protein
XX or gene therapy. The genes are isolated from a range of human tissues
XX disclosed in the specification. The nucleic acids, proteins, antibodies
XX and (ant)agonists are useful in the diagnosis, treatment and prevention
XX of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
XX adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
XX lung, or urogenital; (b) immune disorders e.g. Addison's disease,
XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
XX arthritis and ulcerative colitis; (c) cardiovascular disorders such as
XX myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
XX cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
XX bacterial, fungal and parasitic infections. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 62 AA;

Query Match 97.1%; Score 27; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFVFF 5
Db 31 KFVFF 35
RESULT 37
ABUL2483
ID ABUL2483 standard; protein; 62 AA.
XX AC ABUL2483;
XX DT 26-FEB-2003 (first entry)
XX DE Novel human musculoskeletal system antigen #103.
XX Musculoskeletal system antigen; cancer; metastasis; re-vascularisation;
KW thrombosis; arteriosclerosis; mineral content; cardiovascular condition;
KW wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair;
KW limb regeneration; neuronal growth; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; AIDS-related complex;
KW chondrocyte growth; bone regeneration; periodontal regeneration;
KW tissue transport; bone graft; skin aging; keratinocyte growth; hair loss;
KW melanocyte growth; cell proliferation; cell growth; organ transplant;
KW cell differentiation; body height; weight; hair colour; eye colour; skin;
KW percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism;
KW biorythm; cardiac rhythm; depression; tendency for violence; pain;
KW reproductive capability; hormone level; endocrine level; appetite;
KW libido; memory; stress; storage capability; fat content; lipid content;
KW protein content; carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX Homo sapiens.
OS
XX
XX US2002147140-A1.
XX 10-OCT-2002.
XX
XX 17-JAN-2001; 2001US-00764877.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 28-JUN-2000; 2000US-0214886P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 26-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 22-AUG-2000; 2000US-0225758P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 08-SEP-2000; 2000US-0229513P.
XX 21-SEP-2000; 2000US-0231413P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.

PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239355P.
 PR 20-OCT-2000; 2000US-0240360P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX

(ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;
 WPI; 2003-128199/12.
 N-PSDB; ABX57759.

Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.

Claim 11; SEQ ID NO 1136; 321pp; English.

The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since POF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's metal state or physical state by influencing biorhythms, cardiac rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This is the amino acid sequence of a novel human musculoskeletal system antigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at ftp.segdata.uspto.gov/sequence.html?DocID=20020147140

Sequence 62 AA;

Query Match 87.1%; Score 27; DB 6; Length 62;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 31 KPVFF 35

RESULT 38

ADJ28509
 ID ADJ28509 standard; protein; 62 AA.

AC ADJ28509;

XX 20-MAY-2004 (first entry)

XX Human musculoskeletal system-associated protein - SEQ ID 1136.

XX musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
 XX Gene therapy; vaccine; human.

OS Homo sapiens.

PN US2004009488-A1.

PD 15-JAN-2004.

PF 13-SEP-2002; 2002US-00242515.

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231245P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241828P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2004-090458/09.
XX N-PSDB; ADJ27486.
XX
XX New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer of musculoskeletal tissues or osteoporosis.
XX
XX Claim 11; SEQ ID NO 1136; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-associated nucleic acid molecule. The nucleic acid of the invention demonstrates cytostatic and osteopathic activities and may be useful for preparing a medicament for preventing, treating or ameliorating a medical condition such as cancer of the musculoskeletal tissues or osteoporosis, possibly via gene therapy or vaccine production. The current sequence is that of the human musculoskeletal system-associated polypeptide of the invention. The current sequence is not shown within the specification per se but is available on the USPTO web-site
XX <http://seqdata.uspto.gov/sequence.html?DocID=20040009488>.
XX
XX Sequence 62 AA;
SQ
Query Match 87.1%; Score 27; DB 8; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KVFVF 5
Db 31 KVFVF 35
RESULT 39
AAG00778
ID AAG00778 standard; protein; 82 AA.
XX
AC AAG00778;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein, SEQ ID NO: 4859.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX

PD 06-SEP-2000.
 XX
 XX 21-FEB-2000; 2000BP-00200610.
 XX
 XX 26-FEB-1999; 99US-0122487P.
 XX
 XX (GEST) GENSET.
 XX
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 XX WPI; 2000-500381/45.
 XX
 XX N-PSDB; AAC00784.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 XX Claim 13; SEQ ID NO 4859; 71pp + Sequence Listing; English.
 XX
 XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 XX Sequence 82 AA;
 SQ
 Query Match 87.1%; Score 27; DB 3; Length 82;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 5
 Db 32 KVFVFF 36
 |||||
 |||||
 RESULT 40
 ABG13797
 ID ABG13797 standard; protein; 82 AA.
 XX
 XX AC ABG13797;
 XX
 XX 18-FEB-2002 (first entry)
 XX
 XX Novel human diagnostic protein #13788.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US008631.
 XX
 XX 31-MAR-2000; 2000US-00540217.
 PR
 XX 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR

DR N-PSDB; AAS77984.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 XX Claim 20; SEQ ID NO 44156; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in treating disorders
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have application of mutations
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 82 AA;
 SQ
 Query Match 87.1%; Score 27; DB 4; Length 82;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 6
 Db 11 EFVFFFA 16
 :|||
 |||||
 RESULT 41
 AAO12276
 ID AAO12276 standard; protein; 91 AA.
 XX
 XX AC AAO12276;
 XX
 XX 06-NOV-2001 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 26168.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 XX Homo sapiens.
 OS
 XX WO200164835-A2.
 PN
 XX 07-SEP-2001.
 PD
 XX 26-FEB-2001; 2001WO-US004927.
 XX
 XX 28-FEB-2000; 2000US-00515126.
 PR
 XX 18-MAY-2000; 2000US-00577409.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-514838/56.
 DR

DR N-PSDB; AAI92207.
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 CC
 XX Claim 20; SEQ ID NO 26168; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 91 AA;

Query Match 87.1%; Score 27; DB 4; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 17 KPVFF 21

RESULT 42
 AAO10108
 ID AAO10108 standard; protein; 99 AA.
 XX
 AC AAO10108;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 24000.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.

XX
 XX WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US004927.
 XX
 PR 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AAI90039.
 XX
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 CC
 XX Claim 20; SEQ ID NO 24000; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 99 AA;

Query Match 87.1%; Score 27; DB 4; Length 99;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 39 KPVFF 43

RESULT 43
 AAE12897
 ID AAE12897 standard; protein; 104 AA.
 XX
 AC AAE12897;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Human recombinant beta-amyloid precursor protein (betaAPP) C-83.
 XX
 KW Human; Alzheimer's disease; gamma-secretase; integral-membrane protein;
 KW beta-amyloid precursor protein; betaAPP.
 XX
 OS Homo sapiens.
 XX
 PN WO200175435-A2.
 XX
 PD 11-OCT-2001.

XX
 PF 30-MAR-2001; 2001WO-US010453.
 XX
 PR 03-APR-2000; 2000US-0194495P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Roberts SB, Hendrick JP, Vinitzky A, Lewis M, Smith DW, Pak R;
 PI WPI; 2001-648575/74.
 DR N-PSDB; AAD20982.
 XX
 XX Novel gamma secretase protein, useful in the production of amyloids, is
 PT capable of cleaving beta-amyloid precursor protein to produce beta
 PT amyloid peptide.
 XX
 PS Claim 83; Fig 3; 127pp; English.
 XX

CC The invention relates to the field of plaque amyloid deposits that are
 CC the hallmarks of Alzheimer's disease. In particular, the invention
 CC relates to an isolated, functionally-active protein that has gamma-
 CC secretase activity. Gamma-secretase activity is necessary for amyloid
 CC production. The present invention also relates to methods for isolating
 CC integral-membrane proteins and protein complexes, including the gamma-
 CC secretase protein of the invention. The method is useful for monitoring
 CC the cleavage of beta-amyloid precursor protein (betaAPP) by gamma-
 CC secretase. The present sequence is human recombinant betaAPP protein (C-
 CC 83)

SQ Sequence 104 AA;

Query Match 87.1%; Score 27; DB 4; Length 104;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 21 EFVFFA 26

RESULT 44
AAB93728
ID AAB93728 standard; protein; 114 AA.

AC AAB93728;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human protein sequence SEQ ID NO:13358.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
XX Homo sapiens.
OS
XX EP1074617-A2.
PN
XX
XX 07-FEB-2001.
PD
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
PR
XX 27-AUG-1999; 99JP-00300253.
PR
XX 11-JAN-2000; 2000JP-00118776.
PR
XX 02-MAY-2000; 2000JP-00183767.
PR
XX 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
PA
XX
XX Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PI
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
XX Claim 8; SEQ ID NO 13358; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent polynucleotides, all of which are used in the exemplification of the present invention
XX
XX Sequence 114 AA;
SQ

Query Match 87.1%; Score 27; DB 4; Length 114;

Best Local Similarity 66.7%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 24 KFVFFS 29

RESULT 45
ABP33134
ID ABP33134 standard; protein; 115 AA.

XX
XX ABP33134;
AC
XX
XX 09-JUL-2002 (first entry)
XX
XX Human isomerase-like ORF2107 protein, SEQ ID NO:4214.
XX
XX Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnery; KW vasotropic; antipsoriatic; antidiabetic; cytostatic; neurotropic; KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
XX
XX Homo sapiens.
OS
XX
XX WO200190366-A2.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 24-MAY-2001; 2001WO-US017076.
XX
XX 24-MAY-2000; 2000US-0206690P.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Leach MD, Shimkets RA;
PI
XX
XX WPI; 2002-106200/14.
XX
XX N-PSDB; ABN77160.
DR
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, PT hyperproliferative disorders and disorders related to organ transplantation.
XX
XX Claim 10; Page 1311; 2508pp; English.
XX
XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX CC polynucleotides, the recombinant production of ORFX proteins, antibodies CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and CC polypeptides, methods of screening for modulators of ORFX expression or CC activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide CC range of biological activities, such as cytokine, cell proliferation, CC cell differentiation, immune modulation, haematopoiesis regulation, CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/ CC chemokinetic activity, haemostatic activity, thrombolytic activity, CC receptor/ligand, antiinflammatory activity, tumour inhibition activity, CC and antiinfective activity, and may also be involved in the determination CC

CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases
 XX
 XX Sequence 115 AA;

Query Match 87.1%; Score 27; DB 5; Length 115;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 67 KPVFF 71

RESULT 46

AAO02898
 ID AAO02898 standard; protein; 126 AA.

AC AAO02898;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 16790.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AAI82829.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 16790; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 126 AA;

Query Match 87.1%; Score 27; DB 4; Length 126;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 90 KPVFF 94

RESULT 47

AAO00490
 ID AAO00490 standard; protein; 132 AA.

AC AAO00490;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 14382.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AAI80421.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 14382; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

XX Sequence 132 AA;

Query Match 87.1%; Score 27; DB 4; Length 132;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 5
 Db 22 KVFVFF 26

RESULT 48
 ABG26562
 ID ABG26562 standard; protein; 144 AA.

XX AC ABG26562;
 XX 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #26553.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS90749.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 56921; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 144 AA;

Query Match 87.1%; Score 27; DB 4; Length 144;
 Best Local Similarity 66.7%; Pred. No. 5e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 6
 Db 111 RFIFFA 116

RESULT 49
 AAC07503
 ID AAC07503 standard; protein; 146 AA.

XX AC AAC07503;
 XX 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 21395.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US004927.

XX PR 28-FEB-2000; 2000US-00515126.

XX PR 18-MAY-2000; 2000US-00577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-514838/56.

XX DR N-PSDB; AAI87434.

XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX PS Claim 20; SEQ ID NO 21395; 1399pp + Sequence Listing; English.

XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 146 AA;

Query Match 87.1%; Score 27; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 5
 Db 24 KVFVFF 28

RESULT 50
 ADQ66558
 ID ADQ66558 standard; protein; 148 AA.

XX ADQ66558;
 XX 07-OCT-2004 (first entry)
 XX Novel human protein sequence #1531.
 XX
 XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 XX EP1440981-A2.
 XX
 XX 28-JUL-2004.
 XX
 XX 21-JAN-2004; 2004EP-00001196.
 XX
 XX 21-JAN-2003; 2003JP-00102206.
 XX
 XX 09-MAY-2003; 2003JP-00131392.
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX
 XX WPI; 2004-535376/52.
 XX
 XX N-PSDB; ADQ64370.
 XX
 XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 XX Claim 1; SEQ ID NO 3719; 2449pp; English.
 XX
 XX The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX
 XX Sequence 148 AA;
 SQ
 Query Match 87.1%; Score 27; DB 8; Length 148;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFF 5
 Db 17 KFVFF 21
 RESULT 51
 AAU27710
 ID AAU27710 standard; protein; 173 AA.
 XX
 XX AAU27710;
 AC
 XX 18-DEC-2001 (first entry)
 XX
 XX Human full-length polypeptide sequence #35.
 XX
 XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
 KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 KW nervous system disorder; inflammatory disorder; cell differentiation;
 KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
 KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;

KW cytostatic; antirheumatic; antiarthritic; vulnery; antiinflammatory;
 KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
 KW neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
 KW immunostimulant; analgesic; gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX WO200164834-A2.
 PN
 XX 07-SEP-2001.
 PD
 XX 26-FEB-2001; 2001WO-US004926.
 XX
 XX 28-FEB-2000; 2000US-00515126.
 XX
 XX 18-MAY-2000; 2000US-00577409.
 PR
 XX 17-JUN-2000; 2000US-00597707.
 PR
 XX 14-JUL-2000; 2000US-00616807.
 PR
 XX 19-SEP-2000; 2000US-00664641.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 PI Drmanac R;
 XX
 XX WPI; 2001-589862/66.
 DR
 XX N-PSDB; AAS44610.
 DR
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis, treatment of cancer,
 PT neurological, inflammatory disorders and for use in arrays for detection.
 XX
 XX Claim 10; SEQ ID NO 207; 153pp; English.
 PS
 XX Sequences AAU27676-AAU28019 represent full-length polypeptides and contig
 CC polypeptides of the invention. The proteins and their associated DNA
 CC sequences are useful for the treatment, diagnosis and prevention of
 CC various types of disorder in a mammalian subject such as a human, dog,
 CC monkey, mouse, hamster or rat. The disorders include cancers such as
 CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as
 CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, ankyrotrophic lateral sclerosis, spinal muscular atrophy and
 CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 CC in culture to give rise to neuroepithelial cells that can be used to
 CC augment or replace cells damaged by illness, accidental damage or genetic
 CC disorders. The sequences may also be used for regeneration of bone
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 173 AA;
 SQ
 Query Match 87.1%; Score 27; DB 4; Length 173;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFF 5
 Db 46 KFVFF 50
 RESULT 52
 AAU77842
 ID AAU77842 standard; protein; 173 AA.
 XX
 XX AAU77842;
 AC

XX DT 05-JUN-2002 (first entry)

XX DE Oestrogen receptor associated protein 19.03.

XX KW Oestrogen receptor associated protein 19.03; cytostatic; antiinfertility;

XX KW reproductive system; tumour; sex growth impediment.

XX OS Unidentified.

XX PN WO200212317-A1.

XX PD 14-FEB-2002.

XX PF 11-JUN-2001; 2001WO-CN000930.

XX PR 12-JUN-2000; 2000CN-00116442.

XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX PI Mao Y, Xie Y;

XX WPI; 2002-172145/22.

XX DR N-PSDB; ABK12230.

XX KW Estrogen receptor associated protein 19.03 and encoded polynucleotide,

XX PT used in diagnosis and treatment of reproductive system tumors.

XX PS Claim 1; Page 30; 38pp; Chinese.

XX CC This invention relates to the cDNA and protein sequences of a novel

CC isolated protein estrogen receptor associated protein 19.03 and a method

CC for producing the protein by recombinant means. The protein of the

CC invention may have cytostatic and antiinfertility activities. The DNA and

CC protein sequences of the invention may be used in the diagnosis and

CC treatment of reproductive system tumors and sex growth impediment in the

CC adolescence. The present sequence represents the Estrogen receptor

CC associated protein 19.03 of the invention

XX SQ Sequence 173 AA;

Query Match 87.1%; Score 27; DB 5; Length 173;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

DB 46 KPVFF 50

RESULT 53

ADJ69976

ID ADJ69976 standard; protein; 173 AA.

XX AC ADJ69976;

XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target SeqID1782.

XX KW mitochondrial; human; screening assay; diabetes mellitus;

XX KW Huntington's disease; osteoarthritis;

XX KW Leber's hereditary optic neuropathy; LHON;

XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

XX KW osteopathic; ophthalmological; cytostatic.

XX OS Homo sapiens.

XX PN WO2003087768-A2.

XX PD 23-OCT-2003.

XX PF 04-APR-2003; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

XX PR 17-JUN-2002; 2002US-0389987P.

XX PR 20-SEP-2002; 2002US-0412418P.

XX PA (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX PI Ghosh SS, Faby ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

XX PI Warnock DE;

XX DR WPI; 2003-845369/78.

XX PT Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX PS Claim 1; SEQ ID NO 1782; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC present for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy

CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

CC compositions have neuroprotective, nootropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytostatic activities. This polypeptide sequence is a human heart

CC mitochondrial protein of the invention.

XX SQ Sequence 173 AA;

Query Match 87.1%; Score 27; DB 7; Length 173;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

DB 46 KPVFF 50

RESULT 54

AAG47987

ID AAG47987 standard; protein; 184 AA.

XX AC AAG47987;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 60548.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 184;
 Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6
 ||:|:
 Db 29 KFIFFS 34

RESULT 55
 AEB38594
 ID AEB38594 standard; protein; 186 AA.

XX AC AEB38594;

XX DT 08-SEP-2005 (first entry)

XX DE L. pneumophila protein SEQ ID NO 2926.

XX KW detection; infection; Antibacterial; Vaccine.

XX OS Legionella pneumophila.

XX PN W02005049642-A2.

XX PD 02-JUN-2005.

XX PF 23-SEP-2004; 2004WO-IB003578.

XX PR 21-NOV-2003; 2003FR-00013687.

XX PA (INSP) INST PASTEUR.

XX PA (INRM) INSEPM INST NAT SANTE & RECH MEDICALE.

XX PA (UTLY-) UNIV LYON I BERNARD CLAUDE.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PA Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;

XX PI Rueniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;

XX PI Jarraud S;

XX

DR WPI; 2005-388305/40.
 XX New genome of Legionella pneumophila Paris strain and derived
 PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.
 XX Claim 3; SEQ ID NO 2926; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)
 CC from Legionella pneumophila Paris strain. (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC Legionella, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.

XX Sequence 186 AA;

Query Match 87.1%; Score 27; DB 9; Length 186;

Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6
 :||:
 Db 7 RFIFFA 12

RESULT 56

AAU79255

ID AAU79255 standard; protein; 189 AA.

XX AC AAU79255;

XX DT 13-AUG-2002 (first entry)

XX DE Human membrane-bound matrix metalloproteinase 1 (MT1-MMP) related protein.

XX KW Membrane-bound matrix metalloproteinase; MT-MMP; MT1-MMP; enzyme; human;

XX KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;

XX KW cytostatic; antiallergic; neutropic; neuroprotective.

XX OS Homo sapiens.

XX PN W0200241000-A1.

XX PD 23-MAY-2002.

XX PF 20-NOV-2001; 2001WO-JP010136.

XX PR 20-NOV-2000; 2000JP-00352491.

XX PA (DAII-) DAIICHI FINE CHEM CO LTD.

XX PI Aoki T, Yonezawa K, Fujimoto N, Ogawa M, Iwata K;

XX DR WPI; 2002-435988/46.

XX Immunoassay method for membrane-bound matrix metalloproteinase with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.

XX PS Disclosure; Fig 9; 93pp; Japanese.

XX The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloproteinase (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane

CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a human MT1-MMP related protein
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 Db 60 KVFVF 64

RESULT 57

AAU79257
 ID AAU79257 standard; protein; 189 AA.

XX AC AAU79257;

XX DT 13-AUG-2002 (first entry)

XX DE Rat membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

XX KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rat;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;
 KW cystostatic; antiallergic; neutrophic; neuroprotective.

XX OS Rattus sp.

XX PN WO200241000-A1.

XX PD 23-MAY-2002.

XX PF 20-NOV-2001; 2001WO-JP010136.

XX PR 20-NOV-2000; 2000JP-00352491.

XX PA (DAII-) DAIICHI FINE CHEM CO LTD.

XX PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

XX DR WPI; 2002-435988/46.

XX PT Immunoassay method for membrane-bound matrix metalloprotease with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.

XX PS Disclosure; Fig 9; 93pp; Japanese.

XX CC The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a rat MT1-MMP related protein
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||

Db 60 KVFVF 64

RESULT 58

AAU79258
 ID AAU79258 standard; protein; 189 AA.

XX AC AAU79258;

XX DT 13-AUG-2002 (first entry)

XX DE Rabbit membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.
 XX KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rabbit;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;
 KW cystostatic; antiallergic; neutrophic; neuroprotective.

XX OS Oryctolagus cuniculus.

XX PN WO200241000-A1.

XX PD 23-MAY-2002.

XX PF 20-NOV-2001; 2001WO-JP010136.

XX PR 20-NOV-2000; 2000JP-00352491.

XX PA (DAII-) DAIICHI FINE CHEM CO LTD.

XX PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

XX DR WPI; 2002-435988/46.

XX PT Immunoassay method for membrane-bound matrix metalloprotease with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.

XX PS Disclosure; Fig 9; 93pp; Japanese.

XX CC The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a rabbit MT1-MMP related protein
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||

Db 60 KVFVF 64

RESULT 59

AAU79256
 ID AAU79256 standard; protein; 189 AA.

XX AC AAU79256;

XX DT 13-AUG-2002 (first entry)

XX DE Murine membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

XX KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; mouse;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;

KW cytostatic; antiallergic; nootropic; neuroprotective.

XX Mus sp.

XX WO200241000-A1.

PN 23-MAY-2002.

PD 20-NOV-2001; 2001WO-JP010136.

XX 20-NOV-2000; 2000JP-00352491.

XX (DAII-) DAIICHI FINE CHEM CO LTD.

XX Aoki T, Yonezawa K, Fujimoto N, Ogawa M, Iwata K;

XX WPI; 2002-435988/46.

XX Immunoassay method for membrane-bound matrix metalloproteinase with
PT quantitation using its antibody, applicable in diagnosis of cancer and
PT cancer metastasis, and in drug development.

XX Disclosure; Fig 9; 93pp; Japanese.

XX The invention relates to a method for quantitative immunoassay of a
CC membrane-bound matrix metalloproteinase (MT-MMP), involving using an
CC antibody against MT-MMP selected from groups containing MT-MMPs. The
CC method involves releasing and/or solubilizing MT-MMP from a cell membrane
CC among a group of MT-MMPs by using a surfactant and reductant. Such a
CC method is for detecting a membrane-bound matrix metalloproteinase with
CC quantitation, which is applicable in diagnosis of cancer and cancer
CC metastasis as well as in drug development, and is also used to monitor
CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
CC represents a mouse MT1-MMP related protein

XX Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

DB 60 KPVFF 64

RESULT 60

ABW73888

ID ABW73888 standard; protein; 197 AA.

XX ABW73888;

XX 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #298.

XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX Hordeum vulgare.

XX WO2003057877-A1.

XX 17-JUL-2003.

XX 16-DEC-2002; 2002WO-1B005403.

XX 20-DEC-2001; 2001JP-00387059.

XX 20-DEC-2001; 2001JP-00387131.

XX 20-DEC-2001; 2001JP-00403299.

XX 20-DEC-2001; 2001JP-00403300.

XX 27-SEP-2002; 2002JP-00327515.

XX (UTNI-) UNIV JAPAN OKAYAMA.

XX Sato K, Takeda K, Kohara Y;

XX WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA
PT sequences containing them for analysis and identification of barley
PT varieties and production of barley transformants with desired
PT characteristics.

XX Disclosure; SEQ ID XX; 284pp; Japanese.

XX The present invention relates to oligonucleotide clones originating in
CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
CC varieties, identification of particular varieties and genotype-phenotype
CC analysis, isolation of specific genes and creation of new varieties by
CC transformation of barley varieties with them and production of new barley
CC varieties with desired properties. The present sequence represents an
CC oligonucleotide clone sequence featured in the specification. The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published-pct-sequences

XX Sequence 197 AA;

Query Match 87.1%; Score 27; DB 7; Length 197;

Best Local Similarity 66.7%; Pred. No. 6.8e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6

DB 140 KPIFYA 145

RESULT 61

ABB52559

ID ABB52559 standard; protein; 206 AA.

XX ABB52559;

XX 11-FEB-2002 (first entry)

XX Escherichia coli polypeptide SEQ ID NO 489.

XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
KW systemic infection; non-diarrhoeal infection; septicaemia;
KW pyelonephritis; antibiotic resistance.

XX Escherichia coli.

XX WO200166572-A2.

XX 13-SEP-2001.

XX 12-MAR-2001; 2001WO-EP003445.

XX 10-MAR-2000; 2000FR-00003145.

XX 02-FEB-2001; 2001FR-00001449.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;

XX WPI; 2001-550253/61.

XX A library of DNA fragments of Escherichia coli strains for the phylogenic
PT determination of a given strain comprises polynucleotides of nature B2/D+
PT A-.

XX Example 6; Fig 6; 646pp; English.

CC The invention relates to a library of DNA fragments of Escherichia coli
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and
 CC encoded proteins (AB52459-AB52919 and AB52954-AB53094) of nature
 CC B2/D+A-. The polynucleotides have potential anti-inflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenetic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicemia, pyelonephritis and meningitis this is particularly
 CC advantageous as bacterial resistance is increasing with the more frequent
 CC use of broad spectrum antibiotics

XX
 SQ Sequence 206 AA;
 Query Match 87.1%; Score 27; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFF 5
 Db 25 KFVFF 29
 |||||

RESULT 62
 AEG22983
 ID AEG22983 standard; protein; 221 AA.
 XX
 AC AEG22983;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22974.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 FI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS87170.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 53342; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AEG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 221 AA;
 Query Match 87.1%; Score 27; DB 4; Length 221;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFF 5
 Db 36 KFVFF 40
 |||||

RESULT 63
 ABG06994
 ID ABG06994 standard; protein; 221 AA.
 XX
 AC ABG06994;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #6985.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 FI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS71181.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 37353; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 221 AA;
 SQ

Query Match 87.1%; Score 27; DB 4; Length 221;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 Db 11 EFVFFA 16
 :|||||

RESULT 64
 ADH45453
 ID ADH45453 standard; protein; 227 AA.
 AC
 XX ADH45453;
 XX

DT 25-MAR-2004 (first entry)
 XX

DE Human molecule useful for disease detection and treatment, SEQ ID No 47.
 XX

XX human; molecule; disease detection; treatment; MDDT; cytostatic;
 KW antiarteriosclerotic; anti-HIV; antiallergic; cerebroprotective;
 KW antiparkinsonian; anticonvulsant; nootropic; neuroprotective;
 KW antiinflammatory; ophthalmological; antithyroid; antiaerthritic;
 KW antibacterial; virucide; prozoacide; antiparasitic; fungicide;
 KW anorectic; cardiant; hypotensive; antiinfertility; hepatotropic;
 KW gene therapy.
 KW

XX Homo sapiens.
 OS

XX WO2003093427-A2.
 PN

XX 13-NOV-2003.
 PD

XX 30-APR-2003; 2003WO-US013629.
 PF

XX 30-APR-2002; 2002US-0376988P.
 PR

XX 14-JUN-2002; 2002US-0389095P.
 PR

XX 22-AUG-2002; 2002US-0405860P.
 PR

XX 27-AUG-2002; 2002US-0406512P.
 PR

XX (INCY-) INCYTE CORP.
 PA

XX Swarnakar A, Tran UK, Khare R, Marquis JP, Hafalia AJA; Yue H;
 PI Elliott VS, Becha SD, Ramkumar J, Kable AE, Wilson AD, Jiang X;
 PI Forsythe IJ, Griffin JA, Bulloch SA, Jin P, Jackson AA;
 PI Mason PM, Chawla NK, Chang H, Richardson TW, Tang YT, Lee SY;
 PI Gietzen KJ, Fu GK;
 XX

XX WPI; 2004-022653/02.
 DR

XX N-PSDB; ADH45507.
 DR

XX New human molecules for disease detection and treatment (MDDT) and
 XX encoding polynucleotides, useful for diagnosing, preventing or treating
 XX diseases associated with aberrant MDDT expression, e.g. cancer, stroke,
 XX obesity or AIDS.
 PT

XX Claim 1; SEQ ID NO 47; 267pp; English.
 PS

XX The invention relates to human molecules useful for disease detection and
 XX treatment (MDDT) and also the polynucleotides which encode and identify
 XX and encode MDDT. The MDDT polypeptides and encoding polynucleotides have

CC the following activities: cytostatic, antiarteriosclerotic, anti-HIV,
 CC antiallergic, cerebroprotective, antiparkinsonian, anticonvulsant,
 CC nootropic, neuroprotective, antiinflammatory, ophthalmological,
 CC antithyroid, antiaerthritic, antibacterial, virucide, prozoacide,
 CC antiparasitic, fungicide, anorectic, cardiant, hypotensive,
 CC antiinfertility, and hepatotropic. The MDDT polynucleotide may be used in
 CC gene therapy to treat disorders. The MDDT polynucleotide are
 CC useful in diagnosing, preventing or treating diseases or conditions
 CC associated with the decreased expression or overexpression of MDDT, such
 CC as autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis,
 CC arthritis or thyroiditis), infections (e.g. bacterial, viral, parasitic,
 CC protozoal or fungal), metabolic disorders (e.g. obesity), reproductive
 CC disorders (e.g. infertility), neurological disorders (Parkinson's
 CC disease, Alzheimer's disease, stroke, epilepsy), cardiovascular disorders
 CC (e.g. myocardial infarction or hypertension), eye disorders, or cell
 CC proliferative diseases (e.g. cancer, atherosclerosis, hepatitis). These
 CC are also useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acid and amino acid sequences of MDDT. The MDDT or
 CC its fragments are useful in screening compounds for effectiveness as
 CC agonist or antagonist of the polypeptides, or in altering the expression
 CC of the target polynucleotide and compounds that specifically bind to or
 CC modulate the activity of the polypeptide. The microarray of the invention
 CC is useful in monitoring or measuring protein-protein interactions, drug-
 CC target interactions, and gene expression profiles. This sequence
 CC represents an MDDT polypeptide of the invention.
 XX

XX Sequence 227 AA;
 SQ

Query Match 87.1%; Score 27; DB 8; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 Db 32 KVFVFF 36
 :|||||

RESULT 65
 ABM91660
 ID ABM91660 standard; protein; 238 AA.
 AC
 XX ABM91660;
 XX

DT 02-JUN-2005 (first entry)
 XX

XX M. xanthus protein sequence, seq id 10859.
 XX

XX Transgenic plant; DNA replication; gene regulation; gene expression.
 XX

XX Myxococcus xanthus.
 OS

XX US6833447-B1.
 PN

XX 21-DEC-2004.
 PD

XX 10-JUL-2001; 2001US-00902540.
 PF

XX 10-JUL-2000; 2000US-0217883P.
 PR

XX (MONS) MONSANTO TECHNOLOGY LLC.
 PA

XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
 PI WPI; 2005-028716/03.
 XX

XX New substantially purified Myxococcus xanthus nucleic acid molecule
 XX encoding a nitrite reductase, useful for determining gene expression,
 XX identifying mutations in a gene of interest, and for constructing
 XX mutations in a gene of interest.
 PT

XX Example 2; SEQ ID NO 10859; 25pp; English.
 PS

XX The invention relates to a substantially purified nucleic acid molecule

CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
 CC recombinant DNA construct for expression of a nitrite reductase gene in a
 CC plant cell, and a plant cell comprising the recombinant DNA construct.
 CC The nucleic acid is useful for determining gene expression, identifying
 CC mutations in a gene of interest, and for constructing mutations in a gene
 CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
 CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 XX
 SQ Sequence 238 AA;

Query Match 87.1%; Score 27; DB 9; Length 238;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 DB 132 KVFVF 136

RESULT 66
 ABP40600
 ID ABP40600 standard; protein; 240 AA.

XX AC ABP40600;
 XX DT 24-JUL-2002 (first entry)
 XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5445.
 XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 XX KW antibacterial; gene therapy.
 XX OS Staphylococcus epidermidis.

XX PN US6380370-B1.
 XX PD 30-APR-2002.

XX PF 13-AUG-1998; 98US-00134001.
 XX PR 14-AUG-1997; 97US-00557739.
 XX PR 08-NOV-1997; 97US-0064964P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Doucette-Stamm LA, Bush D;
 XX DR WPI; 2002-381255/41.
 XX DR N-PSDB; ABN93145.
 XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
 XX PT polypeptide, useful for diagnosing and treating bacterial infections.
 XX PS Disclosure; SEQ ID NO 5445; 267pp; English.

XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life cycle
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site
 XX

SQ Sequence 240 AA;

Query Match 87.1%; Score 27; DB 5; Length 240;
 Best Local Similarity 83.3%; Pred. No. 8.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVEFA 6
 DB 168 QVFVEFA 173

RESULT 67
 ADS07805

ID ADS07805 standard; protein; 240 AA.

XX AC ADS07805;

XX DT 04-NOV-2004 (first entry)

XX DE Staphylococcus epidermis polypeptide seqid 7100.

XX KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
 XX KW recombinant expression vector; infection; computer readable medium;
 XX KW computer based system.

XX OS Staphylococcus epidermidis.

XX PN US2004147734-A1.

XX PD 29-JUL-2004.

XX PF 01-DEC-2003; 2003US-00724972.

XX PR 08-NOV-1997; 97US-0064964P.

XX PR 13-AUG-1998; 98US-00134001.

XX PR 29-NOV-1999; 99US-00450969.

XX PA (DOUC/) DOUCETTE-STAMM L.

XX PA (BUSH/) BUSH D.

XX PI Doucette-Stamm L, Bush D;

XX DR WPI; 2004-580138/56.

XX DR N-PSDB; ADS04033.

XX PT New isolated polypeptide and encoding nucleic acid derived from

XX PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or

XX PT treating an S. epidermidis bacterial infection.

XX PS Claim 17; SEQ ID NO 7100; 741pp; English.

XX CC The invention describes an isolated nucleic acid comprising a nucleotide
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
 CC given in the specification. Also described are: a recombinant expression
 CC vector; a cell comprising a recombinant expression vector of (1);
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection, comprising a nucleic acid cited above and a carrier; treating
 CC a subject for S. epidermidis infection; a recombinant or substantially
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a
 CC sample; a computer readable medium having recorded in it the nucleotide
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
 CC system for identifying fragments of the Staphylococcus genome of
 CC commercial importance; a computer based system for identifying fragments
 CC of the Staphylococcus plasmids of commercial importance; identifying
 CC commercially important nucleic acid fragments of the Staphylococcus
 CC genome and/or plasmids; and identifying an expression modulating fragment
 CC of the Staphylococcus genome and/or plasmids. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of an Staphylococcal epidermidis bacterial
 CC infection. This is the amino acid sequence of a S. epidermis protein of
 CC the invention.

XX

```
SQ Sequence 240 AA;
Query Match 87.1%; Score 27; DB 8; Length 240;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KEVFFA 6
Db 168 QVFFA 173

RESULT 68
AAG10914
ID AAG10914 standard; protein; 248 AA.
XX
AC AAG10914;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9429.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000BP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126364P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 21-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
```


PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139751P.
PR 21-JUN-1999; 99US-0139817P.
PR 21-JUN-1999; 99US-0139899P.
PR 22-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 23-JUN-1999; 99US-0140695P.
PR 24-JUN-1999; 99US-0140823P.
PR 28-JUN-1999; 99US-0140991P.
PR 29-JUN-1999; 99US-0141287P.
PR 30-JUN-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142377P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.

PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149428P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156598P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 252;
Best Local Similarity 66.7%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||:|:
Db 210 KFIFYA 215

RESULT 70
AAG10912
ID AAG10912 standard; protein; 270 AA.

XX AC AAG10912; PR 18-JUN-1999; 99US-0139462P.
XX DT 17-OCT-2000 (first entry) PR 18-JUN-1999; 99US-0139463P.
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9427. PR 18-JUN-1999; 99US-0139750P.
XX KW Protein identification; signal transduction pathway; metabolic pathway; PR 18-JUN-1999; 99US-0139763P.
XX KW hybridisation assay; genetic mapping; gene expression control; promoter; PR 21-JUN-1999; 99US-0139817P.
XX KW termination sequence. PR 22-JUN-1999; 99US-0139899P.
XX OS Arabidopsis thaliana. PR 23-JUN-1999; 99US-0140353P.
XX PN EP1033405-A2. PR 23-JUN-1999; 99US-0140354P.
XX PD 06-SEP-2000. PR 24-JUN-1999; 99US-0140695P.
XX PF 25-FEB-2000; 200EP-00301439. PR 28-JUN-1999; 99US-0140823P.
XX PR 25-FEB-1999; 99US-0140931P.
XX PR 05-MAR-1999; 99US-0141287P.
XX PR 09-MAR-1999; 99US-0141287P.
XX PR 23-MAR-1999; 99US-0141842P.
XX PR 25-MAR-1999; 99US-0141842P.
XX PR 29-MAR-1999; 99US-0142055P.
XX PR 01-APR-1999; 99US-0142055P.
XX PR 06-APR-1999; 99US-0142330P.
XX PR 08-APR-1999; 99US-0142803P.
XX PR 16-APR-1999; 99US-0142920P.
XX PR 19-APR-1999; 99US-0142977P.
XX PR 21-APR-1999; 99US-0142977P.
XX PR 23-APR-1999; 99US-0143542P.
XX PR 28-APR-1999; 99US-0143624P.
XX PR 30-APR-1999; 99US-0144005P.
XX PR 04-MAY-1999; 99US-0144086P.
XX PR 05-MAY-1999; 99US-0144331P.
XX PR 06-MAY-1999; 99US-0144332P.
XX PR 07-MAY-1999; 99US-0144333P.
XX PR 11-MAY-1999; 99US-0144334P.
XX PR 14-MAY-1999; 99US-0144335P.
XX PR 14-MAY-1999; 99US-0144632P.
XX PR 14-MAY-1999; 99US-0144884P.
XX PR 18-MAY-1999; 99US-0144814P.
XX PR 19-MAY-1999; 99US-0145086P.
XX PR 14-MAY-1999; 99US-0145088P.
XX PR 14-MAY-1999; 99US-0145088P.
XX PR 14-MAY-1999; 99US-0145087P.
XX PR 14-MAY-1999; 99US-0145089P.
XX PR 14-MAY-1999; 99US-0145192P.
XX PR 14-MAY-1999; 99US-0145145P.
XX PR 14-MAY-1999; 99US-0145218P.
XX PR 14-MAY-1999; 99US-0145224P.
XX PR 14-MAY-1999; 99US-0145276P.
XX PR 14-MAY-1999; 99US-0145913P.
XX PR 18-MAY-1999; 99US-0145918P.
XX PR 19-MAY-1999; 99US-0145919P.
XX PR 20-MAY-1999; 99US-0145951P.
XX PR 21-MAY-1999; 99US-0146386P.
XX PR 24-MAY-1999; 99US-0146388P.
XX PR 25-MAY-1999; 99US-0146389P.
XX PR 27-MAY-1999; 99US-0147038P.
XX PR 28-MAY-1999; 99US-0147204P.
XX PR 01-JUN-1999; 99US-0147302P.
XX PR 03-JUN-1999; 99US-0147302P.
XX PR 04-JUN-1999; 99US-0147303P.
XX PR 07-JUN-1999; 99US-0147303P.
XX PR 08-JUN-1999; 99US-0147416P.
XX PR 10-JUN-1999; 99US-0147433P.
XX PR 10-JUN-1999; 99US-0147935P.
XX PR 14-JUN-1999; 99US-0148171P.
XX PR 16-JUN-1999; 99US-0148319P.
XX PR 16-JUN-1999; 99US-0148341P.
XX PR 17-JUN-1999; 99US-0148565P.
XX PR 18-JUN-1999; 99US-0148684P.
XX PR 18-JUN-1999; 99US-0149368P.
XX PR 18-JUN-1999; 99US-0149175P.
XX PR 18-JUN-1999; 99US-0149457P.
XX PR 18-JUN-1999; 99US-0149722P.
XX PR 18-JUN-1999; 99US-0149723P.
XX PR 18-JUN-1999; 99US-0149929P.
XX PR 18-JUN-1999; 99US-0149902P.
XX PR 18-JUN-1999; 99US-0149930P.

PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0156559P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 25-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 270;
 Best Local Similarity 66.7%; Pred. No. 9.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 6
 ||:|:|
 Db 228 KFIFYA 233

RESULT 71
 AAU80872
 ID AAU80872 standard; protein; 297 AA.
 AC AAU80872;
 XX
 DT 26-MAR-2002 (first entry)
 XX Human CLAN NACHT.
 DE
 XX

KW Caspase recruitment domain; CARD; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 XX Homo sapiens.
 OS WO200190156-A2.
 PN 29-NOV-2001.
 PD 24-MAY-2001; 2001WO-US017158.
 PF 24-MAY-2000; 2000US-00579240.
 PR 10-OCT-2000; 2000US-00686347.
 PR 14-MAR-2001; 2001US-0275980P.
 PR 23-MAY-2001; 2001US-00864921.
 XX (BURN-) BURNHAM INST.
 XX Reed JC, Pio PF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 XX WPI; 2002-083086/11.
 DR N-PSDB; ABK22766.
 PT New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke.
 XX Claim 9; Page 201-202; 216pp; English.
 XX The invention relates to an isolated caspase recruitment domain (CARD) -
 CC containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 CC from it, and the polynucleotides encoding them. Also included are a
 CC recombinant vector comprising the polynucleotide, recombinant cells
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian and
 CC insect cells) and an anti-CARD antibody. The CARD-containing polypeptide
 CC and CARD-encoding nucleic acid are useful for treating a pathology
 CC characterised by abnormal cell proliferation (e.g. cancer), abnormal cell
 CC death (apoptosis), autoimmune diseases or inflammation. In particular,
 CC the polypeptide and nucleic acid are useful for treating keratinocyte
 CC hyperplasia, inflammatory hyperplasia, fibrosis, smooth muscle cell
 CC proliferation in arteries following balloon angioplasty (restenosis),
 CC gliomas, carcinomas, sarcomas, melanomas, leukaemias, allergies,
 CC arthritis, lupus, Schrogen's syndrome, Crohn's disease, graft-versus-host
 CC disease, stroke, myocardial infarction, heart failure, neurodegenerative
 CC diseases (e.g. Parkinson's disease or Alzheimer's disease) or
 CC immunodeficiency associated disease (e.g. human immunodeficiency virus
 CC (HIV) infection). The nucleic acids are useful in a variety of diagnostic
 CC applications. The present sequence is a CARD domain containing protein
 XX
 SQ Sequence 297 AA;

Query Match 87.1%; Score 27; DB 5; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 5
 ||:|:|
 Db 38 KFVFPA 42

RESULT 72
 ABU81731
 ID ABU81731 standard; protein; 297 AA.

XX AC ABU81731;

XX DT 26-JUN-2003 (first entry)

XX DE Human caspase recruitment domain-containing polypeptide #15.

XX DE Human; caspase recruitment domain-containing polypeptide; CARD; NB-ARC; ANGIO-R; leucine rich repeat; LRR; S-adenosyl methionine domain; apoptosis; NF-kappaB induction; cytokine processing; SAM; transcription; cJun N-terminal kinase induction; caspase-mediated proteolysis; cancer; inflammation; cell adhesion; cell proliferation; abnormal cell death; keratinocyte hyperplasia; neoplasia; benign prostatic hyper trophy; lupus; inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation; angioplasty; artery; keloid; restenosis; autoimmune disease; allergy; arthritis; Sjogren's syndrome; Crohn's disease; ulcerative colitis; allograft rejection; graft versus host disease; myocardial infarction; heart failure; neurodegenerative disease; stroke; HIV.

XX OS Homo sapiens.

XX PN US2002176853-A1.

XX PD 28-NOV-2002.

XX PF 23-MAY-2001; 2001US-00864921.

XX PR 24-MAY-2000; 2000US-0325756P.

XX PR 10-OCT-2000; 2000US-0367337P.

XX PR 14-MAR-2001; 2001US-0275980P.

XX (REED/) REED J C.

PA (PIOF/) PIO F F.

PA (GODZ/) GODZIK A.

PA (STEH/) STEHLIK C.

PA (DAMI/) DAMIANO J S.

PA (LEES/) LEE S H.

PA (OLIV/) OLIVEIRA V A.

PA (HAYA/) HAYASHI H.

PA (PAWL/) PAWLOWSKI K.

XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH; Oliveira VA, Hayashi H, Pawlowski K;

PI WPI; 2002-083086/11.

XX N-PSDB; ACA68180.

XX New caspase recruitment domain (CARD)-containing polypeptides and encoding nucleic acids, useful for treating abnormal cell proliferation or cell death, autoimmune diseases or inflammation, e.g. carcinomas, arthritis or stroke.

XX Claim 1; Page 85-86; 106pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)-containing polypeptide, or its CARD, NB-ARC, ANGIO-R, leucine rich repeat (LRR) or S-adenosyl methionine (SAM) domain, and its associated polynucleotide. The DNA is useful for altering the level of a biochemical process (including apoptosis, NF-kappaB induction, cytokine processing, cJun N-terminal kinase induction, caspase-mediated proteolysis, transcription, inflammation and cell adhesion) modulated by the DNA. The sequences are useful for treating a pathology characterised by abnormal cell proliferation, abnormal cell death or inflammation. The treatable diseases include cancer, keratinocyte hyperplasia, neoplasia, keloids, benign prostatic hypertrophy, inflammatory hyperplasia, fibrosis, smooth muscle cell proliferation in arteries following angioplasty, restenosis, autoimmune diseases including allergies, inflammatory diseases including arthritis, lupus, Sjogren's syndrome, Crohn's disease, ulcerative colitis, allograft rejection such as graft versus host disease, stroke, myocardial infarction, heart failure, neurodegenerative diseases such as Parkinson's disease and Alzheimer's disease and immunodeficiency associated diseases such as human immunodeficiency virus (HIV) infection. Sequences ABU81714-ABU81735 represent human CARD-containing polypeptides

CC of the invention

XX Sequence 297 AA;

SQ

Query Match 87.1%; Score 27; DB 5; Length 297;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

Db 38 KVFVF 42

|||||

RESULT 73

ADP47907

ID ADP47907 standard; protein; 312 AA.

XX ADP47907;

AC ADP47907;

XX 12-AUG-2004 (first entry)

DT XX Human CATERPILLER Ipaf nucleotide binding domain (NBD) protein.

DE XX

XX Monarch-1; CATERPILLER 11.2; caspase recruitment domain; CARD, transcription enhancer, R-binding, pyrin, lots of leucine repeat; CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIAS1; cold-induced autoinflammatory syndrome 1; antiinflammatory; cytostatic; inflammatory disease; cancer; gene therapy; human; purine; nucleotide binding domain; NBD; Ipaf.

XX Homo sapiens.

OS

XX WO2004034093-A2.

PN 22-APR-2004.

XX 30-APR-2003; 2003WO-US013562.

PF 30-APR-2002; 2002US-0376626P.

PR (UTNC-) UNIV NORTH CAROLINA.

XX Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'connor W; Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;

PI WPI; 2004-348215/32.

XX New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3, CATERPILLAR 16.1, CATERPILLER 16.2 or CIAS1 polypeptide, useful in preparing a composition for treating inflammatory disease or cancer.

PT Example 1; Fig 3; 205pp; English.

PS

XX The invention relates to a novel isolated nucleic acid encoding a Monarch -1, CATERPILLER (CARD [caspase recruitment domain], transcription enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2, CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 (cold-induced autoinflammatory syndrome 1) polypeptide comprising the amino acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or its fragment. The nucleic acid of the invention demonstrates antiinflammatory and cytostatic activities and may be useful in preparing a composition for treating an inflammatory disease or cancer, possibly via gene therapy. The current sequence is that of a human CATERPILLER nucleotide binding domain (NBD) protein of the invention.

XX Sequence 312 AA;

SQ

Query Match 87.1%; Score 27; DB 8; Length 312;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

|||||

Db 51 KTVFF 55

RESULT 74
AAG33404
ID AAG33404 standard; protein; 313 AA.
XX AC AAG33404;
XX DT 18-OCT-2000 (first entry)
XX Zea mays protein fragment SEQ ID NO: 40468.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX Zea mays subsp. mays.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 13-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 19-MAY-1999; 99US-0134768P.
PR 20-MAY-1999; 99US-0134941P.
PR 21-MAY-1999; 99US-0135124P.
PR 24-MAY-1999; 99US-0135353P.
PR 25-MAY-1999; 99US-0135629P.
PR 27-MAY-1999; 99US-0136021P.
PR 28-MAY-1999; 99US-0136382P.
PR 01-JUN-1999; 99US-0136782P.
PR 03-JUN-1999; 99US-0137222P.
PR 04-JUN-1999; 99US-0137528P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139482P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 06-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142390P.
PR 09-JUL-1999; 99US-0142803P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147260P.
PR 05-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.

```

PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156598P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0158293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159334P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
DB 86 KVFVF 90

RESULT 75
ID ADT58396 standard; protein; 335 AA.
XX

```

```

AC ADT58396;
XX
DT 13-JAN-2005 (first entry)
XX
DE Plant polypeptide, SEQ ID 8473.
XX
KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
OS Viridiplantae.
XX
PN US2004216190-A1.
XX
PD 28-OCT-2004.
XX
PF 18-DEC-2003; 2003US-00739930.
XX
PR 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX
PA (KOVA/) KOVALIC D K.
XX
PI Kovalic DK;
XX
WP: 2004-757369/74.
XX
PS New recombinant DNA constructs useful in the field of biochemistry and
genetics, and in particular for producing transgenic plants with improved
biological characteristics.
XX
PS Claim 2; SEQ ID NO 8473; 14pp; English.
XX
CC The invention relates a recombinant DNA construct comprising a
polynucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO:
1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
(SQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean,
Arabidopsis, wheat and rape but the specification does not indicate which
sequences is derived from which organism. Also included is a method of
producing a plant having an improved property, comprising transforming a
plant with a recombinant DNA construct comprising a promoter region
functional in a plant cell operably joined to a polynucleotide encoding a
polypeptide associated with the property, and growing the transformed
plant. The property is selected from improving plant cold tolerance, for
manipulating growth rate in plant cells by modification of the cell cycle
pathway, for improving plant drought tolerance, for providing increased
resistance to plant disease, for galactomannan production, for production
of plant growth regulators, for improving plant heat tolerance, for
improving plant tolerance to herbicides, for increasing the rate of
homologous recombination in plants, for lignin production, for improving
plant tolerance to extreme osmotic conditions, for improving plant
tolerance to pathogens or pests, for yield improvement by modification of
photosynthesis, for modifying seed oil yield and/or content, for
modifying seed protein yield and/or content, for yield improvement by
modification of carbohydrate, nitrogen or phosphorus use and/or uptake
and for yield improvement by providing improved plant growth and
development under at least one stress condition. The polynucleotide may
also encode a plant transcription factor. The methods and compositions of
the present invention are useful in the field of biochemistry and
genetics, in particular for producing transgenic plants with improved
biological characteristics such as increased yield, improved nitrogen
flow, increasing plant tolerance to cold or heat, improving plant
tolerance to extreme osmotic and drought conditions, and improving plant
tolerance to plant pests or pathogens. They can also be used in physical
arrays of molecules, plant breeding markers, computer-based storage and
analysis systems. The present sequence is one of the 5544 plant protein
sequences of the invention. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20040216190.
XX

```

SQ Sequence 335 AA;

Query Match 87.1%; Score 27; DB 8; Length 335;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
 || ||
 Db 80 KPAFFA 85

Search completed: December 29, 2005, 17:33:39
 Job time : 82.7742 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-10
Perfect score: 29
Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	164	Q73N39_TREDE	Q73N39 treponema d
2	29	100.0	387	Q81FHS_BACCR	Q81FHS bacillus ce
3	29	100.0	450	Q4TRF8_9SPHN	Q4TRF8 erythrobact
4	29	100.0	464	Q4S4T5_TETNG	Q4S4T5 tetraodon n
5	29	100.0	606	Q91VU5_MOUSE	Q91VU5 mus musculu
6	29	100.0	663	Q6RUU2_MOUSE	Q6RUU2 mus musculu
7	29	100.0	690	Q83IB2_TROW8	Q83IB2 tropheryma
8	29	100.0	698	Q83GW3_TROWT	Q83GW3 tropheryma
9	29	100.0	1265	Q6ZQ91_MOUSE	Q6ZQ91 mus musculu
10	29	100.0	1412	Q5F3M1_CHICK	Q5F3M1 gallus gall
11	28	96.6	88	Q4LBQ8_SODGL	Q4LBQ8 sodalis glo
12	28	96.6	183	Q9RQ09_BACTN	Q9RQ09 bacteroides
13	28	96.6	186	GL19_ORYSA	F29835 oryza sativ
14	28	96.6	186	P93414_ORYSA	P93414 oryza sativ
15	28	96.6	231	Q8C6Y8_MOUSE	Q8C6Y8 mus musculu
16	28	96.6	315	Q61C67_CAEBR	Q61C67 caenorhabdi
17	28	96.6	362	Q4HSJ7_CAMUP	Q4HSJ7 campylobact
18	28	96.6	372	Q6D7U3_ERWCT	Q6D7U3 erwania car
19	28	96.6	373	Q7M9N5_WOLSU	Q7M9N5 wolnelliella s
20	28	96.6	382	Q9V7J0_DROME	Q9V7J0 drosophila
21	28	96.6	387	Q9KI10_BACCE	Q9KI10 bacillus ce
22	28	96.6	387	Q4MT39_BACCE	Q4MT39 bacillus ce
23	28	96.6	387	Q63DD4_BACCH	Q63DD4 bacillus th
24	28	96.6	387	Q6HKU6_BACHK	Q6HKU6 bacillus th
25	28	96.6	387	Q73AP3_BACCL	Q73AP3 bacillus ce
26	28	96.6	387	Q81SK9_BACAN	Q81SK9 bacillus an
27	28	96.6	410	Q6L2B4_PICTO	Q6L2B4 picrophilus
28	28	96.6	410	Q8C5T3_MOUSE	Q8C5T3 mus musculu
29	28	96.6	442	Q9PHV5_CAMJE	Q9PHV5 campylobact
30	28	96.6	447	Q59243_PYROH	Q59243 pyrococcus
31	28	96.6	556	Q95S93_DROME	Q95S93 drosophila

32	28	96.6	556	2	Q9V7I9_DROME	Q9V7I9 drosophila
33	28	96.6	703	2	Q5HYE1_HUMAN	Q5HYE1 homo sapien
34	28	96.6	721	2	Q6AG25_LBIXX	Q6AG25 leifsonia x
35	28	96.6	785	2	Q9GQ82_DROME	Q9GQ82 drosophila
36	28	96.6	925	2	Q95786_HUMAN	Q95786 homo sapien
37	28	96.6	925	2	Q5VVT1_HUMAN	Q5VVT1 homo sapien
38	28	96.6	926	2	Q6Q899_MOUSE	Q6Q899 mus musculu
39	28	96.6	940	2	Q9GLV6_PIG	Q9GLV6 sus scrofa
40	28	96.6	1144	1	N0S2_MOUSE	P29477 mus musculu
41	28	96.6	1144	2	Q5SXT3_MOUSE	Q5SXT3 mus musculu
42	28	96.6	1145	2	Q8R410_MOUSE	Q8R410 mus musculu
43	28	96.6	1145	2	Q6P6A0_MOUSE	Q6P6A0 mus musculu
44	28	96.6	1384	2	Q68K27_CHLRE	Q68K27 chlamydomon
45	28	96.6	1408	2	Q7QEF0_ANOGA	Q7QEF0 anopheles g
46	28	96.6	1443	2	Q9VPR0_DROME	Q9VPR0 drosophila
47	28	96.6	1458	2	Q5BI64_DROME	Q5BI64 drosophila
48	28	96.6	1503	2	Q7KTZ4_DROME	Q7KTZ4 drosophila
49	28	96.6	1676	2	Q8A6R7_BACTN	Q8A6R7 bacteroides
50	27	93.1	33	2	Q9UC33_HUMAN	Q9UC33 homo sapien
51	27	93.1	42	2	O56J36_GRAGR	O56J36 grampus gri
52	27	93.1	42	2	Q56J37_TURTR	Q56J37 tursiops tr
53	27	93.1	42	2	Q7M088_CAVPO	Q7M088 cavia porce
54	27	93.1	52	2	Q8WZ99_HUMAN	Q8WZ99 homo sapien
55	27	93.1	57	1	A4_URSWA	Q29149 u alzheimer
56	27	93.1	58	1	A4_CANFA	Q28280 c alzheimer
57	27	93.1	58	1	A4_RABIT	Q28748 o alzheimer
58	27	93.1	58	1	A4_SHEEP	Q28757 o alzheimer
59	27	93.1	59	1	A4_BOVIN	Q28053 b alzheimer
60	27	93.1	79	2	O35463_CRIGR	O35463 cricetulus
61	27	93.1	113	2	Q8JH58_CHESE	Q8JH58 chelydra se
62	27	93.1	137	2	Q7UPR1_RHOBA	Q7UPR1 rhodopirell
63	27	93.1	152	2	Q9STZ9_ARATH	Q9STZ9 arabidopsis
64	27	93.1	203	2	Q6AKB9_DESPS	Q6AKB9 desulfotale
65	27	93.1	218	2	Q8BPV5_MOUSE	Q8BPV5 mus musculu
66	27	93.1	229	2	Q8VY56_ARATH	Q8VY56 arabidopsis
67	27	93.1	231	2	Q9SV79_ARATH	Q9SV79 arabidopsis
68	27	93.1	352	2	Q9XGY6_SINCH	Q9XGY6 simmondsia
69	27	93.1	357	2	Q8U460_PYRFU	Q8U460 pyrococcus
70	27	93.1	357	2	Q8UU18_BRARE	Q8UU18 brachydanio
71	27	93.1	366	2	Q8PPL1_XANON	Q8PPL1 xanthomonas
72	27	93.1	380	2	O67225_AQUAE	O67225 aquifex aeo
73	27	93.1	384	2	Q8BPC7_MOUSE	Q8BPC7 mus musculu
74	27	93.1	391	2	Q4NSU7_THERPA	Q4NSU7 theileria p
75	27	93.1	399	2	O5WPU9_LUTLO	O5WPU9 lutomyia l
76	27	93.1	403	2	Q5L117_GEOKA	Q5L117 geobacillus
77	27	93.1	404	2	Q4UY5S_XANCP	Q4UY5S xanthomonas
78	27	93.1	404	2	Q8P597_XANCP	Q8P597 xanthomonas
79	27	93.1	428	2	Q9M1Q8_ARATH	Q9M1Q8 arabidopsis
80	27	93.1	461	2	Q89329_9POTV	Q89329 zucchini ye
81	27	93.1	470	2	Q7T910_9POTV	Q7T910 zucchini ye
82	27	93.1	472	2	Q8UU00_BRARE	Q8UU00 brachydanio
83	27	93.1	488	2	Q52NV6_9POTV	Q52NV6 zucchini ye
84	27	93.1	490	2	Q7T911_9POTV	Q7T911 zucchini ye
85	27	93.1	490	2	Q7T912_9POTV	Q7T912 zucchini ye
86	27	93.1	493	2	Q5K4D4_9POTV	Q5K4D4 soybean mos
87	27	93.1	493	2	Q5K4D5_9POTV	Q5K4D5 soybean mos
88	27	93.1	508	2	Q5GV5S_XANOR	Q5GV5S xanthomonas
89	27	93.1	534	2	Q93296_CHICK	Q93296 gallus gall
90	27	93.1	569	2	Q9PVL1_CHICK	Q9PVL1 gallus gall
91	27	93.1	612	2	Q919E7_BRARE	Q919E7 brachydanio
92	27	93.1	615	2	Q50Z85_ENTHI	Q50Z85 entamoeba h
93	27	93.1	623	2	Q4WBU2_ASFFU	Q4WBU2 aspergillus
94	27	93.1	630	2	Q5K7B5_CRYNE	Q5K7B5 cryptococcu
95	27	93.1	638	2	Q5B2V4_EMENI	Q5B2V4 aspergillus
96	27	93.1	678	2	Q7ZZT1_BRARE	Q7ZZT1 brachydanio
97	27	93.1	693	2	Q98SG0_XENLA	Q98SG0 xenopus lae
98	27	93.1	695	2	Q5R477_PONPY	Q5R477 pongo pygma
99	27	93.1	695	2	Q6RH29_CANFA	Q6RH29 canis fami
100	27	93.1	695	2	Q56JK3_CANFA	Q56JK3 canis fami
101	27	93.1	695	2	Q6GR78_MOUSE	Q6GR78 mus musculu
102	27	93.1	695	2	Q9DGJ8_CHICK	Q9DGJ8 gallus gall
103	27	93.1	695	2	Q98SF9_XENLA	Q98SF9 xenopus lae
104	27	93.1	695	2	Q7ZXQ0_XENLA	Q7ZXQ0 xenopus lae

105	27	93.1	714	2	Q56JK4	CANFA	Q56jk4	canis famil	178	26	89.7	248	2	Q813W8	PLAF7	Q813w8	plasmodium
106	27	93.1	733	2	Q6P6Q5	RAT	Q6p6q5	rattus norv	179	26	89.7	253	2	Q9KL60	VIBCH	Q9kl60	vibrio chol
107	27	93.1	737	1	A4_FUGRU		Q93279	fugu rubrip	180	26	89.7	270	2	Q7MV75	PORGI	Q7mv75	porphyronon
108	27	93.1	738	1	Q6NUZ1	BRARE	Q6nuz1	brachydanio	181	26	89.7	279	2	Q4ILF1	GIBZE	Q4ilf1	gibberella
109	27	93.1	738	2	Q90W28	BRARE	Q90w28	brachydanio	182	26	89.7	281	2	Q51ZJ1	MAGGR	Q51zj1	magnaporthe
110	27	93.1	747	2	Q31963	9P1PI	Q31963	xenopus. ap	183	26	89.7	281	2	Q4XS11	PLACH	Q4xs11	plasmodium
111	27	93.1	749	2	Q56JK2	STECO	Q56jk2	stenella co	184	26	89.7	284	2	Q4ZX22	PSSEY	Q4zx22	pseudomonas
112	27	93.1	749	2	Q6NR11	XENLA	Q6nr11	xenopus lae	185	26	89.7	292	2	Q4WK19	CAEPFU	Q4wk19	aspergillus
113	27	93.1	750	2	Q6DJB6	XENTR	Q6djb6	xenopus tro	186	26	89.7	300	2	Q9XU61	CAEPL	Q9xu61	caenorhabdi
114	27	93.1	751	1	A4_SAISC		Q95241	s amyloid b	187	26	89.7	301	2	Q5B613	EMENI	Q5b613	aspergillus
115	27	93.1	751	2	Q6SC00	HUMAN	Q6sc00	homo sapien	188	26	89.7	306	2	Q68RL2	THEMI	Q68rl2	glycaerps b
116	27	93.1	751	2	Q6RH28	CANFA	Q6rh28	canis famil	189	26	89.7	312	2	Q9ZZU4	9CAEN	Q9zzu4	littorina s
117	27	93.1	751	2	Q56JK5	CANFA	Q56jk5	canis famil	190	26	89.7	321	1	Y189	RICPR	Q92dx5	rickettsia
118	27	93.1	751	2	Q4R4R8	CANFA	Q4r4r8	macaca fasc	191	26	89.7	333	2	Q6TG00	HELZE	Q6tg00	heliothis z
119	27	93.1	751	2	Q9DGJ7	CHICK	Q9dgj7	gallus gall	192	26	89.7	336	1	RSMC	BUCAP	Q8k9l5	buchera ap
120	27	93.1	754	2	Q4RY33	TETNG	Q4ry33	tetraodon n	193	26	89.7	337	2	Q54NZ2	DICDI	Q54nz2	dictyosteli
121	27	93.1	754	2	Q4S034	TETNG	Q4s034	tetraodon n	194	26	89.7	347	2	Q87PM3	VIBPA	Q87pm3	vibrio para
122	27	93.1	760	2	Q55HW1	CRINE	Q55hw1	cryptococcu	195	26	89.7	349	2	Q9XU59	ANASP	Q9xu59	caenorhabdi
123	27	93.1	770	1	A4_CAVFO		Q60495	c amyloid b	196	26	89.7	352	2	Q8YUK9	ANASP	Q8yuk9	anabaena sp
124	27	93.1	770	1	A4_HUMAN		P53601	m amyloid b	197	26	89.7	360	2	Q7NM29	GLOVI	Q7nm29	gloeobacter
125	27	93.1	770	1	A4_MACFA		P53601	m amyloid b	198	26	89.7	366	2	Q8DI25	SVNEL	Q8di25	synechococc
126	27	93.1	770	1	A4_MOUSE		P12023	m amyloid b	199	26	89.7	380	2	Q7VJCL	HELHP	Q7vjc1	helicobacte
127	27	93.1	770	1	A4_PANTR		Q51s80	p amyloid b	200	26	89.7	382	2	Q9KDE2	BACSD	Q9kde2	bacillus ha
128	27	93.1	770	1	A4_PIG		P79307	s amyloid b	201	26	89.7	390	2	Q5WLG1	BACSK	Q5wlg1	bacillus cl
129	27	93.1	770	1	A4_RAT		P8B592	r amyloid b	202	26	89.7	391	2	Q8A2G6	BACTN	Q8a2g6	bacteroides
130	27	93.1	770	2	Q6RH30	CANFA	Q6rh30	canis famil	203	26	89.7	400	2	Q7PXH6	ANOAG	Q7pxh6	anopheles g
131	27	93.1	770	2	Q56JK6	CANFA	Q56jk6	canis famil	204	26	89.7	402	2	Q9Z1T8	ECOLI	Q9zit8	escherichia
132	27	93.1	770	2	Q53ZT3	MOUSE	Q53zt3	mus musculu	205	26	89.7	402	2	Q7DB96	SCOS7	Q7db96	escherichia
133	27	93.1	770	2	Q547B7	RAT	Q547b7	rattus norv	206	26	89.7	402	2	Q83PPI	SHIFL	Q83ppi	shigella fl
134	27	93.1	770	1	A4_TETFL		Q73683	tetraodon f	207	26	89.7	405	1	SYV	BORBU	Q51343	borrelia bu
135	27	93.1	955	2	Q80R22	9POTV	Q80r22	calla lily	208	26	89.7	405	1	Q661P9	BORGA	Q661p9	borrelia ga
136	27	93.1	962	2	Q4NTK2	9DELT	Q4ntk2	anaeromykob	209	26	89.7	421	2	Q9LH60	ARATH	Q9lh60	arabidopsai
137	27	93.1	1016	2	Q05912	9POTV	Q05912	zucchinni ye	210	26	89.7	468	2	Q616J7	CAEBR	Q616j7	caenorhabdi
138	27	93.1	1056	2	Q6FK46	CANGA	Q6fk46	candida gla	211	26	89.7	472	2	Q4WEZ5	ASPFU	Q4wez5	aspergillus
139	27	93.1	1655	2	Q4SQ4	LEIMA	Q4sq4	leishmania	212	26	89.7	479	2	Q9QDL5	9POTV	Q9qdl5	sarcophilus
140	27	93.1	1916	2	Q8QK04	9POTV	Q8qk04	zucchinni ye	213	26	89.7	479	2	Q4F979	9POTV	Q4f979	eustrephus
141	27	93.1	3080	1	POLG_ZYMYC		P18479	z genome po	214	26	89.7	480	2	Q4N8N8	THEPA	Q4n8n8	theileria p
142	27	93.1	3080	2	Q6WN47	9POTV	Q6wn47	zucchinni ye	215	26	89.7	496	2	Q5K4D0	9POTV	Q5k4d0	dasheen mos
143	27	93.1	3080	2	Q6WN48	9POTV	Q6wn48	zucchinni ye	216	26	89.7	502	2	Q5L1S5	GEOKA	Q5l1s5	geobacillus
144	27	93.1	3080	2	Q6WN49	9POTV	Q6wn49	zucchinni ye	217	26	89.7	522	2	Q4XPM5	PLACH	Q4xpm5	plasmodium
145	27	93.1	3080	2	Q5Y2U7	9POTV	Q5y2u7	zucchinni ye	218	26	89.7	524	2	Q912R1	9POTV	Q912r1	dasheen mos
146	27	93.1	3080	2	Q7T908	9POTV	Q7t908	zucchinni ye	219	26	89.7	539	2	Q9QP99	9POTV	Q9qp99	dasheen mos
147	27	93.1	3080	2	Q7T914	9POTV	Q7t914	zucchinni ye	220	26	89.7	557	2	Q4UGZ4	THEAN	Q4ugz4	theileria a
148	27	93.1	3083	1	POLG_ZYMY5		Q36979	z genome po	221	26	89.7	598	2	Q644G8	9SALA	Q644g8	grinophilu
149	27	93.1	3105	2	Q70XR2	9POTV	Q70xr2	soybean mos	222	26	89.7	604	2	Q645P2	9SALA	Q645f2	stereochilu
150	26	89.7	40	2	Q1FF3	IRV6	Q91ff3	chilo iride	223	26	89.7	606	2	Q8SJ19	URSAM	Q8sj19	ursus ameri
151	26	89.7	66	2	Q728F0	DESVH	P728f0	desulfovibr	224	26	89.7	607	2	Q644P6	9SALA	Q644p6	thorius n.
152	26	89.7	74	1	Y131	MYCGE	P47377	mycoplasma	225	26	89.7	611	2	Q6ZLV9	9TELE	Q6zlv9	ophiurus m
153	26	89.7	81	2	Q6D3D0	ERWCT	Q6d3d0	erwinia car	226	26	89.7	613	2	Q4ZGQ0	9TELE	Q4zgg0	scleropages
154	26	89.7	89	2	Q83VF2	LACLC	Q83vf2	lactococcus	227	26	89.7	620	2	Q29198	ARCFU	Q29198	archaeoglob
155	26	89.7	105	2	Q64CV5	9ARCH	Q64cv5	uncultured	228	26	89.7	624	2	Q6FBJ6	ACIAD	Q6fbj6	acinetobact
156	26	89.7	109	2	Q9X292	THEMA	Q9x292	thermotoga	229	26	89.7	626	2	Q8RM01	ACIAD	Q8rm01	acinetobact
157	26	89.7	145	2	Q5USA9	9PEZI	Q5usa9	monacospor	230	26	89.7	685	1	MDL1	CANAL	P97998	candida alb
158	26	89.7	156	2	Q8DN20	STRP6	Q8dn20	streptococc	231	26	89.7	685	2	Q5A951	CANAL	Q5a951	candida alb
159	26	89.7	156	2	Q8N292	STRP6	Q8n292	streptococc	232	26	89.7	726	2	Q4Y7D6	PLACH	Q4y7d6	plasmodium
160	26	89.7	164	2	Q81Y15	BACAN	Q81y15	bacillus an	233	26	89.7	738	2	Q5A445	CANAL	Q5a445	candida alb
161	26	89.7	190	2	Q82WB8	RHIME	Q82wb8	rhizobium m	234	26	89.7	743	2	Q6BM34	DEBHA	Q6bm34	debaryomyce
162	26	89.7	194	2	Q87G46	CLOAB	Q87g46	clostridium	235	26	89.7	771	2	Q4SDL4	TETNG	Q4sdl4	tetradomyce
163	26	89.7	196	2	Q8HVS9	BACAN	Q8hvs9	bacillus an	236	26	89.7	774	2	Q64777	ARATH	Q64777	arabidopsai
164	26	89.7	202	2	Q7P578	FUSNV	Q7p578	fusobacteri	237	26	89.7	787	2	Q4XMD0	PLACH	Q4xmd0	plasmodium
165	26	89.7	202	2	Q8RE19	FUSNV	Q8re19	fusobacteri	238	26	89.7	804	2	Q64770	ARATH	Q64770	arabidopsai
166	26	89.7	218	2	Q5CYB3	CRYPV	Q5cyb3	cryptospori	239	26	89.7	881	2	Q6BM22	DEBHA	Q6bm22	debaryomyce
167	26	89.7	218	2	Q5CIV9	CRYHO	Q5civ9	cryptospori	240	26	89.7	911	2	Q6MUF5	MYCMS	Q6muf5	mycoplasma
168	26	89.7	220	2	Q5Z2T4	PEMVM	Q5z2t4	peanut mott	241	26	89.7	957	2	Q7T3T7	OREMO	Q7t3t7	oreochromis
169	26	89.7	230	2	Q7RDM9	PLAYO	Q7rdm9	plasmodium	242	26	89.7	969	2	Q71953	9POTV	Q71953	dasheen mos
170	26	89.7	231	2	Q637W5	BACCZ	Q637w5	bacillus ce	243	26	89.7	973	2	Q9VTH1	DROME	Q9vth1	drosophila
171	26	89.7	241	2	Q4XAZ2	PLACH	Q4xaz2	plasmodium	244	26	89.7	1094	2	Q4Q4Z7	LEIMA	Q4q4z7	leishmania
172	26	89.7	241	2	Q4MXQ0	BACCZ	Q4mxq0	bacillus ce	245	26	89.7	1119	2	Q9LM79	ARATH	Q9lm79	arabidopsai
173	26	89.7	241	2	Q438P6	BACCZ	Q438p6	bacillus ce	246	26	89.7	1273	2	Q9LM82	ARATH	Q9lm82	arabidopsai
174	26	89.7	241	2	Q6HG76	BACHK	Q6hg76	bacillus th	247	26	89.7	3099	1	POLG_PENVM		Q56075	p genome po
175	26	89.7	241	2	Q734P7	BACCI	Q734p7	bacillus ce	248	26	89.7	3191	2	Q912R2	9POTV	Q912r2	dasheen mos
176	26	89.7	241	2	Q81B59	BACCR	Q81b59	bacillus ce	249	26	89.7	3381	2	Q81DK4	PLAF7	Q81dk4	plasmodium
177	26	89.7	241	2	Q81N30	BACAN	Q81n30	bacillus an	250	25	86.2	20	2	Q8CYA3	STRR6	Q8cya3	streptococc

251 25 86.2 26 2 Q4XGP1 PLASMODIUM
 252 25 86.2 46 2 Q4YT9 PLASMODIUM
 253 25 86.2 47 2 Q8EXM4 LEPTOSPIRA
 254 25 86.2 46 2 Q8QGY9 FUGU RUBRIP
 255 25 86.2 49 2 Q4XA79 PLASMODIUM
 256 25 86.2 51 2 Q7RF81 PLASMODIUM
 257 25 86.2 51 2 Q4YGE7 PLASMODIUM
 258 25 86.2 55 2 Q8YV8 NITROSONA
 259 25 86.2 59 2 Q4YGP8 PLASMODIUM
 260 25 86.2 62 1 Y078 HELPY
 261 25 86.2 62 1 Y085 HELPY
 262 25 86.2 62 2 Q6AS36 BACFR
 263 25 86.2 72 2 Q4HSS4 CAMUP
 264 25 86.2 72 2 Q5KQ9 CRAGI
 265 25 86.2 77 2 Q5KQ9 CRAGI
 266 25 86.2 79 2 Q5WJL8 BACSK
 267 25 86.2 81 1 MORAD ECOLI
 268 25 86.2 81 2 Q9APF7 9BACT
 269 25 86.2 81 2 Q57RF2 SALCH
 270 25 86.2 81 2 Q6STT0 MANSUM
 271 25 86.2 81 2 Q7MGP4 PHOLL
 272 25 86.2 81 2 Q8D897 VIBVU
 273 25 86.2 81 2 Q9KT78 VIBCH
 274 25 86.2 81 2 Q83S38 SHIFL
 275 25 86.2 81 2 Q7NM72 VIBVU
 276 25 86.2 81 2 Q8X807 ECO57
 277 25 86.2 83 2 Q8CLV3 YERP8
 278 25 86.2 83 2 Q5FG40 SALPA
 279 25 86.2 83 2 Q8Z886 SALT1
 280 25 86.2 85 2 Q8ZQO0 SALT1
 281 25 86.2 108 1 Y3403 METUA
 282 25 86.2 109 2 Q6YVX4 ORYSA
 283 25 86.2 111 2 Q9AI26 ECOLI
 284 25 86.2 116 2 Q49347 MYCGE
 285 25 86.2 121 2 Q4VBR3 BRARE
 286 25 86.2 128 2 Q6DUB9 PSRFL
 287 25 86.2 130 2 Q4KBR9 PSRFP5
 288 25 86.2 138 1 Y613 PASMU
 289 25 86.2 131 2 Q6BXU4 DBBHA
 290 25 86.2 135 2 Q9LIH4 ARATH
 291 25 86.2 141 2 Q5LGT9 BACFN
 292 25 86.2 141 2 Q67684 AQUAE
 293 25 86.2 141 2 Q64XP1 BACFR
 294 25 86.2 143 1 COF1 YEAST
 295 25 86.2 143 2 Q6BWX4 DBBHA
 296 25 86.2 143 2 Q6CQ22 KLJULA
 297 25 86.2 143 2 Q6FV81 CANGA
 298 25 86.2 143 2 Q9HF97 ZYGRO
 299 25 86.2 143 2 Q759P0 ASHGO
 300 25 86.2 143 2 Q8EMC6 OCEIHI

ALIGNMENTS

RESULT 1
 Q73N39 TREDE PRELIMINARY; PRT; 164 AA.
 ID Q73N39 TREDE PRELIMINARY; PRT; 164 AA.
 AC Q73N39;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=TDE1317;
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OC NCBI_TaxID=158;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 35405 / DSM 14222;
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
 Dodson R.J., Davidse T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

RA Selenget J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 Gebregoriss E., Geer K., Tsagaye G., Malek J.A., Ayodeji B.,
 Shatsman S., McLeod M.P., Smajls D., Howell J.K., Fal S., Amin A.,
 Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
 Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
 RT "Comparison of the genome of the oral pathogen Treponema denticola
 with other spirochete genomes";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
 DR EMBL; AE017250; AAS11834.1; -; Genomic_DNA.
 DR TIGR; TDE1317; -;
 KW Complete proteome.
 SQ SEQUENCE 164 AA; 18968 MW; 27B92778DDA9117C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 164;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 50 KIVFFA 55
 RESULT 2
 Q81FH5 BACCR PRELIMINARY; PRT; 387 AA.
 ID Q81FH5 BACCR PRELIMINARY; PRT; 387 AA.
 AC Q81FH5;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Na+/H+ antiporter NAPA (inosine-dependent germination).
 GN OrderedLocusNames=BCI612;
 OC Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 RN [1]
 RN NCBI_TaxID=226900;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,
 Kapralov V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 Chu L., Mazur M., Goldstein E., Larsen N., D'Souza M., Walunas T.,
 Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 Overbeek R., Kyrpides N.C.;
 RA "Genome sequence of Bacillus cereus and comparative analysis with
 other Bacillus anthracis";
 RT Nature 423:87-91(2003).
 RL Nature 423:87-91(2003).
 DR EMBL; AE017003; AAP08591.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; F:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRfams; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41037 MW; 907C03B6BA150B4A CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. No. 2.1e-02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 184 KIVFFA 189
 RESULT 3
 Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.
 ID Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.

```

AC Q4TRF8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Membrane protein.
GN ORFNames=BLI0568;
OS Erythrobacter litoralis H7CC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S.,
RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
RA Friedman R., Venter J.C.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAGG01000001; EAL76762.1; -; Genomic DNA.
SQ SEQUENCE 450 AA; 50280 MW; 077F448E75AD977 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 116 KIVFFA 121

RESULT 4
Q4S4T5_TETNG
ID Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
AC Q4S4T5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAR14738, whole genome shotgun sequence.
DE (Fragment)
GN ORFNames=GSTENG00024047001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygia; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bienmont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Bottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Boeak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter F., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Croliis H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014738; CAG04347.1; -; Genomic DNA.

```

```

FT NON TER 464 464
SQ SEQUENCE 464 AA; 53213 MW; 0F9FF81DB193CE5C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 304 KIVFFA 309

RESULT 5
Q91VU5_MOUSE
ID Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
AC Q91VU5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Wdct2 protein.
GN Name=A1661311; Synonyms=Wdctc2;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RG NIH MGC Project;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009019; AAH09019.1; -; mRNA.
DR Ensemble; ENSMUSG00000024169; Mus musculus.
DR MGI; MGI:2146906; A1661311.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like helical.
SQ SEQUENCE 606 AA; 70392 MW; 4BB6057E07ADA16C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 606;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 376 KIVFFA 381

RESULT 6
Q6RUU2_MOUSE

```

```

ID QGRU2_MOUSE PRELIMINARY; PRT; 663 AA.
AC QGRU2_MOUSE PRELIMINARY; PRT; 663 AA.
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bratwaite M., Waelz P., Dudekula D., Nagaraja R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY491413; AAS21643.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3EED0356F1C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 433 KIVFFA 438

RESULT 7
ID Q831B2_TROW8 PRELIMINARY; PRT; 690 AA.
AC Q831B2_TROW8 PRELIMINARY; PRT; 690 AA.
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Putative helicase regulator.
OS Tropheryma whippelii (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bentley S.D., Mairwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrall B.G., Parkhill J., Rellman D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whippelii."
RL Lancet 361:637-644(2003).
DR EMBL; BX251410; CAD66810.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome.
SQ SEQUENCE 690 AA; 76266 MW; CD3633B94B669E32 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 526 KIVFFA 531

RESULT 8
ID Q83GW3_TROWT PRELIMINARY; PRT; 698 AA.
AC Q83GW3_TROWT PRELIMINARY; PRT; 698 AA.
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE DNA helicase.
OS Tropheryma whippelii (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Raoult D., Ogata H., Audic S., Robert C., Suhre K., Drancourt M.,
RA Claverie J.-M.;
RT "Tropheryma whippelii Twist: a human pathogenic Actinobacteria with a
reduced genome."
RL Genome Res. 13:1800-1809(2003).
DR EMBL; AE016850; AAO44215.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; Helicase.
SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDDE72 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 534 KIVFFA 539

RESULT 9
ID Q6ZQ91_MOUSE PRELIMINARY; PRT; 1265 AA.
AC Q6ZQ91_MOUSE PRELIMINARY; PRT; 1265 AA.
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MKIAA0590 protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
III. the complete nucleotide sequences of 500 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries."
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129167; BAC97977.1; -; mRNA.

```

```

FT NON_TER      1      1
SQ SEQUENCE     1265 AA; 143403 MW; C9C157ABE80FF928 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 1265;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1081 KIVFFA 1086

RESULT 10
Q5F3M1 CHICK
ID Q5F3M1 CHICK PRELIMINARY; PRT; 1412 AA.
AC Q5F3M1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH5263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE     1412 AA; 158448 MW; FA0050885B274747 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 1412;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1225 KIVFFA 1230

RESULT 11
Q4LBQ8_SODGL
ID Q4LBQ8_SODGL PRELIMINARY; PRT; 88 AA.
AC Q4LBQ8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chey protein.
GN Name=cheY;
OS Sodalis glossinidius.
OG Plasmid pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtzis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius.";
```

```

RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE     88 AA; 10177 MW; F4168F2A56B8D0AC CRC64;

Query Match
Best Local Similarity 96.6%; Score 28; DB 2; Length 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      42 KIVFFA 47

RESULT 12
Q9RQ09_BACTN
ID Q9RQ09_BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09; Q7C422;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=93380605; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.10800029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic DNA.
DR EMBL; AE016931; AA076385.1; -; Genomic_DNA.
DR GO; GO:0016987; P:sigma factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF04542; Sigma70_r2; 1.
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Sigma factor; Transcription;
KW Transcription regulation; Transference.
SQ SEQUENCE     183 AA; 22042 MW; 6B24DABC99BEC643 CRC64;

Query Match
Best Local Similarity 96.6%; Score 28; DB 2; Length 183;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      172 KIVFFA 177

RESULT 13
GL19_ORYSA
ID GL19_ORYSA STANDARD; PRT; 186 AA.
AC P29835;
DT 01-APR-1993 (Rel. 25, Created)
```

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 19 kDa globulin precursor (Alpha-globulin).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN NUCLEOTIDE SEQUENCE OF 5-186
 RP STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;
 RC MEDLINE=93277591; PubMed=8503935;
 RX MEDLINE=92119226; PubMed=1731968;
 RA Shorrosh B.S., Wen L., Zen K.C., Huang J.K., Pan J.S., Hermodson M.A.,
 RA Tanaka K., Muthukrishnan S., Reek G.R.;
 RT "A novel cereal storage protein: molecular genetics of the 19 kDa
 RT globulin of rice."
 RL Plant Mol. Biol. 18:151-154(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 5-186
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;
 RX MEDLINE=93277591; PubMed=8503935;
 RA Krishnan H.B., Pueppke S.G.;
 RT "Nucleotide sequence of an abundant rice seed globulin: homology with
 RT the high molecular weight glutelins of wheat, rye and triticale."
 RL Biochem. Biophys. Res. Commun. 193:460-466(1993).
 CC -!- FUNCTION: Seed storage protein.
 CC -!- SIMILARITY: Belongs to the 2S seed storage albumins family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; X63990; CAA45400.1; -; mRNA.
 DR EMBL; L12252; AA72362.1; ALT_INIT; mRNA.
 DR FIR; S20024; WNRZ19.
 DR HSSP; P24565; LPNB.
 DR Gramene; P29835; -.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR PANTHER; PTHR14054; Glutenin; 1.
 DR Pfam; PF00234; Tryp_alpha_amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 DR Direct protein sequencing; Seed storage protein; Signal;
 KW Storage protein.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 186 19 kDa globulin.
 SQ SEQUENCE 186 AA; 21050 MW; 9E09BA74CB0B6810 CRC64;
 Query Match 96.6%; Score 28; DB 1; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVEFFA 6
 DB 4 KVVFFA 9
 RESULT 14
 P93414 ORYZA
 ID P93414 ORYZA PRELIMINARY; PRT; 186 AA.
 AC P93414;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE 26 kDa globulin (Alpha-globulin).
 GN Name=P0010D04.16; Synonyms=QJ1057 B02.5;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Endosperm;
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,
 RA Tanaka K., Matsuda T.;
 RT "Cloning of the rice seed alpha-globulin-encoding gene: sequence
 RT similarity of the 5'-flanking region to those of the genes encoding
 RT wheat high molecular-weight glutenin and barley D hordein."
 RL Gene 170:223-226(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RT "Oryza sativa BAC QJ1057 B02 genomic sequence."
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; P50643; BA009308.1; -; Genomic DNA.
 DR EMBL; AC130605; AAT44292.1; -; Genomic DNA.
 DR EMBL; AC133332; AAT93857.1; -; Genomic DNA.
 DR FIR; JC4784; JC4784.
 DR HSSP; P24565; LPNB.
 DR Gramene; P93414; -.
 DR GO; GO:0045735; P.nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR Pfam; PF00234; Tryp_alpha_amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 186 AA; 21055 MW; AE288F1107C8BC94 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVEFFA 6
 DB 4 KVVFFA 9
 RESULT 15
 Q8C6Y8 MOUSE
 ID Q8C6Y8 MOUSE PRELIMINARY; PRT; 231 AA.
 AC Q8C6Y8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
 DE library, clone:D830015B12 product:hypothetical DEAD/DEAH box helicase
 DE containing protein, full insert sequence. (Fragment).
 GN Name=Ddx58;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Suehara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani J., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saichoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagaki A., Takahashi F., Takaku-Akaira S., Tanaka Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK052871; BAC35183.1; -; mRNA.
 DR MGI; MGI:2442858; Ddx58.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0004386; P:helicase activity; IEA.
 DR GO; GO:0003676; P:nucleic acid binding; IEA.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR Pfam; PF00270; DEAD; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR NON_TER 231 231
 SQ SEQUENCE 231 AA; 25524 MW; 1D191607390D7FBB CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 231;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 145 KIVFFA 150
 RESULT 16
 Q61C67 CAEBR
 ID Q61C67 CAEBR PRELIMINARY; PRT; 315 AA.
 AC Q61C67;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG13055 (Fragment).
 GN Name=CBG13055;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C. briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CAAC01000061; CAB67532.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Hypothetical protein; Receptor;
 KW Transducer; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 315 315
 SQ SEQUENCE 315 AA; 35855 MW; 579B590D01874512 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 315;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 117 KIVFFA 122
 RESULT 17
 Q4HSJ7 CAMUP
 ID Q4HSJ7 CAMUP PRELIMINARY; PRT; 362 AA.
 AC Q4HSJ7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hydrogenase expression/formation protein Hypd.
 GN Name=Hypd; ORFNames=CUP0294;
 OS Campylobacter upsaliensis RM3195.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=306264;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RM3195;
 RA Foute D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Raeko D.A.,
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
 RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
 RA Nelson K.E.;
 RT "Major structural and novel potential virulence mechanisms from the
 RT genomes of multiple Campylobacter species."
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAFJ0100002; EAL53713.1; -; Genomic DNA.
 SQ SEQUENCE 362 AA; 40365 MW; 1580A8B12D60CABD CRC64;

Query Match 96.6%; Score 28; DB 2; Length 362;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 DB 132 KIIFFA 137

RESULT 18
 Q6D7U3 ERWCT
 ID Q6D7U3 ERWCT PRELIMINARY; PRT; 372 AA.
 AC Q6D7U3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hydrogenase isoenzymes formation protein.
 GN Name=hypp; OrderedLocustNames=EAL1232;
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=29471;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Ackin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
 RT "Genome sequence of the enterobacterial phytopathogen Erwinia
 RT carotovora subsp. atroseptica and characterization of virulence
 RT factors."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
 RL EMBL; BX950851; CAG74142.1; -; Genomic DNA.
 DR InterPro; IPR002780; Hypp.
 DR Pfam; PF01924; Hypp; 1.
 DR PIRSF; PIRSF005622; Hydrn_mat_hypp; 1.
 DR TIGRFAMs; TIGR00075; hypp; 1.
 KW Complete proteome.
 SQ SEQUENCE 372 AA; 41130 MW; A001A18AC015E620 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 372;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 DB 139 KIVFFA 144

RESULT 19
 Q7M9N5 WOLSU
 ID Q7M9N5 WOLSU PRELIMINARY; PRT; 373 AA.
 AC Q7M9N5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE HYDROGENASE PROTEIN.
 GN Name=HYPD; OrderedLocustNames=WS0793;
 OS Wolinella succinogenes.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Wolinella.
 OX NCBI_TaxID=844;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=DSMZ 1740;
 RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
 RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
 RA Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
 RA Meyer P., Lederer H., Schuster S.C.;
 RT "Complete genome sequence and analysis of Wolinella succinogenes."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
 DR EMBL; BX571659; CAB0906.1; -; Genomic DNA.
 DR InterPro; IPR002780; Hypp.
 DR Pfam; PF01924; Hypp; 1.
 DR PIRSF; PIRSF005622; Hydrn_mat_hypp; 1.
 DR TIGRFAMs; TIGR00075; hypp; 1.
 KW Complete proteome.
 SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 373;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 DB 138 KIVFFA 143

RESULT 20
 Q9V7J0 DROME
 ID Q9V7J0 DROME PRELIMINARY; PRT; 382 AA.
 AC Q9V7J0; Q9CG81;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE CG8421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).
 GN Name=Asph; ORFNames=CG8421;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriodes; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwee R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Eosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali K., Kalush B., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser K.N., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "*Drosophila melanogaster* release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
RA Friedman P.A.;

RT "Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
RT isoform of Asph missing the catalytic domain share exons with
RT junctin.";
RL J. Biol. Chem. 275:39543-39554(2000).
DR EMBL; AE003808; AAP58063.2; -; Genomic_DNA.
DR EMBL; AF289494; AAG40807.1; -; mRNA.
DR Ensembl; CG8421; *Drosophila melanogaster*.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 382 AA; 43287 MW; 60E5C03AEBFC6E8B CRC64;

Query Match 96.6%; Score 28; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
||:||||
Db 53 KIIFFA 58

RESULT 21

O9KI10_BACCE PRELIMINARY; PRT; 387 AA.
AC O9KI10;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GerN.
GN Name=gerN;
OS *Bacillus cereus*.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*;
OC *Bacillus cereus* group.
OX NCBI_TaxID=1396;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC10876;
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;
RT "GerN, an antiporter homologue important in germination of *Bacillus*
RT *cereus* endospores.";
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na H Exchanger; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
||:||||
Db 184 KVFFFA 189

RESULT 22

Q4MT39_BACCE PRELIMINARY; PRT; 387 AA.
AC Q4MT39;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Na+/H+ antiporter.
GN ORFNames=BCE_G9241_1647;

OS Bacillus cereus G9241.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=269801;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=G9241;
 RC PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hofmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
 RA Ripsone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Fraser C.M.;
 RT "Identification of anthrax toxin genes in a Bacillus cereus associated
 RT with an illness resembling inhalation anthrax.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAEK01000008; EAL15336.1; -; Genomic DNA.
 SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79B12C38 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 DB 184 KVVFFA 189

RESULT 23
 Q63DD4_BACCC PRELIMINARY; PRT; 387 AA.
 ID Q63DD4_BACCC PRELIMINARY;
 AC Q63DD4_BACCC PRELIMINARY;
 DT 25-OCT-2004 (TREMELrel. 28, Created)
 DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
 DE Na+/H+ exchanger family protein.
 GN Name=gerN;
 OS Bacillus cereus (strain 2K).
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=288681;
 [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus cereus 2K.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CP000001; AAU18770.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRFAMs; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 DB 184 KVVFFA 189

RESULT 24
 Q6HKU6_BACHK PRELIMINARY; PRT; 387 AA.
 ID Q6HKU6_BACHK PRELIMINARY;
 AC Q6HKU6;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Na+/H+ exchanger family protein.
 GN Name=gerN; OrderedLocusNames=BT9727_1493;
 OS Bacillus thuringiensis (subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=180856;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=97-27;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017355; AAT63168.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRFAMs; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41076 MW; DFECAD90985F951 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 DB 184 KVVFFA 189

RESULT 25
 Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
 ID Q73AP3_BACCI PRELIMINARY;
 AC Q73AP3;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Germination protein gerN.
 GN OrderedLocusNames=BCE1729;
 OS Bacillus cereus (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=222523;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=14960714; DOI=10.1093/nar/gkh258;
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angioli S.V., Kolonay J.F.,
 RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
 RT adaptations and a large plasmid related to Bacillus anthracis pXOI.";
 RL Nucleic Acids Res. 32:1977-988(2004).
 DR EMBL; AE017269; AAS40658.1; -; Genomic DNA.
 DR TIGR; BCE1729; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.

```

DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na Hporter.
DR Pfam; PF00999; Na H Exchanger; 1.
DR TIGRFAMs; TIGR00932_2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEBA3 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 184 KVVFFA 189

RESULT 26
QB1SK9_BACAN
ID QB1SK9_BACAN PRELIMINARY; PRT; 387 AA.
AC QB1SK9; Q610U3; Q6KUP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Germination protein genX.
GN OrderedLocNames=BAL1639, BAS1521, GBAAL1639;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=225608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.C., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate 0581;
RX Ravel J., Rasko D.A., Shumway M.P., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017029; AAP25572.1; -; Genomic DNA.
DR EMBL; AE017334; AAT30749.1; -; Genomic DNA.
DR EMBL; AE017225; AAT53839.1; -; Genomic DNA.
DR TIGR; BA1639; -.
DR TIGR; GBAAL1639; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0008324; F: cation transporter activity; IEA.
DR GO; GO:0015299; F: solute:hydrogen antiporter activity; IEA.

DR GO; GO:0006812; P: cation transport; IEA.
DR GO; GO:0006885; P: regulation of pH; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na Hporter.
DR Pfam; PF00999; Na H Exchanger; 1.
DR TIGRFAMs; TIGR00932_2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 184 KVVFFA 189

RESULT 27
Q6L2B4_PICTO
ID Q6L2B4_PICTO PRELIMINARY; PRT; 410 AA.
AC Q6L2B4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lipopolysaccharide N-acetylglucosaminyltransferase.
GN OrderedLocNames=PT00303;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AE017261; AAT42888.1; -; Genomic DNA.
DR GO; GO:0016757; F: transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0009058; P: biosynthesis; IEA.
DR InterPro; IPR001296; Glyco trans.1.
DR Pfam; PF00534; Glycos transf 1; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 410 AA; 48120 MW; C192F0152E66E9B0 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 410;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 235 KIVFFA 240

RESULT 28
Q8C5I3_MOUSE
ID Q8C5I3_MOUSE PRELIMINARY; PRT; 410 AA.
AC Q8C5I3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box
DE helicase containing protein, full insert sequence.
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.145100;
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Katsunai T., Tashiro H., Itoh M.,
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hata M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Tananashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL: AK078287; BAC37205.1; -; mRNA.
 DR Ensembl: ENSMUSG0000040296; Mus musculus.
 DR MGI: MGI:2442858; Ddx58.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0004386; F:helicase activity; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR Pfam: PF00270; DEAD; 1.
 DR SMART: SM00487; DEXDC; 1.
 KW Helicase; Hypothetical protein; Nuclear protein.
 SQ SEQUENCE 410 AA; 46841 MW; ECC9E3D2D2BC5FE0 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 410;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 293 KVVFFA 298
 ID Q9PHV5 CAMJE PRELIMINARY; PRT; 442 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Putative integral membrane protein.
 GN OrderedLocustNames=Cj0560;
 OS Campylobacter jejuni
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OC NCBI_TaxID=197;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCITC 11168;
 RX MEDLINE=20150912; PubMed=10689204; DOI=10.1038/35001088;
 RA Parkhill J., Wren B.W., Mungall K.L., Kelsey J.M., Churcher C.M.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jagsis K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream A.M., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 DR EMBL: AL139075; CAB75196.1; -; Genomic DNA.
 DR PIR: H81402; H81402.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0015237; F:antipporter activity; IEA.
 DR GO: GO:0015238; F:drug transporter activity; IEA.
 DR GO: GO:0006855; P:multidrug transport; IEA.
 DR InterPro: IPR002114; HPr SerP_S.
 DR InterPro: IPR002528; MatE.
 DR Pfam: PF01554; MateE; 1.
 DR TIGRPFAM9; TIGR00797; mate; 1.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 442 AA; 49452 MW; 38EA04E7AB1A8F3E CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 442;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 313 KVVFFA 318

```

RESULT 30
O59243 PYRHO PRELIMINARY; PRT; 447 AA.
AC O59243;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PH1606.
GN OrderedLocusNames=PH1606;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosooyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:58-76(1998).
DR EMBL; BA000001; BAA30718.1; -; Genomic_DNA.
DR PIR; F71039; F71039.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005355; P:glucose transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000803; Gluc transporter.
DR PRINTS; PR00172; GLUCTRNSPOT.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 207 KIIFFA 212

RESULT 31
O95593 DROME PRELIMINARY; PRT; 556 AA.
AC O95593;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM05229p.
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060905; AAL28453.1; -; mRNA.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11FE8 CRC64;

```

```

Query Match 96.6%; Score 28; DB 2; Length 556;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 53 KIIFFA 58

RESULT 32
O9V719 DROME PRELIMINARY; PRT; 556 AA.
AC O9V719;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doul L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen C.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

```

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs E.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RL melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celisner S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celisner S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RP FlyBase;
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION:
 CC O46085:EG:63B12.5; NBExp=1; IntAct=EBI-123244, EBI-151469;
 DR EMBL; AE003808; AAF58064.2; -; Genomic_DNA.
 DR IntAct; Q9V719; -;
 DR Ensembl; CG8421; Drosophila melanogaster.
 DR FlyBase; FBgn0034075; Asph.
 DR FlyBase; FBgn0034075; CG8421.
 SQ SEQUENCE 556 AA; 63144 MW; B420980C8D6C357A CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 556;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 53 KIIFFA 58
 RESULT 33
 QSHYEL HUMAN
 ID QSHYEL HUMAN PRELIMINARY; PRT; 703 AA.
 AC QSHYEL;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein DKFZp686N19181 (Fragment).
 GN Name=DKFZp686N19181;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa;
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Skin endothel;

RG The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Meves H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX647917; CAI46068.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00490; HELICc; 1.
 KW Hypothetical protein.
 FT NON_TER 703
 SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 703;
 Best Local Similarity 83.3%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 247 KIVFFA 252
 RESULT 34
 Q6AG25 LEIXX
 ID Q6AG25 LEIXX PRELIMINARY; PRT; 721 AA.
 AC Q6AG25;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE ATP-dependent RNA helicase.
 GN OrderedLocusNames=Lxx07490;
 OS Leifsonia xyl (subsp. xyl).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococineae; Microbacteriaceae; Leifsonia.
 OX NCBI_TaxID=59736;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=CTC807.
 RC PubMed=15305603;
 RX Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
 RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
 RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
 RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
 RA Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorri H.A.,
 RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
 RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
 RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
 RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
 RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.;
 RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
 RT xyl subsp. xyl.";
 RL Mol. Plant Microbe Interact. 17:827-836(2004).
 DR EMBL; AE016822; AAT88670.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00490; HELICc; 1.
 KW Complete proteome; DNA-binding; Helicase; Hydrolase.
 SQ SEQUENCE 721 AA; 78860 MW; 73F5D2A8435BADE3 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 721;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 KIVFFA 6
Db      564 KIVFFA 569

RESULT 35
Q9GQ82 DROME PRELIMINARY;      PRT;      785 AA.
ID      Q9GQ82 DROME PRELIMINARY;      PRT;      785 AA.
AC      Q9GQ82;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE      Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).
GN      Name=Asph; ORFNames=CG8421;
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
RA      Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
RA      O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
RA      Friedman P.A.;
RT      "Aspartyl beta-hydroxylase (Asph) and an evolutionarily conserved
RT      isoform of Asph missing the catalytic domain share exons with
RT      junctin."
RL      J. Biol. Chem. 275:39543-39554(2000).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA      Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Branton R.C., Rogers Y.-H.C., Blasej R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA      Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA      Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA      Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA      Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.B.,
RA      Palazzolo M., Pittman G.S., Pan S., Pollard J.S., Puri V., Reese M.G.,
RA      Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA      Williams S.M., Woodge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      "The genome sequence of Drosophila melanogaster."
RL      Science 287:2185-2195(2000).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.

```

```

RX      MEDLINE=22426065; PubMed=12537568;
RA      Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA      Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA      George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA      Pacle J.B., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA      Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA      Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT      "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT      melanogaster euchromatic genome sequence."
RL      Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22426070; PubMed=12537573;
RA      Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskaas R.,
RA      Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA      Ashburner M., Celnik S.E.;
RT      "The transposable elements of the Drosophila melanogaster euchromatin:
RT      a genomics perspective."
RL      Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN      [5]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22426069; PubMed=12537572;
RA      Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA      Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA      Smith C.D., Tupy J.B., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA      Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
RA      Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA      Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA      Lewis S.E.;
RT      "Annotation of the Drosophila melanogaster euchromatic genome: a
RT      systematic review."
RL      Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN      [6]
RP      NUCLEOTIDE SEQUENCE.
RX      Berkeley Drosophila Genome Project;
RA      Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA      Hoskins R., Stapleton M., Pacle J., Park S., Svirskaas R., Smith E.,
RA      Yu C., Rubin G.;
RT      "Drosophila melanogaster release 4 sequence."
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [7]
RP      NUCLEOTIDE SEQUENCE.
RX      FlyBase;
RL      Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF289493; AAG40806.1; -; mRNA.
DR      EMBL; AE003808; AAM70947.1; -; Genomic DNA.
DR      Ensembl; CG8421; Drosophila melanogaster.
DR      FlyBase; FBgn0034075; Asph.
DR      FlyBase; FBgn0034075; CG8421.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IEA.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005488; F:binding; IEA.
DR      GO; GO:0004597; F:peptide-aspartate beta-dioxygenase activity; IEA.
DR      GO; GO:0018193; P:peptidyl-amino acid modification; IEA.
DR      InterPro; IPR007803; Asp Arg Hydrol.
DR      InterPro; IPR006025; Pept_M_Zn_BS.
DR      InterPro; IPR001440; TPR.
DR      InterPro; IPR011990; TPR-like helical.
DR      Pfam; PF05118; Asp Arg Hydrol; 1.
DR      PROSITE; PS0293; TPR REGION; 1.
DR      PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ      SEQUENCE 785 AA; 89843 MW; 30A8DFCD6836F7F1 CRC64;

```

Query Match 96.6%; Score 28; DB 2; Length 785;
 Best Local Similarity 83.3%; Pred. No. 6.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6

Db 53 KIVFFA 58

RESULT 36

```

O95786 HUMAN
ID O95786 HUMAN PRELIMINARY; PRT; 925 AA.
AC O95786;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=DDX58; Synonyms=RIG-I;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun Y.W.;
RT "RIG-I, a human homolog gene of RNA helicase, is induced by retinoic
RT acid during the differentiation of acute promyelocytic leukemia
RT cell.";
RL Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
RL Shanghai Second Medical University.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yi-Wu S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038963; AAD19826.1; -; mRNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR HGNC; HGNC:19102; DDX58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase.
SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3DD0F00D4 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 292 KVVFFA 297
|:|||||

RESULT 37
QSVYTI HUMAN
ID QSVYTI HUMAN PRELIMINARY; PRT; 925 AA.
AC QSVYTI;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OTTHUMP0000021185.
GN Name=RP11-334P12.2; ORFNames=RP11-334P12.2-001;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

```

RA Sehra H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL353671; CAH71251.1; -; Genomic DNA.
DR EMBL; AL161783; CAH72600.1; -; Genomic DNA.
DR EMBL; AL161783; CAH71251.1; JOINED; Genomic DNA.
DR EMBL; AL353671; CAH72600.1; JOINED; Genomic DNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein.
SQ SEQUENCE 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 292 KVVFFA 297
|:|||||

RESULT 38
Q6Q899 MOUSE
ID Q6Q899 MOUSE PRELIMINARY; PRT; 926 AA.
AC Q6Q899;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DEAD/H box polypeptide RIG-I.
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wei J.; Gu J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY553221; AAS59532.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR006935; Resili.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF04851; Resili; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
SQ SEQUENCE 926 AA; 105877 MW; 632462010107698E CRC64;

Query Match 96.6%; Score 28; DB 2; Length 926;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 293 KVVFFA 298
|:|||||

RESULT 39
Q9GLV6 PIG
ID Q9GLV6_PIG PRELIMINARY; PRT; 940 AA.

```

```

AC Q9GLV6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=RHIV-1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261798; PubMed=10799277; DOI=10.1006/mpat.1999.0349;
RA Zhang X., Wang C., Schock L.B., Hawken R.J., Rutherford M.S.;
RT "An RNA helicase, RHIV -1, induced by porcine reproductive and
RT respiratory syndrome virus (PRRSV) is mapped on porcine chromosome
RT 10q13.";
RL Microb. Pathog. 28:267-278(2000).
CC 1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF181119; AAC09428.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR Helicase; Hydrolase; Nuclear protein; Repeat.
KW Helicase; Hydrolase; Nuclear protein; Repeat.
SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 940;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 290 KIVFFPA 295
:|||||
:|||||

RESULT 40
NOS2 MOUSE
ID NOS2 MOUSE STANDARD; PRT; 1144 AA.
AC P29477; O70515; O70516;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
GN Name=Nos2; Synonyms=iNOS;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92229444; PubMed=1373522;
RA Xie Q.-W., Ding H.-J., Calaycay J., Munford R.A., Swiderek K.M.,
RA Lee T.D., Cho A., Troso T., Nathan C.;
RT "Cloning and characterization of inducible nitric oxide synthase from
RT mouse macrophages.";
RL Science 256:225-228(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92357701; PubMed=1379716;
RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
RT "Cloned and expressed macrophage nitric oxide synthase contrasts with
RT the brain enzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
RN [3]

```

```

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92210618; PubMed=1372907;
RA Lyons C.R., Orloff G.J., Cunningham J.M.;
RT "Molecular cloning and functional expression of an inducible nitric
RT oxide synthase from a murine macrophage cell line.";
RL J. Biol. Chem. 267:6370-6374(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96088781; PubMed=7503239;
RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;
RT "Role of NF-kappa B in the regulation of inducible nitric oxide
RT synthase in an M2AL cell line.";
RL Am. J. Physiol. 269:F718-F729(1995).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.
RX STRAIN=B10.S/J, BALB/cByJ, DBA/2J, NOD/LtJ, and SUL/J; TISSUE=Spleen;
MEDLINE=93370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scya2
RT (monocyte chemoattractant protein (MCP)-1) and Scya12 (MCP-5) are
RT candidates for sae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
RN [6]
RP EFFECT OF ASPIRIN.
RC TISSUE=Macrophage;
RX MEDLINE=95372392; PubMed=7544010;
RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
RA Weissmann G., Abramson S.B.;
RT "The mode of action of aspirin-like drugs: effect on inducible nitric
RT oxide synthase.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
RX MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;
RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Getzoff E.D.,
RA Stuehr D.J., Tainer J.A.;
RT "The structure of nitric oxide synthase oxygenase domain and inhibitor
RT complexes.";
RL Science 278:425-431(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
RX MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;
RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
RA Tainer J.A.;
RT "Structure of nitric oxide synthase oxygenase dimer with pterin and
RT substrate.";
RL Science 279:2121-2126(1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
RX MEDLINE=20031637; PubMed=10562538; DOI=10.1093/emboj/18.22.6260;
RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
RT hook and pterin-binding segment in dimerization and
RT tetrahydrobiopterin interaction.";
RL EMBO J. 18:6260-6270(1999).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
RX MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;
RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,
RA Tainer J.A., Stuehr D.J., Getzoff E.D.;
RT "N-terminal domain swapping and metal ion binding in nitric oxide
RT synthase dimerization.";
RL EMBO J. 18:6271-6281(1999).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
RX MEDLINE=20233702; PubMed=10769116; DOI=10.1021/bi992409a;
RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,
RA Tainer J.A.;
RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible
RT nitric oxide synthase oxygenase dimer with active and inactive

```


DR	PDB; 1M8E; X-ray; A/B=65-498.
DR	PDB; 1M8H; X-ray; A/B=65-498.
DR	PDB; 1M8I; X-ray; A/B=65-498.
DR	PDB; 1M9T; X-ray; A/B=65-498.
DR	PDB; 1N2N; X-ray; A/B=77-495.
DR	PDB; 1NOC; X-ray; A=115-498.
DR	PDB; 1NOD; X-ray; A/B=77-499.
DR	PDB; 1NOS; X-ray; @=115-498.
DR	PDB; 1QOM; X-ray; A/B=65-498.
DR	PDB; 1QW4; X-ray; A/B=77-495.
DR	PDB; 1OW5; X-ray; A/B=77-495.
DR	PDB; 1R35; X-ray; A/B=66-498.
DR	PDB; 1VAP; X-ray; A/B=77-495.
DR	PDB; 2BHJ; X-ray; A=77-498.
DR	PDB; 2NOD; X-ray; A/B=77-499.
DR	PDB; 2NOS; X-ray; @=115-498.
DR	PDB; 3NOD; X-ray; A/B=77-499.
DR	IntAct; P29477; -
DR	Ensembl; ENSMUSG0000020826; Mus musculus.
DR	MGI; MGI:97361; N082.
DR	GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR	GO; GO:0005829; C:cytosol; TAS.
DR	GO; GO:0048471; C:perinuclear region; IDA.
DR	GO; GO:0005516; P:calmodulin binding; TAS.
DR	GO; GO:0020037; F:heme binding; NAS.

Query Match 96.6%; Score 28; DB 1; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1 KIVFFPA 6 :
Dd	514 KVVFFFA 519

RESULT 41
 QSSXT3 MOUSE
 ID QSSXT3_MOUSE PRELIMINARY; PRT; 1144 AA.
 AC QSSXT3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Nitric oxide synthase 2, inducible, macrophage (inducible nitric oxide synthase).
 DE Names=Nos2; ORFNames=RP23-341J22.2-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hopkins B.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
 RC [2]
 RN NUCLEOTIDE SEQUENCE.
 RA STRAIN=CD-1;
 RC CoGe P., Levacher B., Rique H., Leopold O., Boutin J.A., Galizzi J.-P.;
 RA "Genomic structure of the murine inducible nitric oxide synthase (i-NOS) gene";
 RT NT
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL592185; CAI25275.1; -; Genomic DNA.
 DR EMBL; AF427516; AAL24076.1; -; Genomic DNA.
 SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457P CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1 KIVFFPA 6 :
Dd	514 KVVFFFA 519

```

RESULT 42
Q8R410 MOUSE
ID Q8R410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q8R410;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ICR;
RA Hagiwara K., Endo Y., Xin H., Takahashi M., Huguin, Nukiwa T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090567; AAM11887.1; -; mRNA.
DR HSSP; P29477; 1DNV.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005823; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxid_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130685 MW; DAD5AAPF3680B005 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 515 KVVFFA 520

RESULT 43
Q6P6A0 MOUSE
ID Q6P6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q6P6A0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nos2 protein.

```

```

GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062378; AAHG2378.1; -; mRNA.
DR HSSP; P29477; 1JWK.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042803; F:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; IMP.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; IMP.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxid_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130671 MW; C26E09F536923295 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 515 KVVFFA 520

```

FT NON_TER 1408 1408
SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1408;
Best Local Similarity 83.3%; Pred.No.1.le+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
||:||||
Db 1212 KIIFPA 1217

RESULT 46
QSVPRO DROME PRELIMINARY; PRT; 1443 AA.
AC QSVPRO;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE CG11838-PA, isoform A.
GN Names=Ose93; ORFNames=CG11838;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Spheroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthanathan P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.;
RP "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22425065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE001589; AAF51483.1; -; Genomic_DNA.
DR FlyBase; FBgn0031262; Oreg3.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1443 AA; 161316 MW; A8C5997678040888 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1443;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1204 KIIFFA 1209
RESULT 47
ID Q5BI64_DROME PRELIMINARY; PRT; 1458 AA.
AC Q5BI64;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LP14662p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT021360; AAX33508.1; -; mRNA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
KW Repeat.
SQ SEQUENCE 1458 AA; 163133 MW; 2D704C8970E541EC CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1458;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1219 KIIFFA 1224
RESULT 48
ID Q7KTZ4_DROME PRELIMINARY; PRT; 1503 AA.
AC Q7KTZ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG11838-PB, isoform B.
GN Name=Oreg3; ORFNames=CG11838;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidel-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE-22426065; PubMed-12537568;
 RA Celisner S.E., Wheeler D.A., Kronmiller B., Carlsson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE-22426070; PubMed-12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlsson J.W., Swirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celisner S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE-22426069; PubMed-12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celisner S., Carlsson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Swirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003589; AAS64635.1; -; Genomic_DNA.
 DR InterPro; IPR011990; TPR-like_helical.
 DR InterPro; IPR001680; WD40.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
 DR PROSITE; PSS0294; WD_REPEATS_REGION; 1.
 KW Repeat.
 SQ SEQUENCE 1503 AA; 167957 MW; A0DD3F532590486 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1503;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 Db 1264 KIIFFA 1269

RESULT 49
 Q8A6R7 BACTN PRELIMINARY; PRT; 1676 AA.
 AC Q8A6R7; 2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Conserved protein, with weak BamHI domain.
 GN OrderedLocustNames-Brl809;
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN-VPI-5482 / ATCC 29148;
 RX MEDLINE-22550858; PubMed-12663928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 DR EMBL; AE016933; AAO76916.1; -; Genomic_DNA.
 DR InterPro; IPR002048; EF-hand.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1676;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 Db 1656 KIIFFA 1661

RESULT 50

Q9UC33 HUMAN PRELIMINARY; PRT; 33 AA.
 ID Q9UC33 HUMAN PRELIMINARY;
 AC Q9UC33;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-amyloid peptide (Fragment).
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE-93024877; PubMed-1406936; DOI=10.1038/359325a0;
 RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
 RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
 RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
 RT biological fluids.";
 RL Nature 359:325-327(1992).
 DR HSSP; Q16019; 1BA4.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETA-APP; 1.
 DR PROSITE; PS00204; BETA-APP; 1.
 SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 33;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 Db 16 KIVFFA 21

RESULT 51
 Q56JG6 GRAGR PRELIMINARY; PRT; 42 AA.
 AC Q56JG6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)

```

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 52
Q56JJ7 TURTR
ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.
AC Q56JJ7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottlenose dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 53
Q7M088 CAVPO
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]

```

```

RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
protein fragment for NK-1 substance P receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR PIR; P05112; P05112.
DR HSSP; Q16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 54
Q8WZ99 HUMAN
ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.
AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
RA Ninomiya H., Saïdo TC., Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
probable familial Alzheimer's disease.";
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
DR EMBL; AB066441; BAB71958.2; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5597 MW; 3F08E9E9EC18011AD CRC64;

Query Match 93.1%; Score 27; DB 2; Length 52;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 16 KLVFFA 21

RESULT 55
A4 URSWA
ID A4 URSWA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)

```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE Alpha-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Fragment).
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Fragment).
 DE Name=APP;
 GN Ursus maritimus (Polar bear) (Thalartos maritimus).
 OS Ursus maritimus (Polar bear) (Thalartos maritimus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
 OC Ursus.
 OX NCBI_TaxID=29073;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RA "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; X56128; CAA39593.1; -; mRNA.
 DR FIR; B60045; B60045.
 DR HSSP; P08592; INMW.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 5 Soluble APP-beta (By similarity).
 FT CHAIN 6 >57 CTF-alpha (By similarity).
 FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
 FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 33 Extracellular (Potential).
 FT TRANSMEM 34 57 Potential.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
 Query Match 93.18; Score 27; DB 1; Length 57;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 DB 21 KLVFFA 26
 RESULT 56
 ID A4_CANFA STANDARD; PRT; 58 AA.
 AC Q28280;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Fragment).
 DE Name=APP;
 GN Canis familiaris (Dog).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RA "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; X56125; CAA39590.1; -; mRNA.
 DR HSSP; P08592; INMW.
 DR Ensembl; ENSCAF00000008557; Canis familiaris.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 6 Soluble APP-beta (By similarity).
 FT CHAIN 7 >58 CTF-alpha (By similarity).
 FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
 FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 34 Extracellular (Potential).
 FT TRANSMEM 35 58 Potential.
 FT NON_TER 1 1
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
 Query Match 93.18; Score 27; DB 1; Length 58;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 DB 22 KLVFFA 27
 RESULT 57
 ID A4_RABIT STANDARD; PRT; 58 AA.
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DT Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);

```

DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56129; CAA39594.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5
FT CHAIN 6 >58 Soluble APP-beta (By similarity).
FT CHAIN 6 >47 CTF-alpha (By similarity).
FT CHAIN 6 >45 Beta-amyloid protein 42 (By similarity).
FT CHAIN 46 >58 Beta-amyloid protein 40 (By similarity).
FT CHAIN 48 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 21 KLVFFA 26

RESULT 58
A4 SHEEP
ID_ A4 SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;

```

```

DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56130; CAA39595.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5
FT CHAIN 6 >58 Soluble APP-beta (By similarity).
FT CHAIN 6 >47 CTF-alpha (By similarity).
FT CHAIN 6 >45 Beta-amyloid protein 42 (By similarity).
FT CHAIN 46 >58 Beta-amyloid protein 40 (By similarity).
FT CHAIN 48 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 21 KLVFFA 26

RESULT 59
A4 BOVIN
ID_ A4 BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;

```


OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Brain;
 RC MEDLINE=92017079; PubMed=156157; DOI=10.1016/0169-328X(91)90088-F;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RA "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis".
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; X56124; CAA39589.1; -; mRNA.
 CC EMBL; X56126; CAA39591.1; -; mRNA.
 CC HSSP; P08592; 1NMJ.
 CC InterPro; IPR008155; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PRINTS; PR00204; BETAAMYLOID.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 6 Soluble APP-beta (By similarity).
 FT CHAIN 7 >59 CTF-alpha (By similarity).
 FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
 FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
 FT CHAIN <1 34 Extracellular (Potential).
 FT TRANSMEM 35 58 Potential.
 FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
 FT NON_TER 1 1
 FT NON_TER 59 59
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 59;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 Db 22 KLVFFA 27
 RESULT 60
 ID O35463_CRIGR PRELIMINARY; PRT; 79 AA.
 AC O35463;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alzheimer's amyloid beta protein (Fragment).
 GN Name-beta APP;
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetinae; Cricetus.
 ON NCBI_TaxID=10029;

[1] NUCLEOTIDE SEQUENCE.
 RP Sambamurti K., Finnix I., Gandhi S.;
 RA Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF030413; AAB86608.1; -; mRNA.
 DR HSSP; P08592; 1NMJ.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 79;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 Db 36 KLVFFA 41
 RESULT 61
 Q8UH58_CHESE PRELIMINARY; PRT; 113 AA.
 ID Q8UH58;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Amyloid beta protein (Fragment).
 OS Chelydra serpentina serpentina (common snapping turtle).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
 ON NCBI_TaxID=134619;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP MEDLINE=21876906; PubMed=11882478;
 RX Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
 RT "Octylphenol (OP) alters the expression of members of the amyloid
 RT protein family in the hypothalamus of the snapping turtle, Chelydra
 RT serpentina serpentina.";
 RL Environ. Health Perspect. 110:269-275(2002).
 DR EMBL; AF541917; AAN04908.1; -; mRNA.
 DR HSSP; Q16019; 1IYT.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1 1
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 113;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 Db 30 KLVFFA 35
 RESULT 62
 Q7UPR1_RHOBA PRELIMINARY; PRT; 137 AA.
 ID Q7UPR1;
 AC Q7UPR1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```

DE Hypothetical protein.
GN OrderedLocusNames=RB6777;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann K., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294144; CAD75000.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 15530 MW; 5DCC133B06CC5FC0 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 85 KLVFFA 90
|:|||||

RESULT 63
QST29 ARATH PRELIMINARY; PRT; 152 AA.
ID Q9ST29;
AC Q9ST29;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein T20K18.220 (Hypothetical protein AT4g12870).
GN Name=T20K18.220; Synonyms=AT4g12870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049640; CAB41004.1; -; Genomic DNA.
DR EMBL; AL161535; CAB78329.1; -; Genomic DNA.
DR PIR; T06645; T06645.
DR InterPro; IPR004911; GILF.
DR Pfam; PF03227; GILF; 1.
KW Hypothetical protein.
SQ SEQUENCE 152 AA; 17095 MW; ED47CEAF607B131 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KIVFFA 6
Db 9 KLVFFA 14
|:|||||

RESULT 64
Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.
ID Q6AKE9;
AC Q6AKE9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to McbG protein.
GN OrderedLocusNames=DP2447;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSv54 / DSM 12343;
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG37176.1; -; Genomic DNA.
DR InterPro; IPR001646; Septide repeat.
DR Pfam; PF00805; Pentapeptide; 3.
KW Complete proteome.
SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;

Query Match 93.1%; Score 27; DB 2; Length 203;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 52 KVIFFA 57
|:|||||

RESULT 65
Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.
ID Q8BPV5;
AC Q8BPV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone:D430025B14 product:amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279255; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

```

DR Pfam, PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 135 KLVFFA 140

RESULT 66
Q8VY56 ARATH PRELIMINARY; PRT; 229 AA.
AC Q8VY56;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12870.
GN Name=At4g12870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072432; AAL62424.1; -; mRNA.
DR EMBL; AY128863; AAN91263.1; -; mRNA.
DR InterPro; IPR004911; GILT.
DR Pfam; PF03227; GILT.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25707 MW; BF3DD2587EAA82D6 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 9 KLVFFA 14

RESULT 67
Q9SV79 ARATH PRELIMINARY; PRT; 231 AA.
AC Q9SV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12900.
GN Name=At4g12900; Synonyms=AT4g12900;

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OX NCBI_TaxID=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Bevan M., Robben J., Grymonprez B., Volckaert G., Bancroft I.,

RA Mewes H.W., Rudd S., Schoof H., Mayer K.F.X.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,

RA Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE.

RA Robben J., Grymonprez B., Volckaert G., Mewes H.W., Lemcke K.,

RA Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

RP NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [6]

DR EMBL; AL079349; CAB53090.1; -; Genomic DNA.

DR EMBL; AL161535; CAB78332.1; -; Genomic DNA.

DR FIRM; H85138; H85138.

DR InterPro; IPR004911; GILT.

DR Pfam; PF03227; GILT. 1.

DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 231 AA; 26025 MW; 734109A78E942295 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 231;

Best Local Similarity 83.3%; Pred. No. 4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 12 KLVFFA 17

RESULT 68

ID Q9XGY6 SIMCH PRELIMINARY;

AC Q9XGY6; PRT; 352 AA.

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Wax synthase.

OS Simmondsia chinensis (Jojoba).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllales; Simmondsiaceae; Simmondsia.

OX NCBI_TaxID=3999;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=20177844; PubMed=10712527; DOI=10.1104/pp.122.3.645;

RA Lardizabal K.D., Metz J.G., Sakamoto T., Hutton W.C., Pollard M.R.,

RA Laesner M.W.;

RT "Purification of a jojoba embryo wax synthase, cloning of its cDNA and

production of high levels of wax in seeds of transgenic Arabidopsis."

RL Plant Physiol. 122:645-655(2000).

DR EMBL; AF149919; AAD38041.1; -; mRNA.

DR PIR; T48903; T48903.

DR InterPro; IPR004299; MBOAT_fam.

DR Pfam; PF03062; MBOAT; 1.

SQ SEQUENCE 352 AA; 40156 MW; F91D6BD896003629 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 352;

Best Local Similarity 83.3%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 135 KLVFFA 140

RESULT 69

ID Q8U460 PYRFU

AC Q8U460; PRT; 357 AA.

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein PF0234.

GN OrderedLocusNames=PF0234;

OS Pyrococcus furiosus.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.

OX NCBI_TaxID=2261;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

RT "The complete sequence of the Pyrococcus furiosus genome."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE010148; AAL80358.1; -; Genomic DNA.

DR InterPro; IPR008553; DUF835.

DR Pfam; PF05763; DUF835; 1.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 357 AA; 39940 MW; 9EEFE2540CF8D65 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 357;

Best Local Similarity 83.3%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 197 KLVFFA 202

RESULT 70

ID Q8UUI8 BRARE

AC Q8UUI8; PRT; 357 AA.

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative membrane protein (Fragment).

GN Name=appa;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole embryo;

RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;

RA Musa A., Leirach H., Russo V.B.A.;

RT "Distinct expression patterns of two zebrafish homologues of the human

APP gene during embryonic development."

RL Dev. Genes Evol. 211:563-567(2001).

DR EMBL; AJ315637; CAC85734.1; -; mRNA.

DR HSSP; Q16019; 1HZ3.

DR SMR; Q8UUI8; 62-170.

DR ZFIN; ZDB-GENE-000616-13; appa.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR008155; A4_APP.

DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR PROSITE; PS00204; BETAAMYLOID.
 FT NON TER 1
 SQ SEQUENCE 357 AA; 40962 MW; 07D99BEF6C55B2D8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 357;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 Db 274 KLVFFPA 279

RESULT 71

O8PPL1_XANAC PRELIMINARY; PRT; 366 AA.

AC Q8PPL1; 22, Created
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein XAC0675.

GN OrderedLocusNames=XAC0675;

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

RA Almeida N.B., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,

RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,

RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

RA Ferro M.I.T., Foghieri E.P., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RL Nature 417:459-463(2002).

DR EMBL; AE011696; AM35564.1; -: Genomic DNA.

SQ Complete proteome; Hypothetical protein

KW SEQUENCE 366 AA; 40845 MW; 6EF65B2BEC89844 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 366;
 Best Local Similarity 83.3%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 Db 340 KLVFFPA 345

RESULT 72

O67225_AQUAE

ID O67225_AQUAE PRELIMINARY; PRT; 380 AA.

AC O67225;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hydrogenase expression/formation protein HypD.

GN Name=hypD; OrderedLocusNames=AQ_1157;
 OS Aquifex aeolicus
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Shortbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,

RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex

aeolicus."

RL Nature 392:353-358(1998).

DR EMBL; AE000726; AAC07185.1; -: Genomic DNA.

DR PIR; F70399; F70399.

DR InterPro; IPR002780; HypD.

DR Pfam; PF01924; HypD; 1.

DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.

DR TIGRFAMs; TIGR00075; hypD; 1.

KW Complete proteome.

SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 380;
 Best Local Similarity 66.7%; Pred. No. 6.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 Db 141 KVIFFPA 146

RESULT 73

QB8PC7_MOUSE

ID QB8PC7_MOUSE PRELIMINARY; PRT; 384 AA.

AC QB8PC7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched

DE library, clone:4833432109 product:amyloid beta (A4) protein, full

DE insert sequence. (Fragment).

GN Name=App;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning."

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK076506; BAC36369.1; -, mRNA.
 DR HSP; P08592; 1NMJ.
 DR SMR; Q8BPC7; 74-183.
 DR MGI; MGI:88059; App.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. .; IGI.
 DR InterPro; IPR008155; A4 APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA.
 DR PRINTS; PR00204; BETAMYLOID.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 384;
 Best Local Similarity 83.3%; Pred No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVEFFA 6
 Db 301 KLVFFA 306
 I:|||||
 301 KLVFFA 306
 RESULT 74
 Q4NSU7 THEPA
 ID Q4NSU7 THEPA PRELIMINARY; PRT; 391 AA.
 AC Q4NSU7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=TP02_0195;
 OS Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OX NCBI_TaxID=5875;
 RN [1]
 RC STRAIN=Muguga;
 RP NUCLEOTIDE SEQUENCE.
 RA Gardner W.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
 RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
 RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
 RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
 RA Venter J.C., Fraser C.M., Nene V.;
 RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
 RT lymphocytes.";
 RL Science 309:134-137(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;
 RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
 RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
 RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AKG01000002; EAN32476.1; -, Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 391 AA; 44445 MW; 129227F0ABAF933C CRC64;

Query Match 93.1%; Score 27; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVEFFA 6
 Db 130 KLVFFA 135
 I:|||||

RESULT 75
 Q5WPU9 LUTLO
 ID Q5WPU9 LUTLO PRELIMINARY; PRT; 399 AA.
 AC Q5WPU9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE 43.2 kDa salivary protein.
 GN ORFNames=LJ111 Clu9;
 OS Lutzomyia longipalpis (Sand fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
 OC Psychodidae; Lutzomyia; Lutzomyia.

```

OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Salivary gland;
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT "Identification of the most abundant secreted proteins from the
RT salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT Leishmania chagasi.";
RL J. Exp. Biol. 207:3717-3729(2004).
DR EMBL; AY445935; AAS05318.1; -; mRNA.
DR InterPro: IPR003534; Royaljelly.
DR Pfam: PF03022; MRJP; 1
SQ SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 399;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 305 KVIFFA 310

```

Search completed: December 29, 2005, 17:47:27
Job time : 79.1936 secs

THIS PAGE BLANK (USPTO)

; Publication No. US20040172684A1

; GENERAL INFORMATION: David K.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53335)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 31699

; LENGTH: 206

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C102839_1.pep

US-10-767-701-31699

Query Match 89.7%; Score 26; DB 4; Length 206;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPPA 6

Db 6 KAVPFS 11

RESULT 73

; Sequence 39451, Application US/10450763

; Publication No. US20050196754A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 39451

; LENGTH: 208

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(208)

; OTHER INFORMATION: Xaa = X or * as defined in Table 2

US-10-450-763-39451

Query Match 89.7%; Score 26; DB 5; Length 208;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPPA 6

Db 37 RAVPPA 42

RESULT 74

US-10-282-122A-61639

; Sequence 6139, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 61639

; LENGTH: 210

; TYPE: PRT

; ORGANISM: Mycobacterium avium

US-10-282-122A-61639

Query Match 89.7%; Score 26; DB 4; Length 210;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPPA 6

Db 54 RAVPPA 59

RESULT 75

US-10-425-115-286732

; Sequence 286732, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 286732

; LENGTH: 258

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_24595C.1.pep

US-10-425-115-286732

Query Match 89.7%; Score 26; DB 4; Length 258;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 ||:||
 Db 212 KAMFFA 217

Search completed: December 29, 2005, 18:49:44
 Job time : 71.2903 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVFFPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

PIR_80:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	261	2 D64166	hypothetical prote
2	29	100.0	469	2 T02325	probable selenum-
3	29	100.0	660	1 A28153	gelatinase A (EC 3
4	29	100.0	662	2 S70365	gelatinase A (EC 3
5	29	100.0	662	2 A42496	gelatinase A (EC 3
6	29	100.0	662	2 S34780	gelatinase A (EC 3
7	29	100.0	663	1 S46492	gelatinase A (EC 3
8	29	100.0	1147	1 I53165	nitric-oxide synth
9	29	100.0	1147	1 I56575	nitric-oxide synth
10	29	100.0	1147	1 S38253	nitric-oxide synth
11	29	100.0	1147	1 S47647	nitric-oxide synth
12	29	100.0	1147	2 JC5029	nitric-oxide synth
13	29	100.0	1147	2 JC5029	nitric-oxide synth
14	29	100.0	1147	2 JC5027	nitric-oxide synth
15	29	100.0	1147	2 S65440	nitric-oxide synth
16	28	96.6	169	2 A22630	hypothetical prote
17	28	96.6	283	2 T20734	hypothetical prote
18	26	89.7	58	2 B44358	cysteine-rich prot
19	26	89.7	150	2 S27597	hypothetical prote
20	26	89.7	156	1 P69857	conserved hypotet
21	26	89.7	166	2 D71049	probable L(+)-tart
22	26	89.7	185	2 E70445	C-terminal fumarat
23	26	89.7	192	2 A49648	cysteine-rich prot
24	26	89.7	192	2 S38879	LIM-domain protein
25	26	89.7	229	2 E75252	molybdopter in bios
26	26	89.7	244	2 T16110	hypothetical prote
27	26	89.7	285	2 T01119	hypothetical prote
28	26	89.7	299	1 ZBBE13	33.1K zinc-binding
29	26	89.7	421	2 S40819	probable transport

30	26	89.7	421	2 C86075	probable resistanc
31	26	89.7	421	2 D91228	probable resistanc
32	26	89.7	457	2 AH1799	Grpase homolog lin
33	26	89.7	464	1 VCXFTI	major capsid prote
34	26	89.7	467	1 JQ2215	major capsid prote
35	26	89.7	472	1 VCXFSI	major capsid prote
36	26	89.7	479	2 T50726	hypothetical prote
37	26	89.7	715	2 AB0805	3-hydroxyacyl-CoA
38	26	89.7	1139	2 B54962	sterol regulatory
39	26	89.7	1204	2 S62506	alpha-glucan synth
40	26	89.7	1701	2 T09127	probable erythrocy
41	25	86.2	100	2 AG2447	hypothetical prote
42	25	86.2	120	1 QQSACC	hypothetical prote
43	25	86.2	132	2 I40566	hypothetical prote
44	25	86.2	186	1 WMR219	19K globulin precu
45	25	86.2	186	2 JC4784	alpha-globulin pre
46	25	86.2	191	2 H64441	hypothetical prote
47	25	86.2	202	2 B64668	carbonic anhydrase
48	25	86.2	209	2 AG2405	hypothetical prote
49	25	86.2	210	2 C81216	conserved hypotet
50	25	86.2	210	2 G81793	hypothetical prote
51	25	86.2	212	2 AB3270	threonine efflux p
52	25	86.2	226	2 F69125	conserved hypotet
53	25	86.2	247	2 A71847	carbonic anhydrase
54	25	86.2	260	2 B69983	conserved hypotet
55	25	86.2	263	2 C95942	probable transcrip
56	25	86.2	282	1 A28171	phenylethanolamine
57	25	86.2	285	2 A82458	hypothetical prote
58	25	86.2	298	2 B90435	hypothetical prote
59	25	86.2	302	2 H90717	hypothetical prote
60	25	86.2	308	2 T24732	hypothetical prote
61	25	86.2	321	2 G72347	hypothetical prote
62	25	86.2	323	2 H85567	hypothetical prote
63	25	86.2	326	2 S51509	pectase lyase - As
64	25	86.2	331	2 C72015	glycerol-3-phospha
65	25	86.2	331	2 D86610	glycerol-3-P acylt
66	25	86.2	332	2 E72597	probable alcohol d
67	25	86.2	342	2 AD2306	hypothetical prote
68	25	86.2	347	2 T21067	hypothetical prote
69	25	86.2	352	2 H97272	histidinol-phospha
70	25	86.2	384	2 H64161	hypothetical prote
71	25	86.2	411	2 AF0203	probable membrane
72	25	86.2	420	2 T05877	hypothetical prote
73	25	86.2	442	2 H81402	probable integral
74	25	86.2	462	2 G95233	Cof family protein
75	25	86.2	462	2 AS6717	conserved hypotet
76	25	86.2	463	2 JS0376	hypothetical 53.0K
77	25	86.2	468	2 AD0585	probable outer mem
78	25	86.2	468	2 H64802	YbfM protein - Esc
79	25	86.2	472	2 A99098	conserved hypotet
80	25	86.2	483	2 S25606	bleomycin hydrolas
81	25	86.2	499	2 JH0313	potassium channel
82	25	86.2	537	2 T31009	hypothetical prote
83	25	86.2	555	2 AC2467	hypothetical prote
84	25	86.2	560	2 I38065	gene NMB protein -
85	25	86.2	564	2 B81735	conserved hypotet
86	25	86.2	573	2 F89719	protein F09B12.1 [
87	25	86.2	573	2 B96639	protein TIF9.16 [i
88	25	86.2	573	2 S65826	hypothetical prote
89	25	86.2	656	2 S65826	DNA topoisomerase
90	25	86.2	769	2 F81415	hypothetical prote
91	25	86.2	800	2 G84740	hypothetical prote
92	25	86.2	800	2 A84293	helicase [imported
93	25	86.2	1005	2 A64465	hypothetical prote
94	25	86.2	1057	2 T46193	hypothetical prote
95	25	86.2	1144	1 A43271	nitric-oxide synth
96	25	86.2	2526	2 T20531	hypothetical prote
97	25	86.2	2722	2 T20532	hypothetical prote
98	25	86.2	2738	2 B88320	protein F07A11.6 [
99	25	86.2	33	2 S23094	beta-amyloid prote
100	24	82.8	42	2 PN0512	beta-amyloid prote
101	24	82.8	57	2 A60045	Alzheimer's diseas
102	24	82.8	57	2 D60045	Alzheimer's diseas

249 79.3 230 2 B98203 nonF-related prote
250 23 B66154 T6A9.7 protein - A
251 23 AD3612 multidrug resistan
252 23 B63612 hypothetical prote
253 23 H95396 sec-independent pr
254 23 H82790 hypothetical prote
255 23 F87454 repB protein - Cam
256 23 S49371 T23339
257 23 T23339 hypothetical prote
258 23 S73385 hypothetical prote
259 23 D72103 glucose-6-p dehydro
260 23 F90372 conserved hypothet
261 23 B97509 hypothetical prote
262 23 A56641 probable membrane
263 23 G89833 teichoic acid tran
264 23 H64054 site-specific DNA-
265 23 C87208 conserved hypothet
266 23 D95168 membrane protein [
267 23 T33218 hypothetical prote
268 23 T41674 probable edoplasm
269 23 PC4287 protein kinase (EC
270 23 AE0963 probable carbohydr
271 23 A88040 protein F47f6.1 [1
272 23 S73736 MG302 homolog A05
273 23 AB2032 conserved hypothet
274 23 B98034 conserved hypothet
275 23 H71729 hypothetical prote
276 23 D82435 D-3-phosphoglycer
277 23 D88109 protein T24E12.6 [1
278 23 B46678 endoglycosidase F3
279 23 S77441 oligopeptide trans
280 23 S77441 cytochrome-c oxida
281 23 T06516 protein farnesyltr
282 23 B95290 hypothetical prote
283 23 MMB85 cell fusion protei
284 23 AC1920 ABC phosphate tran
285 23 A95230 conserved hypothet
286 23 D98094 conserved hypothet
287 23 C71281 conserved hypothet
288 23 G72378 glycerol dehydroge
289 23 W2WU18 E2 protein - human
290 23 AB2423 hypothetical prote
291 23 AH2200 two-component hybr
292 23 T32601 hypothetical prote
293 23 A69253 cyanate transport
294 23 B69325 LPS biosynthesis p
295 23 A03223 transposase, IS285
296 23 AB0193 transposase, IS285
297 23 T14710 probable transposa
298 23 AE0267 transposase, IS285
299 23 A02356 transposase, IS285
300 23 AH0298 transposase, IS285
300 23 AG0264 transposase, IS285

ALIGNMENTS

RESULT 1
D64166
hypothetical protein H11086 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: D64166
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64166
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-261 <TIGR>
A;Cross-references: UNIPROT:P45030; UNIPARC:UPI0000013BFPAD; GB:U32788; GB:L42023; NID:gi
A;Note: Best homolog was a hypothetical protein from Escherichia coli
C;Superfamily: conserved hypothetical protein H11086
Query Match 100.0%; Score 29; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFPA 6
Db 205 KAVFFPA 210
|||||
RESULT 2
T02325
probable selenium-binding protein [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F13P17.21
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02325; G84755
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence.
A;Reference number: Z14657
A;Accession: T02325
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-469 <ROU>
A;Cross-references: UNIPROT:Q8S807; UNIPARC:UPI000009FA17; EMBL:AC004481; NID:93337347;
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-469 <STO>
A;Cross-references: UNIPARC:UPI000009FA17; GB:AE002093; NID:G6598404; PIDN:AAC26713.2;
C;Genetics:
A;Gene: F13P17.21; At2g34370
A;Map position: 2

Query Match 100.0%; Score 29; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFPA 6
Db 213 KAVFFPA 218
|||||
RESULT 3
A28153
gelatinase A (EC 3.4.24.24) precursor - human
N;Alternate names: collagenase type IV; matrix metalloproteinase 2 (MMP2); progelatinas
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1989 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A28153; A34202; A42225; A60187; S13858; S39436; A31480; S44432; A61498; S5
R;Collier, I.E.; Wilhelm, S.M.; Eisen, A.Z.; Marner, B.L.; Grant, G.A.; Seltzer, J.L.;
J. Biol. Chem. 263, 6579-6587, 1988
A;Title: H-ras oncogene-transformed human bronchial epithelial cells (TBB-1) secrete a
A;Reference number: A28153; MUID:88198218; PMID:2834383
A;Accession: A28153
A;Molecule type: mRNA
A;Residues: 30-660 <COL>
A;Cross-references: UNIPROT:P08253; UNIPARC:UPI0000172CE7; GB:J03210; NID:gi180670; PIDN
R;Huhtala, P.; Eddy, R.L.; Fan, Y.S.; Byers, M.G.; Shows, T.B.; Tryggvason, K.
Genomics 6, 554-559, 1990
A;Title: Completion of the primary structure of the human type IV collagenase preproenz

A;Reference number: A34202; MUID:90228972; PMID:2158484
A;Accession: A34202
A;Molecule type: DNA
A;Residues: 1-51 <HU2>
A;Cross-references: UNIPARC:UPI000016A6E3; GB:M33789; NID:g180600; PIDN:AAAS2027.1; PID:
R;Huhtala, P.; Chow, L.T.; Tryggvason, K.
J. Biol. Chem. 265, 11077-11082, 1990
A;Title: Structure of the human type IV collagenase gene.
A;Reference number: A42225; MUID:90293047; PMID:2162831
A;Accession: A42225
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-51;220-393 <HUH>
A;Cross-references: UNIPARC:UPI000016A6E3; UNIPARC:UPI0000172CE8; GB:M55593; GB:J05471;
A;Note: neither the complete amino acid nor the complete nucleotide sequence is given in
R;Frisch, S.M.; Reich, R.; Collier, I.E.; Genrich, L.I.; Martin, G.; Goldberg, G.I.
Oncogene 5, 75-83, 1990
A;Title: Adenovirus E1A represses protease gene expression and inhibits metastasis of hu
A;Reference number: A60187; MUID:90206614; PMID:2157183
A;Accession: A60187
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-58 <PRI>
A;Cross-references: UNIPARC:UPI0000172CE9
R;Okada, Y.; Morodomi, T.; Enghild, J.J.; Suzuki, K.; Yasui, A.; Nakanishi, I.; Salvesen
Eur. J. Biochem. 194, 721-730, 1990
A;Title: Matrix metalloproteinase 2 from human rheumatoid synovial fibroblasts. Purifica
A;Reference number: S13858; MUID:91099351; PMID:2269296
A;Accession: S13858
A;Molecule type: protein
A;Residues: 30-45;110-124 <OKA>
A;Cross-references: UNIPARC:UPI0000172CEA; UNIPARC:UPI0000172CEB
R;Crabbe, T.; Ioannou, C.; Docherty, A.J.P.
Eur. J. Biochem. 218, 431-438, 1993
A;Title: Human progelatinase A can be activated by autolysis at a rate that is concentra
A;Reference number: S39436; MUID:94094834; PMID:8269931
A;Accession: S39436
A;Molecule type: protein
A;Residues: 30-44;444-456 <CR2>
A;Cross-references: UNIPARC:UPI00000723BF; UNIPARC:UPI0000172CEC
R;Stetler-Stevenson, W.G.; Kruttsch, H.C.; Wachter, M.P.; Margulies, I.M.K.; Liotta, L.A.
J. Biol. Chem. 264, 1353-1356, 1989
A;Title: The activation of human type IV collagenase proenzyme. Sequence identification
A;Reference number: A31480; MUID:89109136; PMID:2536363
A;Accession: A31480
A;Molecule type: protein
A;Residues: 110-123 <STE>
A;Cross-references: UNIPARC:UPI0000158DA9
R;Crabbe, T.; Smith, B.; O'Connell, J.; Docherty, A.
FEBS Lett. 345, 14-16, 1994
A;Title: Human progelatinase A can be activated by matrixlysin.
A;Reference number: S44432; MUID:94252395; PMID:8194591
A;Accession: S44432
A;Molecule type: protein
A;Residues: 110-115 <CRA>
A;Cross-references: UNIPARC:UPI0000172CED
R;Brown, D.; Chwa, M.; Escobar, M.; Kenney, M.C.
Exp. Eye Res. 52, 5-16, 1991
A;Title: Characterization of the major matrix degrading metalloproteinase of human corne
A;Reference number: A61498; MUID:91330998; PMID:1868885
A;Accession: A61498
A;Molecule type: protein
A;Residues: 'X', '31', 'X', '33-46', 'X', '48-50', 'Q' <BRO>
A;Cross-references: UNIPARC:UPI0000172CEE
A;Experimental source: corneal stroma
R;Ittoh, Y.; Binner, S.; Nagase, H.
Biochem. J. 308, 645-651, 1995
A;Title: Steps involved in activation of the complex of pro-matrix metalloproteinase 2
A;Reference number: S55327; MUID:95290003; PMID:7772054
A;Accession: S55327
A;Molecule type: protein
A;Residues: 110-114 <ITO>
A;Cross-references: UNIPARC:UPI0000172CEF

C;Genetics:
A;Gene: GDB:MMP2; CLG4; CLG4A
A;Cross-references: GDB:120592; OMIM:120360
A;Map position: 16q13-16q13
A;Introns: 51/3; 127/2; 178/1; 220/1; 278/1; 336/1; 394/1; 446/1; 491/2; 537/1; 590/2; 6;
C;Function:
A;Description: proteolytic cleavage of gelatin type I and collagen types IV, V, VII, and
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homolo
C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase,
F;1-29/Domains: signal sequence #status predicted <SIG>
F;30-660/Product: progelatinase A #status predicted <ACT>
F;30-109/Domains: activation peptide #status predicted <MAT>
F;70-219,394-446/Domains: matrix metalloproteinase homology #status atypical <MMP>
F;110-660/Product: gelatinase A #status predicted <MAT>
F;233-390/Region: collagen binding #status predicted
F;233-274/Domains: fibronectin type II repeat homology <2F1>
F;291-332/Domains: fibronectin type II repeat homology <2F8>
F;349-390/Domains: fibronectin type II repeat homology <2F9>
F;463-660/Domains: hemopexin repeat homology <PXN>
F;102,403,407,413/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
F;404/Active site: Glu #status predicted
F;469-660/Dissulfide bonds: #status predicted
F;573,642/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 29; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 531 KAVFFA 536
RESULT 4
S70365
Gelatinase A (EC 3.4.24.24) precursor - rabbit
N;Alternate names: matrix metalloproteinase-2; type IV collagenase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S70365
R;Matsumoto, S.; Katoh, M.; Watanabe, T.; Masuho, Y.
Biochim. Biophys. Acta 1307, 137-139, 1996
A;Title: Molecular cloning of rabbit matrix metalloproteinase-2 and its broad expressio
A;Reference number: S70365; MUID:96283805; PMID:8679695
A;Accession: S70365
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <MAT>
A;Cross-references: UNIPROT:P50757; UNIPARC:UPI000012F23F; EMBL:D63579; NID:g944816; PI
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homo
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;233-274/Domains: fibronectin type II repeat homology <2F1>
F;291-332/Domains: fibronectin type II repeat homology <2F2>
F;349-390/Domains: fibronectin type II repeat homology <2F9>
F;465-662/Domains: hemopexin repeat homology <PXN>
F;102,403,407,413/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
F;404/Active site: Glu #status predicted
Query Match 100.0%; Score 29; DB 2; Length 662;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 533 KAVFFA 538
RESULT 5
A42496
Gelatinase A (EC 3.4.24.24) precursor - mouse
N;Alternate names: collagenase type IV, 72K

RESULT 7

S46492

gelatinase A (EC 3.4.24.24) precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S46492

R:Aimes, R.T.; French, D.L.; Quigley, J.P.

Biochem. J. 300, 729-736, 1994

A:Title: Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from chicken embryo

A:Reference number: S46492; MUID:94280397; PMID:8010954

A:Accession: S46492

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-663 <AIM>

A:Cross-references: UNIPROT:Q90611; UNIPARC:UPI000012P23E; EMBL:U07775; NID:G504475; PI

A:Note: in the authors' translation 205-Asp is shown after homology; hemopexin repeat homo

C:Superfamily: gelatinase A; fibronectin type II repeat

C:Keywords: hydrolase; metalloproteinase; zinc; zymogen

F:67-216/Domain: matrix metalloproteinase homology #status atypical <NMP>

F:230-271/Domain: fibronectin type II repeat homology <2F1>

F:288-329/Domain: fibronectin type II repeat homology <2F8>

F:346-387/Domain: fibronectin type II repeat homology <2F9>

F:466-663/Domain: hemopexin repeat homology <PXN>

F:99,400,404,410/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:400,404,410/Binding site: zinc, catalytic (His) (active) #status predicted

F:401/Active site: Glu #status predicted

Query Match 100.0%; Score 29; DB 1; Length 663;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFFA 6
|||||

Db 534 KAVFFFA 539

RESULT 8

I53165

nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004

C:Accession: I53165

R:Karlsen, A.B.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.;

Diabetes 44, 753-758, 1995

A:Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from r

A:Reference number: I53165; MUID:95309542; PMID:7540573

A:Accession: I53165

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1147 <RES>

A:Cross-references: UNIPROT:Q6518; UNIPARC:UPI00001707E9; EMBL:U26686; NID:G886072; PI

C:Genetics:

A:Gene: NOS2

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduc

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; meta

F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1147;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFFA 6
|||||

Db 517 KAVFFFA 522

RESULT 9

I56575

nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
C:Accession: I56575
J. Neurosci. Res. 37, 406-414, 1994
A:Title: Cloning and expression of inducible nitric oxide synthase from rat astrocytes.
A:Reference number: I56575; MUID:94231594; PMID:7513765
A:Accession: I56575
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1147 <RES>
A:Cross-references: UNIPROT:Q06518; UNIPARC:UPI00001707BD; EMBL:U03699; NID:9430718; PIR:
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:538-674/Domain: flavodoxin homology <FLX>
F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1147;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 517 KAVFFA 522

RESULT 10
S38253
nitric-oxide synthase (EC 1.14.13.39) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C:Accession: S38253; JN0457
R:Adachi, H.; Iida, S.; Oguchi, S.; Ohshima, H.; Suzuki, H.; Nagasaki, K.; Kawasaki, H.;
Eur. J. Biochem. 217, 37-43, 1993
A:Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitric-
A:Reference number: S38253; MUID:94039059; PMID:7693462
A:Accession: S38253
A:Molecule type: mRNA
A:Residues: 1-1147 <ADA>
A:Cross-references: UNIPROT:Q06518; UNIPARC:UPI0000170A6C; GB:D12520; NID:9391858; PIR:
A:Experimental source: liver
R:Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Biophys. Res. Commun. 191, 767-774, 1993
A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxid
A:Reference number: JN0457; MUID:93221515; PMID:7682072
A:Accession: JN0457
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-41, 'SS', 44-103, 105-190, 'Q', 192-213, 'R', 215-247, 'T', 249-263, 'I', 265-373, 'F'
'S', 896-1000, 'LG', 'SS', 1003-1015, 'RR', 1018-1026, 'EQ', 1029-1147 <WOO>
A:Cross-references: UNIPARC:UPI000017223C; PIR:AA26037.1
A:Experimental source: liver
C:Genetics:
A:Gene: NOS
C:Function:
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:538-674/Domain: flavodoxin homology <FLX>
F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1147;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 517 KAVFFA 522

RESULT 11

547647
nitric-oxide synthase (EC 1.14.13.39) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C;Accession: S47647; JCI1472
R;Gang, Y.; Almqvist, M.; Hansson, G.K.
Biochim. Biophys. Acta 1218, 421-424, 1994
A;Title: cDNA cloning and expression of inducible nitric oxide synthase from rat vascula
A;Reference number: S47647; MUID:94325351; PMID:7519448
A;Accession: S47647
A;Molecule type: mRNA
A;Residues: 1-1147 <RGN>
A;Cross-references: UNIPROT:Q06518; UNIPARC:UPI0000170BE9; EMBL:X76881; NID:G*39283; PID:
R;Nunokawa, Y.; Iehida, N.; Tanaka, S.
Biochem. Biophys. Res. Commun. 191, 89-94, 1993
A;Title: Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells.
A;Reference number: JCI1472; MUID:93191721; PMID:7680561
A;Accession: JCI1472
A;Molecule type: DNA
A;Residues: 1-71,'Y',73-347,'VP',350-678,'FV',681-720,'L',722-739,'L',741-843,'G',845-10
A;Cross-references: UNIPARC:UPI0000170BA7; DDBJ:D14051; NID:G286260; PIDN:BA003138.1; PI
A;Experimental source: vascular smooth muscle
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FLX>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match	100.0%;	Score 29;	DB 1;	Length 1147;
Best Local Similarity	100.0%;	Pred. No. 73;		
Matches	6;	Conservative	0;	Mismatches
			0;	Gaps
0;				
Db	517 KAVFFA 522			

RESULT 12
JC5029
nitric-oxide synthase (EC 1.14.13.39) U - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5029
R;Tsutsunishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Furaki, S.; Niwa, I
Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and
A;Reference number: JC5027; MUID:97070590; PMID:8913516
A;Accession: JC5029
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1147 <TSU>
A;Cross-references: UNIPROT:Q9R0W4; UNIPARC:UPI000017526E
A;Experimental source: uterus
C;Comment: This protein synthesizes nitric oxide from L-arginine.
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; meta
F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FLX>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match	100.0%;	Score 29;	DB 2;	Length 1147;
Best Local Similarity	100.0%;	Pred. No. 73;		
Matches	6;	Conservative	0;	Mismatches
			0;	Gaps
0;				
Db	517 KAVFFA 522			

RESULT 13
JC5028
nitric-oxide synthase (EC 1.14.13.39) L - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5028
R;Tsutsunishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Furaki, S.; Niwa, I
Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and
A;Reference number: JC5027; MUID:97070590; PMID:8913516
A;Accession: JC5029
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1147 <TSU>
A;Cross-references: UNIPROT:Q9R0W4; UNIPARC:UPI000017526E
A;Experimental source: uterus
C;Comment: This protein synthesizes nitric oxide from L-arginine.
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; meta
F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FLX>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match	100.0%;	Score 29;	DB 2;	Length 1147;
Best Local Similarity	100.0%;	Pred. No. 73;		
Matches	6;	Conservative	0;	Mismatches
			0;	Gaps
0;				
Db	517 KAVFFA 522			

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
 C;Accession: JC5028
 R;Tautsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M
 Biol. Pharm. Bull. 19, 1374-1376, 1996
 A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u
 A;Reference number: JC5027; MUID:97070590; PMID:8913516
 A;Accession: JC5028
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-1147 <TSU>
 A;Cross-references: UNIPROT:Q9R0W4; UNIPARC:UPI0000017526D
 A;Experimental source: lung
 C;Comment: This protein synthesizes nitric oxide from L-arginine.
 C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
 C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
 F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FLX>
 F;538-674/Domain: flavodoxin homology <FLX>
 F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 DB 517 KAVFFFA 522

RESULT 14
 JC5027
 nitric-oxide synthase (EC 1.14.13.39) K - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
 C;Accession: JC5027
 R;Tautsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M
 Biol. Pharm. Bull. 19, 1374-1376, 1996
 A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u
 A;Reference number: JC5027; MUID:97070590; PMID:8913516
 A;Accession: JC5027
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-1147 <TSU>
 A;Cross-references: UNIPROT:Q06518; UNIPARC:UPI0000170A6D; DBJ:D83661; NID:g1209382; PI
 A;Experimental source: kidney
 C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
 C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
 F;191-199/Domain: heme-binding #status predicted <HMB>
 F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FLX>
 F;538-674/Domain: flavodoxin homology <FLX>
 F;620-647/Domain: FMN binding #status predicted <FMN>
 F;764-775,899-910/Domain: FAD binding #status predicted <FAD>
 F;975-993,1054-1067/Domain: NADP binding #status predicted <NDP>
 F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 DB 517 KAVFFFA 522

RESULT 15
 S65440
 nitric-oxide synthase (EC 1.14.13.39) - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S65440
 R;Iwashina, M.; Hirata, Y.; Inai, T.; Sato, K.; Marumo, F.
 Eur. J. Biochem. 237, 668-673, 1996
 A;Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from rat
 A;Reference number: S65440; MUID:96235231; PMID:8647111

A;Accession: S65440
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1147 <IWA>
 C;Cross-references: UNIPROT:Q9R0W4; UNIPARC:UPI0000017526F
 C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduc
 C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; meta
 F;506-535/Region: calmodulin binding
 F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F;538-674/Domain: flavodoxin homology <FLX>
 F;599-618/Region: biopterin binding
 F;620-647/Region: FMN binding #status predicted
 F;764-775/Region: FAD binding #status predicted
 F;901-910/Region: FAD binding #status predicted
 F;975-993/Region: NADPH binding #status predicted
 F;1074-1087/Region: NADPH binding #status predicted
 F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 DB 517 KAVFFFA 522

RESULT 16
 AF2630
 hypothetical protein Atu0441 [imported] - Agrobacterium tumefaciens (strain C58, Dupont
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AF2630
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, B.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AF2630
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-169 <KUR>
 A;Cross-references: UNIPROT:Q8UI59; UNIPARC:UPI00000D17ED; GB:AE008688; PIDN:AAL41460.1
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu0441
 A;Map position: circular chromosome

Query Match 96.6%; Score 28; DB 2; Length 169;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 DB 114 KAIFFA 119

RESULT 17
 T20734
 hypothetical protein M79.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T20734; T23833
 R;Harris, B.
 submitted to the EMBL Data Library, August 1995
 A;Reference number: Z19316
 A;Accession: T20734
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-283 <WIL>

A;Cross-references: UNIPROT:Q19334; UNIPARC:UPI000007F46F; EMBL:Z50857; PIDN:CAA90720.1;
A;Experimental source: clone F1A1
R;Mortimore, B.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19805
A;Accession: T23833
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-283 <W12>
A;Cross-references: UNIPARC:UPI000007F46F; EMBL:Z50806; PIDN:CAA90692.1; GSPDB:GN000028;
A;Experimental source: clone M79
C;Genetics:
A;Gene: CBSP:M79.2
A;Map position: X
A;Introns: 42/1; 71/2; 108/3; 126/3; 167/2; 196/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M79.2
Query Match 96.6%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
||:||||
Db 157 KAIFFA 162
RESULT 18
B44358
cysteine-rich protein hCRP homolog - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: B44358
R;Sadler, I.; Crawford, A.W.; Michelsen, J.W.; Beckerle, M.C.
J. Cell Biol. 119, 1573-1587, 1992
A;Title: Zyxin and cCRP: two interactive LIM domain proteins associated with the cytoske
A;Reference number: A44358; MUID:93107157; PMID:1469049
A;Accession: B44358
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-58 <SAD>
A;Cross-references: UNIPROT:P32965; UNIPARC:UPI00001799R8
A;Note: sequence extracted from NCBI backbone (NCBIP:121176)
C;Superfamily: cysteine and glycine-rich protein; LIM metal-binding repeat homology
F;9-58/Domain: LIM metal-binding repeat homology (fragment) <LIM>
Query Match 89.7%; Score 26; DB 2; Length 58;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
||:||||
Db 14 KAVFFA 19
RESULT 19
S27597
hypothetical protein - Nostoc sp.
C;Species: Nostoc sp.
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S27597
R;Walton, D.K.; Gendel, S.M.; Atherly, A.G.
submitted to the EMBL Data Library, February 1992
A;Reference number: S27596
A;Accession: S27597
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <WAL>
A;Cross-references: UNIPROT:Q51314; UNIPARC:UPI00000B0C14; EMBL:M81381; NID:g150381; PID

QY 1 KAVFFA 6
||:||||
Db 36 KALFFA 41
RESULT 20
F69857
conserved hypothetical protein ykna - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: F69857
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Asevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Scanlon,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69857
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-156 <KUN>
A;Cross-references: UNIPROT:O34598; UNIPARC:UPI00000602B4; GB:Z99110; GB:AL009126; NID:g
C;Genetics:
A;Experimental source: strain 168
C;Gene: ykna
C;Superfamily: deaminase
Query Match 89.7%; Score 26; DB 1; Length 156;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
||:||||
Db 96 KAVFFA 101
RESULT 21
D71049
probable L(+)-tartarate dehydratase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C;Accession: D71049
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71049
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-166 <KAW>
A;Cross-references: UNIPROT:O59317; UNIPARC:UPI00000668B7; GB:AP000006; NID:g3236133; P
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1684
C;Superfamily: iron-dependent tartrate dehydratase beta chain
F;14-165/Domain: iron-dependent tartrate dehydratase beta chain homology <TTDB>
Query Match 89.7%; Score 26; DB 2; Length 166;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||:|
Db 107 KAVYFA 112

RESULT 22

E70445

C-terminal fumarate hydratase, class I - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C/Accession: E70445

V.; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ory

Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: E70445

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-185 <AQF>

A/Cross-references: UNIPROT:O67590; UNIPARC:UPI00000566AD; GB:AE000750; NID:g2983999; PMID

C/Genetics: strain VF5

A/Gene: funx

F/13-175/Domain: iron-dependent tartrate dehydratase beta chain; iron-dependent tartrate d

F/13-175/Domain: iron-dependent tartrate dehydratase beta chain homology <TTDB>

Query Match 89.7%; Score 26; DB 2; Length 185;

Best Local Similarity 83.3%; Pred. No. 71;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||:|
Db 117 KAVYFA 122

RESULT 23

A49648

cysteine-rich protein - chicken

N/Alternate names: zyxin-binding protein

C/Species: Gallus gallus (chicken)

C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Oct-2004

C/Accession: A49648; S34179

R/Crawford, A.W.; Pino, J.D.; Beckerle, M.C.

J. Cell Biol. 124, 117-127, 1994

A/Title: Biochemical and molecular characterization of the chicken cysteine-rich protein

A/Reference number: A49648; MUID:94124603; PMID:8294495

A/Accession: A49648

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-192 <CRA>

A/Cross-references: UNIPROT:P32965; UNIPARC:UPI00001711EC; EMBL:X73831; NID:g313286; PMID

C/Species: Gallus gallus (chicken)

C/Suprafamily: cysteine and glycine-rich protein; LIM metal-binding repeat homology

F/10-61/Domain: LIM metal-binding repeat homology <LIM1>

F/118-169/Domain: LIM metal-binding repeat homology <LIM2>

Query Match 89.7%; Score 26; DB 2; Length 192;

Best Local Similarity 83.3%; Pred. No. 73;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||:|
Db 15 KAVYFA 20

RESULT 24

S38879

LIM-domain protein CRP1 - Japanese quail

C/Species: Coturnix coturnix japonica (Japanese quail)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C/Accession: S38879

R; Weiskirchen, R.; Beckerle, M.C.; Bister, K.

submitted to the EMBL Data Library, November 1993

A/Description: The CRP family of LIM-domain proteins: identification of two different a

A/Reference number: S38879

A/Accession: S38879

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-192 <WEI>

A/Cross-references: UNIPROT:P32965; UNIPARC:UPI00001711EC; EMBL:Z28333; NID:g429159; PI

C/Species: Caenorhabditis elegans

C/Suprafamily: cysteine and glycine-rich protein; LIM metal-binding repeat homology

F/10-61/Domain: LIM metal-binding repeat homology <LIM1>

F/118-169/Domain: LIM metal-binding repeat homology <LIM2>

Query Match 89.7%; Score 26; DB 2; Length 192;

Best Local Similarity 83.3%; Pred. No. 73;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||:|
Db 15 KAVYFA 20

RESULT 25

E75252

molybdopterin biosynthesis protein D/E DR2607 [similarity] - Deinococcus radiodurans (s

N/Alternate names: moaD-moaE fusion protein; molybdopterin-converting factor

C/Species: Deinococcus radiodurans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004

C/Accession: E75252

R/White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: E75252

A/Molecule type: DNA

A/Residues: 1-229 <WHI>

A/Cross-references: UNIPROT:Q9RR88; UNIPARC:UPI000003FEF; GB:AE002090; GB:AE000513; NI

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR2607

A/Map position: 1

C/Suprafamily: Molybdopterin biosynthesis protein D/E

C/Keywords: molybdopterin biosynthesis

Query Match 89.7%; Score 26; DB 2; Length 229;

Best Local Similarity 83.3%; Pred. No. 86;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||:|
Db 4 KAVYFA 9

RESULT 26

T16110

hypothetical protein F20D12.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C/Accession: T16110

R; Wu, X.

submitted to the EMBL Data Library, November 1995

A/Description: The sequence of C. elegans cosmid F20D12.

A/Reference number: Z18462

A/Accession: T16110

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-244 <WUX>

A/Cross-references: UNIPARC:UPI000017B915; EMBL:U40933; NID:g1072142; PID:g1072144; PID

C/Genetics:

A/Gene: CESP:F20D12.5

A/Introns: 14/1; 47/3; 84/3; 118/1; 203/3

Query Match 89.7%; Score 26; DB 2; Length 244;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
:|||||
Db 9 KAVYFA 14

RESULT 27
T01119
Hypothetical protein At2g32880 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T21L14.18
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01119; F84738
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, December 1997
A:Description: Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence.
A:Reference number: Z14209
A:Accession: T01119
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-285 <R0U>
A:Cross-references: UNIPROT:Q48777; UNIPARC:UPI00009E1EC; EMBL:AC003033; NID:g2702261;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84738
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-285 <STO>
A:Cross-references: UNIPARC:UPI00009E1EC; GB:AE002093; NID:g2702282; PIDN:AAB91985.1; C
C:Genetics:
A:Gene: T21L14.18; At2g32880
A:Map position: 2; 105/1; 206/2
A:Introns: 11/1; 54/2; 105/1; 206/2
C:Superfamily: Arabidopsis thaliana hypothetical protein A_TW018A10.12

Query Match 89.7%; Score 26; DB 2; Length 285;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
:|||||
Db 137 KAVYFA 142

RESULT 28
ZBBE13
33.1K zinc-binding protein - ictalurid herpesvirus 1 (strain auburn 1)
C:Species: ictalurid herpesvirus 1
A:Note: host Ictalurus punctatus [channel catfish]
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: D36787
R:Davidson, A.J.
submitted to GenBank, January 1992
A:Description: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A36804
A:Accession: D36787
A:Molecule type: DNA
A:Residues: 1-299 <DAV>
A:Cross-references: UNIPROT:Q00165; UNIPARC:UPI00001384D1; GB:M75136; NID:g331209; PIDN:
R:Davidson, A.J.
Virology 186, 9-14, 1992
A:Title: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A39447; MUID:92087490; PMID:1727613
A:Contents: annotation
A:Note: neither amino acid nor nucleotide sequence is given

C:Genetics:
A:Gene: 12
C:Superfamily: ictalurid herpesvirus 33.1K zinc binding protein
C:Keywords: zinc finger

Query Match 89.7%; Score 26; DB 1; Length 299;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
:|||||
Db 39 RAVFFA 44

RESULT 29
S40819
Probable transport protein yihN - Escherichia coli (strain K-12)
N:Alternate names: hypothetical protein 0421
C:Species: Escherichia coli
C:Date: 19-May-1994 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S40819; E65192
R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 21, 3391-3398, 1993
A:Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8
A:Reference number: S40802; MUID:93347969; PMID:8346018
A:Accession: S40819
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-421 <PLU>
A:Cross-references: UNIPROT:P32135; UNIPARC:UPI000003EB31; EMBL:L19201; NID:g304961; PID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65192
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-421 <BLAT>
A:Cross-references: UNIPARC:UPI000003EB31; GB:AE0000463; GB:U00096; NID:g2367320; PIDN:A
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yihN
C:Superfamily: Escherichia coli probable transport protein yqce
C:Keywords: transmembrane protein; transport protein

Query Match 89.7%; Score 26; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
:|||||
Db 332 RAVFFA 337

RESULT 30
C86075
probable resistance protein (transport) yihN [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C86075
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C86075
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-421 <STO>
A:Cross-references: UNIPROT:Q8X8F3; UNIPARC:UPI00000075F3; GB:AE005174; NID:g12518756;
A:Experimental source: strain O157:H7, substrain EDL933

C;Genetics:
A;Gene: yibN
C;Superfamily: Escherichia coli probable transport protein yqcE

Query Match 89.7%; Score 26; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
:|||||

Db 332 RAVFFPA 337

RESULT 31

D91228
probable resistance protein [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D91228
R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91228
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-421 <HAY>
A;Cross-references: UNIPROT:Q8X8F3; UNIPARC:UPI00000D75F3; GB:BA000007; PIDN:BA038219.1
A;Experimental source: strain O157:H7, substrain RIMD 050952
C;Genetics:
A;Gene: ECe4796
C;Superfamily: Escherichia coli probable transport protein yqcE

Query Match 89.7%; Score 26; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
:|||||

Db 332 RAVFFPA 337

RESULT 32

AH1799
GTPase homolog lin2943 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1799
R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1799
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-457 <GLA>
A;Cross-references: UNIPROT:Q926U7; UNIPARC:UPI000013744F; GB:AL592022; PIDN:CAC98168.1
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2943
C;Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu hom

Query Match 89.7%; Score 26; DB 2; Length 457;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
:|||||

Db 332 RAVFFPA 337

Db 374 KALFFPA 379

RESULT 33

VCXFTI
major capsid protein - Tipula iridescent virus (type 1)
C;Species: Tipula iridescent virus
A;Note: host Tipula paludosa (European crane fly)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A33558
R;Tajbakhsh, S.; Lee, P.B.; Watson, D.C.; Seligy, V.L.
J. Virol. 64, 125-136, 1990
A;Title: Molecular cloning, characterization, and expression of the Tipula iridescent v
A;Reference number: A33558; MUID:90080113; PMID:2293661
A;Accession: A33558
A;Molecule type: DNA
A;Residues: 1-464 <PAJ>
A;Cross-references: UNIPROT:PI8162; UNIPARC:UPI0000127D5B; EMBL:M33542; NID:G331317; PI
C;Superfamily: Tipula iridescent virus major capsid protein
C;Keywords: capsid protein

Query Match 89.7%; Score 26; DB 1; Length 464;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
:|||||

Db 302 KALFFPA 307

RESULT 34

JQ2215
major capsid protein - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ2215
R;Stolwasser, R.; Raab, K.; Schnitzler, P.; Janssen, W.; Darai, G.
J. Gen. Virol. 74, 873-879, 1993
A;Title: Identification of the gene encoding the major capsid protein of insect irides
A;Reference number: JQ2215; MUID:93260401; PMID:8492091
A;Accession: JQ2215
A;Molecule type: DNA
A;Residues: 1-467 <STO>
A;Cross-references: UNIPROT:Q05815; UNIPARC:UPI00001749ED; GB:M99395; NID:G292992; PIDN
A;Note: the authors translated codon G1T for residue 231 as Tyr, codon TAT for residue
C;Superfamily: Tipula iridescent virus major capsid protein
C;Keywords: capsid protein

Query Match 89.7%; Score 26; DB 1; Length 467;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
:|||||

Db 306 KALFFPA 311

RESULT 35

VCXFSI
major capsid protein - Simulium iridescent virus (type 22)
C;Species: Simulium iridescent virus
A;Note: host Simulium spp. (blackfly)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B37075; C37075
R;Cameron, I.R.
Virol. 178, 35-42, 1990
A;Title: Identification and characterization of the gene encoding the major structural
A;Reference number: A37075; MUID:90357789; PMID:2389558
A;Accession: B37075
A;Molecule type: DNA
A;Residues: 1-472 <CAM>
A;Cross-references: UNIPROT:P22166; UNIPARC:UPI0000127D5D; EMBL:M32799; NID:G331321; PI
A;Accession: C37075

Query Match 89.7%; Score 26; DB 1; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
:|||||

Db 306 KALFFPA 311

A;Molecule type: protein
A;Residues: 72-81;89-116 <CA2>
A;Cross-references: UNIPARC:UPI00001749EB; UNIPARC:UPI00001749EC
C;Species: Cricetus griseus (Chinese hamster)
C;Superfamily: Tipula iridescent virus major capsid protein
C;Keywords: capsid protein

Query Match 89.7%; Score 26; DB 1; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 302 KALFFA 307

RESULT 36
T50726
hypothetical protein 479 [imported] - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50726
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2
A;Reference number: Z25222; MUID:20115911; PMID:10648776
A;Accession: T50726
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-479 <CHO>
A;Cross-references: UNIPROT:Q9RFP8; UNIPARC:UPI0000082P99; EMBL:AF195122; PIDN:AAF24270.
A;Experimental source: strain 2.4.1

Query Match 89.7%; Score 26; DB 2; Length 479;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 349 KAMFFA 354

RESULT 37
AB0805
3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - Salmonella enterica subsp. enterica sero
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0805
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-715 <PAR>
A;Cross-references: UNIPARC:UPI0000059B21; GB:AL513382; PIDN:CAD07620.1; PID:g16503611;
C;Genetics:
C;Keywords: oxidoreductase

Query Match 89.7%; Score 26; DB 2; Length 715;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 286 RAVFFA 291

RESULT 38
B54962
sterol regulatory element binding protein 2 precursor - Chinese hamster
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: B54962
R;Yang, J.; Sato, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
A;Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that t
A;Reference number: A54962; MUID:95047343; PMID:7958866
A;Accession: B54962
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1139 <YAN>
A;Cross-references: UNIPROT:Q60429; UNIPARC:UPI0000178926; GB:U12330
A;Note: 493 Ser was also found
C;Superfamily: sterol regulatory element binding protein
C;Keywords: DNA binding; membrane protein

Query Match 89.7%; Score 26; DB 2; Length 1139;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 916 KAVFFA 921

RESULT 39
S62506
alpha-glucan synthase (EC 2.4.1.-) mok11 - fission yeast (Schizosaccharomyces pombe) (fr
N;Alternate names: morphological/kinase-inhibitor supersensitive protein mok11
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: T38290; T43430; S62506
R;Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21783
A;Accession: T38290
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1204 <NT2>
A;Cross-references: UNIPROT:Q09854; UNIPARC:UPI000016208E; EMBL:Z64354; NID:g10393338; P
R;Katayama, S.; Toda, T.
submitted to the EMBL Data Library, October 1998
A;Description: Fission yeast alpha-glucan synthase Mok1 localizes closely with actin an
A;Reference number: Z22509
A;Accession: T43430
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1204 <KAT>
A;Cross-references: UNIPARC:UPI000016208E; EMBL:AB018380; PIDN:BAA76557.1
A;Experimental source: strain h- 972
C;Genetics:
A;Gene: mok11
A;Map position: 1R
C;Function:
A;Description: Involved in cell morphogenesis interdependently of the actin cytoskeleton
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 89.7%; Score 26; DB 2; Length 1204;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 120 KAVFFA 125

RESULT 40
T09127
probable erythrocyte-binding protein MAEBL - Plasmodium yoelii

C;Species: Plasmodium yoelii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09127
R;Kapke, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: 216577; MUID:98115903; PMID:9448314
A;Accession: T09127
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1701 <RAP>
A;Cross-references: UNIPROT:O61164; UNIPARC:UPI000007D433; EMBL:AF031886; NID:G2947227;
A;Experimental source: subspecies yoelii; strain YM
C;Genetics:
A;Gene: maeb1
A;Introns: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion

Query Match 89.7%; Score 26; DB 2; Length 1701;
Best Local Similarity 83.3%; Pred. No. 5.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
Db 1648 KAVYFA 1653

RESULT 41
AG2447
hypothetical protein alr5135 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2447
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <KUR>
A;Cross-references: UNIPROT:Q8TM06; UNIPARC:UPI00000CED8A; GB:BA000019; PIDN:BA076834.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr5135

Query Match 86.2%; Score 25; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 70; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||
Db 37 KAVFF 41

RESULT 42
Q0SACC
hypothetical protein C-120 - Staphylococcus aureus plasmid pC194
C;Species: Staphylococcus aureus
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A04490
R;Horinouchi, S.; Weisblum, B.
J. Bacteriol. 150, 815-825, 1982
A;Title: Nucleotide sequence and functional map of pC194, a plasmid that specifies inducible
A;Reference number: A91791; MUID:82167188; PMID:6950931
A;Accession: A04490
A;Molecule type: DNA
A;Residues: 1-120 <HOR>
A;Cross-references: UNIPROT:P03861; UNIPARC:UPI0000013BD18
C;Genetics:
A;Genome: plasmid

C;Superfamily: Staphylococcus aureus plasmid pC194 hypothetical 14.6K protein
Query Match 86.2%; Score 25; DB 1; Length 120;
Best Local Similarity 83.3%; Pred. No. 83; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
Db 62 KATFFA 67

RESULT 43
I40566
hypothetical protein 5.60 - Bacillus subtilis plasmid pTA1060
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40566
R;Meijer, W.J.; Venema, G.; Bron, S.
Nucleic Acids Res. 23, 612-619, 1995
A;Title: Characterization of single strand origins of cryptic rolling-circle plasmids
A;Reference number: I40549; MUID:95206941; PMID:7899081
A;Accession: I40566
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-132 <RES>
A;Cross-references: UNIPROT:Q45455; UNIPARC:UPI00000B6E18; EMBL:U32380; NID:G1049123; P
A;Experimental source: plasmid pTA1060
C;Genetics:
A;Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 132;
Best Local Similarity 83.3%; Pred. No. 90; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
Db 94 KGVFFA 99

RESULT 44
WMR219
19K globulin precursor - rice
N;Alternate names: alpha-globulin
C;Species: Oryza sativa (rice)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004
C;Accession: S20024; S25735; PNO497
R;Shorttosh, B.S.; Wen, L.; Zen, K.C.; Huang, J.K.; Pan, J.S.; Hermodson, M.A.; Tanaka, K.
Plant Mol. Biol. 18, 151-154, 1992
A;Title: A novel cereal storage protein: molecular genetics of the 19 kDa globulin of rice
A;Reference number: S20024; MUID:92119226; PMID:1731968
A;Accession: S20024
A;Molecule type: mRNA
A;Residues: 1-186 <SHO>
A;Cross-references: UNIPROT:P29835; UNIPARC:UPI000012B4D1; EMBL:X63990; NID:G20158; PID
A;Accession: S25735
A;Molecule type: protein
A;Residues: 66-74;108-133;171-186 <SH2>
A;Cross-references: UNIPARC:UPI0000173296; UNIPARC:UPI0000173297; UNIPARC:UPI0000173298
R;Kishan, H.B.; Pueppke, S.G.
Biochem. Biophys. Res. Commun. 193, 460-466, 1993
A;Title: Nucleotide sequence of an abundant rice seed globulin: homology with the high
A;Reference number: PNO497; MUID:93277591; PMID:8503935
A;Accession: PNO497
A;Molecule type: mRNA
A;Residues: 6-186 <KRI>
A;Cross-references: UNIPARC:UPI0000173299; GB:L12252
A;Experimental source: seed
C;Superfamily: Alpha amylase inhibitor
C;Keywords: storage protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-186/Product: 19K globulin #status predicted <MAT>

Query Match 86.2%; Score 25; DB 1; Length 186;

```

Best Local Similarity 83.3%; Pred. NO. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      | | | |
Db      4 KVVFFA 9

RESULT 45
JC4784
alpha-globulin precursor - rice
C:Species: Oryza sativa (rice)
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 31-Dec-2004
C:Accession: JC4784
R:R; Nakase, M.; Hotta, H.; Adachi, T.; Aoki, N.; Nakamura, R.; Masumura, T.; Tanaka, K.; M
Gene 170, 223-226, 1996
A:Title: Cloning of the rice seed alpha-globulin-encoding gene: Sequence similarity of t

```

A;Reference number: JC4784; MUID:962351139; PMID:8666249
A;Accession: JC4784
A;Molecule type: DNA
A;Residues: 1-186 <NAK>
A;Cross-references: UNIPROT:P93414; UNIPARC:UPI00000A4C3C; DDBJ:D50643; NID:g840704; PDB:
A;Experimental source: seed
C;Genetics:
A;Gene: G1b
C;Superfamily: Alpha amylase inhibitor
C;Keywords: Globulin; seed
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-186/Product: alpha-globulin #status predicted <NAK>

Query Match	86.2%	Score 25;	DB 2;	Length 186;
Best Local Similarity	83.3%;	Pred. No. 1.2e+02;		
Matches 5;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	KAVEFFA	6	
Db	4	KVEFFA	9	

RESULT 46
 H64441
 hypothetical protein MJ1137 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: H64441
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodok, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.N.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:868087
 A:Accession: H64441
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-191 <BUL>
 A:Cross-references: UNIPROT:Q58537; UNIPARC:UPI0000065085; GB:U67556; GB:L77117; NID:gis
 C:Genetics:
 A:Map position: REV1078609-1078034
 A:Start codon: TTG

```

Query Match      86.2%; Score 25; DB 2; Length 191;
Best Local Similarity 100.0%; Pred.No. 1.13e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVPF 5
        |||||
Db      89 KAVPF 93

RESULT 47
B64668

```

carbonic anhydrase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: B64668
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64668
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-202 <TOM>
A:Cross-references: UNIPROT:O25Y98; UNIPARC:UPI00000D3059; GB:AEO000624; GB:AEO000511; NID
C:Superfamily: carbonate dehydratase; carbonic anhydrase homology

```

Query Match      86.2%; Score 25; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      |||||
Db      78 KAVFF 82

RESULT 48
AG2405
Hypochemical protein all4799 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2405
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
  Nakazaki, N.; Shimpu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, I.;
  DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209 <KUR>
A:Cross-references: UNIPROT:Q8YMK5; UNIPARC:UPI000000C8C5F; GB:BA0000019; PIDN:BA876498.1;
A:Experimental source: strain PCC 7120

```

```

C:Genetics:
A:Gene: all4799
C:Superfamily: probable alkaline phosphatase yngC

Query Match      86.2%;   Score 25;   DB 2;   Length 209;
Best Local Similarity 100.0%;   Pred. No. 1.4e+02;
Matches 5;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 KAVFF 5
        |||||
Db      113 KAVFF 117

RESULT 49
CB1216
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: CB1216
R;Pettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiagnani, V.; Pizsa, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: CB1216
A>Status: preliminary

```


A:Molecule type: DNA
 A:Residues: 1-210 <TET>
 A:Cross-references: UNIPROT:Q9KL84; UNIPARC:UPI000000C4451; GB:AE002385; GB:AE002098; NID
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0283

Query Match 86.2%; Score 25; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
 |||||
 Db 116 KAVFF 120

RESULT 50

G81793

hypothetical protein NMA2204 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: G81793

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: G81793

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-210 <PAR>

A:Cross-references: UNIPROT:Q9JSP2; UNIPARC:UPI000000C4D6C; GB:ALL162758; GB:ALL157959; NID

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA2204

Query Match 86.2%; Score 25; DB 2; Length 210;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||||

Db 116 KAVFF 120

RESULT 51

AB3270

threonine efflux protein [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: AB3270

R;DelVecchio, V.G.; Kapatal, R.J.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:1175668

A:Accession: AB3270

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <KUR>

A:Cross-references: UNIPROT:Q9L6H7; UNIPARC:UPI0000057B7C; GB:AE008917; PIDN:ANL51325.1;

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI0143

A:Map position: I

Query Match

Best Local Similarity 86.2%; Score 25; DB 2; Length 212;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||||

Db 131 KAVFF 135

RESULT 52

F69125

conserved hypothetical protein MTH209 - Methanobacterium thermoautotrophicum (strain De

C;Species: Methanobacterium thermoautotrophicum

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: F69125

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: F69125

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-226 <MTH>

A:Cross-references: UNIPROT:Q26311; UNIPARC:UPI0000066675; GB:AE000808; GB:AE000666; NID

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH209

C;Superfamily: hypothetical protein MJ1437

Query Match

Best Local Similarity 86.2%; Score 25; DB 2; Length 226;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||||

Db 3 KAVFF 7

RESULT 53

A71847

carbonic anhydrase - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori

A:Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: A71847

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: A71847

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-247 <ARN>

A:Cross-references: UNIPROT:Q9ZK30; UNIPARC:UPI000000D36F4; GB:AE001539; GB:AE001439; NI

A:Experimental source: strain J99

C:Genetics:

A:Gene: jhp112

C;Superfamily: carbonate dehydratase; carbonic anhydrase homology

Query Match

Best Local Similarity 86.2%; Score 25; DB 2; Length 247;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||||

Db 78 KAVFF 82

RESULT 54

B69983

conserved hypothetical protein ysaA - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: B69983

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmerson, F.T.; Entian, K.D.; Brrington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallei, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.; Koeter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadia, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: B69983

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-260 <N>

A;Cross-references: UNIPROT:P94512; UNIPARC:UPI00000608A7; GB:Z99118; GB:AL009126; NID:9

A;Experimental source: strain 168

C;Genetics:

A;Gene: ysaA

C;Superfamily: hypothetical protein MJ1437

Query Match 86.2%; Score 25; DB 2; Length 260;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0;

QY 1 KAVFF 5

DB 2 KAVFF 6

RESULT 55

C95942

Probable transcription regulator, deoR family protein [imported] - *Sinorhizobium meliloti*

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: C95942

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: C95942

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-263 <KUR>

A;Cross-references: UNIPROT:Q92VA5; UNIPARC:UPI00000CB676; GB:AL591985; PIDN:CAC49203.1

A;Experimental source: strain 1021, megaplasmid pSymb

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

Science 293, 568-572, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, heault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: deoR; SM21299

A;Genome: plasmid

C;Superfamily: deo operon repressor

Query Match 86.2%; Score 25; DB 2; Length 263;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 6

DB 218 KAVFF 223

RESULT 56

A28171

phenylethanolamine N-methyltransferase (BC 2.1.1.28) - human

C;Species: *Homo sapiens* (man)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A28171; S10894; A28210

R;Kaneda, N.; Ichinose, H.; Kobayashi, K.; Oka, K.; Kishi, F.; Nakazawa, A.; Kurosawa, Y J. Biol. Chem. 263, 7672-7677, 1998

A;Title: Molecular cloning of cDNA and chromosomal assignment of the gene for human phen

A;Reference number: A28171; MUID:88227966; PMID:3372503

A;Accession: A28171

A;Molecule type: mRNA

A;Residues: 1-282 <KAN>

A;Cross-references: UNIPROT:P11086; UNIPARC:UPI0000111BE4; GB:J03727; NID:gl90141; PIDN: R;Sasaoka, T.; Kaneda, N.; Kurosawa, Y.; Fujita, K.; Nagatsu, T.

Neurochem. Int. 15, 555-565, 1989

A;Title: Structure of human phenylethanolamine N-methyltransferase gene: existence of tw

A;Reference number: S10894

A;Accession: S10894

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-282 <SAS>

A;Cross-references: UNIPARC:UPI0000111BE4; EMBL:X52730; NID:G35560; PIDN:CAA36944.1; PID R;Baetge, E.E.; Behringer, R.R.; Messing, A.; Brinster, R.L.; Palmiter, R.D.

Proc. Natl. Acad. Sci. U.S.A. 85, 3648-3652, 1988

A;Title: Transgenic mice express the human phenylethanolamine N-methyltransferase gene i

A;Reference number: A28210; MUID:88217959; PMID:2835776

A;Accession: A28210

A;Molecule type: mRNA

A;Residues: 1-168, 'AQ', 171-282 <BAE>

A;Cross-references: UNIPARC:UPI000016AED9; GB:J03280; NID:gl90143; PIDN:AAA60131.1; PID: C;Genetics:

A;Gene: GDB:PNMT; PENT

A;Cross-references: GDB:120271; OMIM:171190

A;Map position: 1pter-17qter

A;Introns: 68/1; 137/2

C;Superfamily: phenylethanolamine N-methyltransferase

C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 86.2%; Score 25; DB 1; Length 282;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 6

DB 270 KGVFF 275

RESULT 57

A82458

hypothetical protein VCA0458 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: A82458

R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: A82458

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-285 <HEI>

A;Cross-references: UNIPROT:Q9KMB5; UNIPARC:UPI00000C352C; GB:AE004378; GB:AE003853; NTI A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0458

A;Map position: 2

Query Match 86.2%; Score 25; DB 2; Length 285;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 217 KAVFF 221
|||||

RESULT 58

B90435
hypothetical protein dppC-3 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90435
R;Shen, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <KUR>
A;Cross-references: UNIPROT:Q97VK7; UNIPARC:UPI00000647C9; GB:AE006641; NID:gl3815922; F
C;Genetics:
C;Superfamily: oligopeptide permease protein oppB

Query Match 86.2%; Score 25; DB 2; Length 298;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
Db 156 KATFFA 161

RESULT 59

H90717
hypothetical protein ECs0712 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90717
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90717
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <HAY>
A;Cross-references: UNIPROT:Q8X9H6; UNIPARC:UPI00001653CA; GB:BA0000007; PIDN:BA034135.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs0712

Query Match 86.2%; Score 25; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||||
Db 189 KAVFF 193

RESULT 60

T24732
hypothetical protein T09B9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24732
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24732

A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: DNA
A;Residues: 1-308 <WIL>
A;Cross-references: UNIPROT:Q10049; UNIPARC:UPI000013C01F; EMBL:Z47070; PIDN:CAA87343.1
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CBSP:T09B9.3
A;Map position: X
A;Introns: 33/3; 65/3; 96/3; 149/2; 182/3; 220/2; 242/2

Query Match 86.2%; Score 25; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||||
Db 66 KAVFF 70

RESULT 61

G72347
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72347
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke-
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se-
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72347
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-321 <ARN>
A;Cross-references: UNIPROT:Q9WZ88; UNIPARC:UPI00000C13B4; GB:AE001740; GB:AE000512; NT1
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0682

Query Match 86.2%; Score 25; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||||
Db 179 KAVFF 183

RESULT 62

H85567
hypothetical protein ybfM [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85567
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe-
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85567
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <STO>
A;Cross-references: UNIPROT:Q8X9H6; UNIPARC:UPI00000D0807; GB:AE005174; NID:g12513583;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ybfM

Query Match 86.2%; Score 25; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D86610
glycerol-3-P acyltransferase [imported] - Chlamydomonadales pneumoniae (strain J138)
C:Species: Chlamydomonadales pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86610
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise,
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: AB6491; PMID:20330349; PMID:10871362
A:Accession: D86610
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <STO>
A:Cross-references: UNIPROT:Q9ZSV0; UNIPARC:UPI00000D411C; GB:BA000008; NID:g8979332; P1:
A:Experimental source: strain J138
C:Genetics:
A:Gene: plsB
C:Superfamily: glycerol-3-phosphate O-acyltransferase

Query Match 86.2%; Score 25; DB 2; Length 311;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 -|||
DB 278 RAIFFA 283

RESULT 66
E72597
probable alcohol dehydrogenase APE1245 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72597
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara,
H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; PMID:99310339; PMID:10382966
A:Accession: E72597
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332 <KAW>
A:Cross-references: UNIPROT:Q9YCH2; UNIPARC:UPI000005DE88; DDBJ:AF000061; NID:G5104821;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1245
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 86.2%; Score 25; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFF 5
 |||||
DB 197 KAVFFF 201

RESULT 67
AD2306
hypothetical protein all4003 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2306
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakasaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic
A:Reference number: AB1807; PMID:21595285; PMID:11759840
A:Accession: AD2306
A>Status: preliminary
A:Molecule type: DNA

Db 102 KTVFFA 107

Fri Dec 30 10:25:19 2005

A;Experimental source: cultivar Columbia; BAC clone T29A15	
C;Genetics:	
A;Map position: 4	
A;Introns: 51/1; 99/2; 155/3; 246/1; 334/3; 378/3	
A;Note: T29A15.210	
C;Superfamily: Arabidopsis thaliana hypothetical protein F2K15.170	
Query Match 86.2%; Score 25; DB 2; Length 420;	
Best Local Similarity 100.0%; Pred. No. 2.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 KAVFF 5	
Db 169 KAVFF 173	
RESULT 73	
H81402	
probable integral membrane protein Cj0560 [imported] - Campylobacter jejuni (strain NCTC	
C;Species: Campylobacter jejuni	
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004	
C;Accession: H81402	
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling	
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell	
Nature 403, 665-668, 2000	
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp	
A;Reference number: A81250; MUID:20150912; PMID:10688204	
A;Accession: H81402	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-442 <PAR>	
A;Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI00000C217E; GB:ALJ139075; GB:ALJ111168; NID	
A;Experimental source: serotype O2, strain NCTC 11168	
C;Genetics:	
A;Gene: Cj0560	
Query Match 86.2%; Score 25; DB 2; Length 442;	
Best Local Similarity 83.3%; Pred. No. 2.7e+02;	
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy 1 KAVFFA 6	
Db 313 KVVFFA 318	
RESULT 74	
G95233	
Cof family protein [imported] - Streptococcus pneumoniae (strain TIGR4)	
C;Species: Streptococcus pneumoniae	
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004	
C;Accession: G95233	
R;Fetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid	
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,	
nson, T.; Hickey, E.K.; Holt, I.E.	
Science 293, 498-506, 2001	
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,	
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.	
A;Reference number: A95000; MUID:21357209; PMID:11463916	
A;Accession: G95233	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-462 <KUR>	
A;Cross-references: UNIPROT:Q9TNM3; UNIPARC:UPI00000C9CFF; GB:AE005672; PIDN:AAK76064.1;	
A;Experimental source: strain TIGR4	
C;Genetics:	
A;Gene: SP1997	
Query Match 86.2%; Score 25; DB 2; Length 462;	
Best Local Similarity 100.0%; Pred. No. 2.9e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 KAVFF 5	
Db 169 KAVFF 173	

Db 4 KAVFF 8	
RESULT 75	
A86717	
conserved hypothetical protein yheD [imported] - Lactococcus lactis subsp. lactis (strain	
C;Species: Lactococcus lactis subsp. lactis	
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004	
C;Accession: A86717	
R;Bolotin, A.; Wincker, P.; Mauer, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich	
Genome Res. 11, 731-753, 2001	
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp	
A;Reference number: A86625; MUID:21235186; PMID:11337471	
A;Accession: A86717	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-462 <STO>	
A;Cross-references: UNIPROT:Q9CHJ4; UNIPARC:UPI00000C68CE; GB:AE005176; PID:gl2723652; PJ	
A;Experimental source: strain IL1403	
C;Genetics:	
A;Gene: yheD	
Query Match 86.2%; Score 25; DB 2; Length 462;	
Best Local Similarity 100.0%; Pred. No. 2.9e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 KAVFF 5	
Db 4 KAVFF 8	
Search completed: December 29, 2005, 17:49:19	
Job time : 13.9677 secs	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVFPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	660	7	US-11-186-284-125
2	29	100.0	708	6	US-10-821-234-917
3	25	86.2	210	6	US-10-467-657-6318
4	25	86.2	560	6	US-10-623-155-225
5	25	86.2	563	6	US-10-821-234-1067
6	24	82.8	19	6	US-10-923-605-5
7	24	82.8	19	6	US-10-934-818-5
8	24	82.8	40	7	US-11-016-706-36
9	24	82.8	40	7	US-11-098-674-12
10	24	82.8	42	6	US-10-923-605-1
11	24	82.8	42	6	US-10-934-818-1
12	24	82.8	42	7	US-11-016-706-37
13	24	82.8	43	6	US-10-934-818-6
14	24	82.8	43	6	US-10-250-581-1
15	24	82.8	43	6	US-10-250-581-1
16	24	82.8	288	6	US-10-467-657-1272
17	24	82.8	423	6	US-10-525-710-44
18	24	82.8	489	6	US-10-467-657-7846
19	24	82.8	770	6	US-10-982-545-15
20	24	82.8	770	6	US-10-789-273-38
21	23	79.3	9	6	US-10-982-891-44
22	23	79.3	114	6	US-10-467-657-5012
23	23	79.3	283	7	US-11-082-389-252
24	23	79.3	283	7	US-11-082-389-254
25	23	79.3	310	6	US-10-454-437-328
26	23	79.3	26	6	US-10-793-626-2080
27	23	79.3	557	6	US-10-467-657-5540
28	23	79.3	974	6	US-10-995-561-895
29	23	79.3	997	6	US-10-995-561-896
30	22	75.9	190	6	US-10-467-657-3436
31	22	75.9	211	6	US-10-821-234-1372
32	22	75.9	216	6	US-10-467-657-5376
33	22	75.9	269	7	US-11-179-977-11
34	22	75.9	335	7	US-11-092-353-2
35	22	75.9	341	7	US-10-131-826A-256
36	22	75.9	341	7	US-11-099-691-6
37	22	75.9	397	7	US-10-467-657-2684
38	22	75.9	478	7	US-11-092-353-4
39	22	75.9	550	6	US-10-467-657-234
40	22	75.9	550	6	US-10-467-657-924
41	22	75.9	645	6	US-10-510-386-32
42	22	75.9	989	6	US-10-821-234-975
43	22	75.9	1070	7	US/11/062
44	22	75.9	1095	7	US/11/062
45	22	75.9	1169	7	US-11-077-550-20
46	21	72.4	28	6	US-10-250-581-14
47	21	72.4	28	6	US-10-250-581-17
48	21	72.4	28	6	US-10-250-581-14
49	21	72.4	28	6	US-10-250-581-17
50	21	72.4	40	6	US-10-250-581-15
51	21	72.4	40	6	US-10-250-581-18
52	21	72.4	40	6	US-10-250-581-15
53	21	72.4	40	6	US-10-250-581-18
54	21	72.4	42	6	US-10-250-581-16
55	21	72.4	42	6	US-10-250-581-19
56	21	72.4	42	6	US-10-250-581-16
57	21	72.4	42	6	US-10-250-581-19
58	21	72.4	54	6	US-10-467-657-4978
59	21	72.4	71	7	US-11-123-896-344
60	21	72.4	73	7	US-11-123-896-335
61	21	72.4	105	6	US-10-467-657-9209
62	21	72.4	105	7	US-11-000-463-759
63	21	72.4	115	6	US-10-793-626-1554
64	21	72.4	127	6	US-10-467-657-3152
65	21	72.4	134	6	US-10-467-657-6860
66	21	72.4	153	6	US-10-467-657-4112
67	21	72.4	162	6	US-10-467-657-9046
68	21	72.4	167	6	US-10-467-657-5306
69	21	72.4	189	6	US-10-467-657-6854
70	21	72.4	189	6	US-10-467-657-7856
71	21	72.4	191	6	US-10-467-657-818
72	21	72.4	213	6	US-10-981-873-40
73	21	72.4	227	6	US-10-980-388-86
74	21	72.4	230	6	US-10-510-386-198
75	21	72.4	244	6	US-10-454-437-238
76	21	72.4	244	6	US-10-454-437-240
77	21	72.4	264	6	US-10-873-528-70
78	21	72.4	299	6	US-10-467-657-4424
79	21	72.4	355	6	US-10-467-657-7996
80	21	72.4	358	6	US-10-467-657-7030
81	21	72.4	366	6	US-10-467-657-7024
82	21	72.4	372	6	US-10-467-657-7964
83	21	72.4	406	6	US-10-467-657-590
84	21	72.4	418	6	US-10-467-657-7420
85	21	72.4	422	6	US-10-467-657-5788
86	21	72.4	422	6	US-10-525-710-40
87	21	72.4	429	6	US-10-858-730-79
88	21	72.4	439	6	US-10-793-626-2408
89	21	72.4	481	6	US-10-995-561-959
90	21	72.4	483	6	US-10-793-626-3132
91	21	72.4	495	6	US-10-613-744-5
92	21	72.4	500	7	US-10-957-569-18
93	21	72.4	550	7	US-11-055-822-866
94	21	72.4	613	6	US-10-467-657-5796
95	21	72.4	616	6	US-10-613-744-4
96	21	72.4	716	6	US-10-131-826A-512
97	21	72.4	716	7	US-11-147-047-52
98	21	72.4	801	6	US-10-467-657-6470

99	21	72.4	897	6	US-10-821-234-1523	Sequence 1523, Ap	172	20	69.0	338	6	US-10-467-657-6798	Sequence 6798, Ap
100	21	72.4	898	7	US-11-099-691-7	Sequence 7, Appli	173	20	69.0	347	6	US-10-467-657-2014	Sequence 2014, Ap
101	21	72.4	1141	6	US-10-995-561-1009	Sequence 1009, Ap	174	20	69.0	355	7	US-10-454-437-102	Sequence 102, Ap
102	21	72.4	1141	6	US-10-995-561-1010	Sequence 1010, Ap	175	20	69.0	355	7	US-11-088-686-4	Sequence 4, Appli
103	20	69.0	5	7	US-11-098-674-1	Sequence 1, Appli	176	20	69.0	356	7	US-11-075-185-16	Sequence 16, Appl
104	20	69.0	9	7	US-11-032-498-28	Sequence 28, Appl	177	20	69.0	357	6	US-10-467-657-2500	Sequence 2500, Ap
105	20	69.0	28	6	US-10-250-581-2	Sequence 2, Appli	178	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
106	20	69.0	38	6	US-10-250-581-2	Sequence 2, Appli	179	20	69.0	363	6	US-10-995-561-602	Sequence 602, Ap
107	20	69.0	38	6	US-10-467-657-2058	Sequence 2058, Ap	180	20	69.0	363	6	US-10-624-932-24	Sequence 24, Appl
108	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	181	20	69.0	376	6	US-10-995-561-844	Sequence 844, App
109	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	182	20	69.0	376	6	US-10-995-561-848	Sequence 848, App
110	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	183	20	69.0	380	6	US-10-624-932-20	Sequence 20, Appl
111	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	184	20	69.0	380	6	US-10-624-932-22	Sequence 22, Appl
112	20	69.0	47	6	US-10-467-657-5436	Sequence 5436, Ap	185	20	69.0	380	6	US-10-995-561-846	Sequence 846, App
113	20	69.0	48	6	US-10-467-657-4322	Sequence 4322, Ap	186	20	69.0	380	7	US-11-108-528-28	Sequence 28, Appl
114	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	187	20	69.0	387	6	US-10-467-657-5522	Sequence 5522, Ap
115	20	69.0	75	6	US-10-467-657-1496	Sequence 1496, Ap	188	20	69.0	390	6	US-10-995-561-847	Sequence 847, App
116	20	69.0	92	6	US-10-467-657-2378	Sequence 2378, Ap	189	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
117	20	69.0	95	6	US-10-467-657-8785	Sequence 8785, Ap	190	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
118	20	69.0	100	7	US-11-123-896-137	Sequence 137, App	191	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
119	20	69.0	104	6	US-10-821-234-1227	Sequence 1227, App	192	20	69.0	400	6	US-10-793-626-1056	Sequence 1056, Ap
120	20	69.0	107	6	US-10-793-626-1586	Sequence 1586, Ap	193	20	69.0	401	7	US-11-055-822-336	Sequence 336, App
121	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	194	20	69.0	402	6	US-10-467-657-9070	Sequence 9070, Ap
122	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	195	20	69.0	402	7	US-11-000-463-449	Sequence 449, App
123	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	196	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
124	20	69.0	131	6	US-10-467-657-9073	Sequence 9073, Ap	197	20	69.0	426	6	US-10-467-657-2120	Sequence 2120, Ap
125	20	69.0	133	6	US-10-467-657-9195	Sequence 9195, Ap	198	20	69.0	428	7	US-11-000-463-448	Sequence 448, App
126	20	69.0	137	6	US-10-793-626-530	Sequence 530, App	199	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
127	20	69.0	137	6	US-10-467-657-6584	Sequence 6584, Ap	200	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
128	20	69.0	155	6	US-10-467-657-2420	Sequence 2420, Ap	201	20	69.0	450	6	US-10-467-657-7094	Sequence 7094, Ap
129	20	69.0	156	6	US-10-793-626-2452	Sequence 2452, Ap	202	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
130	20	69.0	168	7	US-11-000-463-824	Sequence 824, App	203	20	69.0	451	6	US-10-467-657-7104	Sequence 7104, Ap
131	20	69.0	175	6	US-10-467-657-7504	Sequence 7504, Ap	204	20	69.0	453	7	US-11-082-389-198	Sequence 198, App
132	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	205	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
133	20	69.0	196	6	US-10-793-626-630	Sequence 630, App	206	20	69.0	472	6	US-10-467-657-2268	Sequence 2268, Ap
134	20	69.0	196	6	US-10-967-527A-26	Sequence 26, Appl	207	20	69.0	485	6	US-10-821-234-934	Sequence 934, App
135	20	69.0	201	6	US-10-467-657-458	Sequence 458, App	208	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appli
136	20	69.0	202	7	US-11-082-389-364	Sequence 364, App	209	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
137	20	69.0	207	6	US-10-467-657-1816	Sequence 1816, Ap	210	20	69.0	494	6	US-10-467-657-4376	Sequence 4376, Ap
138	20	69.0	211	6	US-10-467-657-6932	Sequence 6932, Ap	211	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
139	20	69.0	215	6	US-10-131-826A-4	Sequence 4, Appli	212	20	69.0	507	6	US-10-467-657-1612	Sequence 1612, Ap
140	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	213	20	69.0	513	6	US-10-467-657-5464	Sequence 5464, Ap
141	20	69.0	227	6	US-10-467-657-1514	Sequence 1514, Ap	214	20	69.0	514	7	US-11-186-284-228	Sequence 228, App
142	20	69.0	228	6	US-10-793-626-1862	Sequence 1862, Ap	215	20	69.0	523	6	US-10-131-826A-246	Sequence 246, App
143	20	69.0	228	6	US-10-467-657-568	Sequence 568, App	216	20	69.0	524	6	US-10-689-742-13	Sequence 13, Appl
144	20	69.0	228	6	US-10-467-657-4838	Sequence 4838, Ap	217	20	69.0	525	7	US-11-082-389-350	Sequence 350, App
145	20	69.0	229	6	US-10-131-826A-410	Sequence 410, App	218	20	69.0	528	6	US-10-793-626-1930	Sequence 1930, Ap
146	20	69.0	233	6	US-10-821-234-1322	Sequence 1322, Ap	219	20	69.0	540	6	US-10-858-730-293	Sequence 293, App
147	20	69.0	239	6	US-10-980-388-78	Sequence 78, Appl	220	20	69.0	554	7	US-11-000-463-240	Sequence 240, App
148	20	69.0	240	6	US-10-467-657-6276	Sequence 6276, Ap	221	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
149	20	69.0	242	6	US-10-821-234-1073	Sequence 1073, Ap	222	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
150	20	69.0	254	7	US-11-103-957-27	Sequence 27, Appl	223	20	69.0	560	7	US-11-080-991-62	Sequence 62, Appl
151	20	69.0	255	7	US-11-185-111-36	Sequence 36, Appl	224	20	69.0	572	6	US-10-467-657-1022	Sequence 1022, Ap
152	20	69.0	257	7	US-11-102-240-94	Sequence 94, Appl	225	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
153	20	69.0	269	6	US-10-467-657-330	Sequence 330, App	226	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appl
154	20	69.0	272	6	US-10-467-657-2520	Sequence 2520, Ap	227	20	69.0	592	6	US-10-467-962B-95	Sequence 95, Appl
155	20	69.0	288	6	US-10-873-528-18	Sequence 18, Appl	228	20	69.0	592	6	US-10-524-647-112	Sequence 112, App
156	20	69.0	291	6	US-10-432-483-12	Sequence 12, Appl	229	20	69.0	599	6	US-10-467-657-3972	Sequence 3972, Ap
157	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	230	20	69.0	614	7	US-11-126-841A-2	Sequence 2, Appli
158	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	231	20	69.0	614	7	US-11-126-841A-13	Sequence 13, Appl
159	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	232	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
160	20	69.0	311	6	US-10-793-626-2450	Sequence 2450, Ap	233	20	69.0	677	6	US-10-131-826A-230	Sequence 230, App
161	20	69.0	311	6	US-10-467-657-2334	Sequence 2334, Ap	234	20	69.0	693	6	US-10-467-657-6176	Sequence 6176, Ap
162	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appl	235	20	69.0	721	6	US-10-467-962B-49	Sequence 49, Appl
163	20	69.0	318	6	US-10-131-826A-374	Sequence 374, App	236	20	69.0	724	7	US-11-184-380-4	Sequence 4, Appli
164	20	69.0	324	6	US-10-467-657-2504	Sequence 2504, Ap	237	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
165	20	69.0	321	6	US-10-467-657-7692	Sequence 7692, Ap	238	20	69.0	835	7	US-11-186-283-2	Sequence 2, Appli
166	20	69.0	325	6	US-10-467-657-8440	Sequence 8440, App	239	20	69.0	835	7	US-11-186-283-8	Sequence 8, Appli
167	20	69.0	324	6	US-10-467-657-142	Sequence 142, App	240	20	69.0	852	6	US-10-467-657-5004	Sequence 5004, Ap
168	20	69.0	330	6	US-10-510-386-82	Sequence 82, Appl	241	20	69.0	858	6	US-10-613-744-6	Sequence 6, Appli
169	20	69.0	333	7	US-11-082-389-202	Sequence 202, App	242	20	69.0	907	7	US-11-103-957-82	Sequence 82, Appl
170	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap	243	20	69.0	916	6	US-10-467-657-4242	Sequence 4242, Ap
171	20	69.0	338	6	US-10-467-657-136	Sequence 136, App	244	20	69.0	964	7	US-11-103-957-13	Sequence 13, Appl

20	69.0	1027	6	US-10-793-626-3106	Sequence 3106, Ap
20	69.0	1076	6	US-10-467-657-5708	Sequence 5708, Ap
20	69.0	1144	6	US-10-467-962B-89	Sequence 89, Appl
20	69.0	1259	6	US-10-467-657-5510	Sequence 5510, Ap
20	69.0	1274	6	US-10-454-437-360	Sequence 360, App
20	69.0	1362	7	US-11-043-693-33	Sequence 33, Appl
20	69.0	1363	7	US-11-043-693-32	Sequence 32, Appl
20	69.0	1368	7	US-11-043-693-34	Sequence 34, Appl
20	69.0	1531	7	US-11-103-957-85	Sequence 15, Appl
20	69.0	2004	6	US-10-467-657-84	Sequence 84, Appl
20	69.0	2004	6	US-10-467-657-6322	Sequence 6322, Ap
20	69.0	3433	6	US-10-714-781A-67	Sequence 67, Appl
20	69.0	3623	6	US-10-995-561-593	Sequence 593, App
20	69.0	4128	6	US-10-770-726-77	Sequence 77, Appl
19	65.5	28	6	US-10-250-581-5	Sequence 5, Appli
19	65.5	28	6	US-10-250-581-8	Sequence 8, Appli
19	65.5	28	6	US-10-250-581-11	Sequence 11, Appl
19	65.5	28	6	US-10-250-581-5	Sequence 5, Appli
19	65.5	28	6	US-10-250-581-8	Sequence 8, Appli
19	65.5	28	6	US-10-250-581-11	Sequence 11, Appl
19	65.5	39	6	US-10-467-657-2174	Sequence 2174, Ap
19	65.5	40	6	US-10-250-581-6	Sequence 6, Appli
19	65.5	40	6	US-10-250-581-9	Sequence 9, Appli
19	65.5	40	6	US-10-250-581-12	Sequence 12, Appl
19	65.5	40	6	US-10-250-581-6	Sequence 6, Appli
19	65.5	40	6	US-10-250-581-9	Sequence 9, Appli
19	65.5	40	6	US-10-250-581-12	Sequence 12, Appl
19	65.5	42	6	US-10-250-581-7	Sequence 7, Appli
19	65.5	42	6	US-10-250-581-10	Sequence 10, Appl
19	65.5	42	6	US-10-250-581-13	Sequence 13, Appl
19	65.5	50	6	US-10-467-657-7892	Sequence 7892, Ap
19	65.5	52	6	US-10-467-657-3656	Sequence 3656, Ap
19	65.5	83	6	US-10-467-657-5366	Sequence 5366, Ap
19	65.5	95	7	US-11-055-822-238	Sequence 238, App
19	65.5	95	7	US-11-055-822-632	Sequence 632, App
19	65.5	96	7	US-11-055-822-1102	Sequence 1102, Ap
19	65.5	96	7	US-10-467-657-3380	Sequence 3380, Ap
19	65.5	97	6	US-10-650-326B-2	Sequence 2, Appli
19	65.5	97	6	US-10-995-561-900	Sequence 900, App
19	65.5	98	6	US-10-467-657-3490	Sequence 3490, Ap
19	65.5	102	6	US-10-667-295-43	Sequence 43, Appl
19	65.5	102	6	US-10-793-628-2392	Sequence 2592, Ap
19	65.5	107	6	US-10-467-657-1018	Sequence 1018, Ap
19	65.5	113	7	US-11-073-605-10	Sequence 10, Appl
19	65.5	124	6	US-10-467-657-8548	Sequence 8548, Ap
19	65.5	128	6	US-10-793-626-1208	Sequence 1208, Ap
19	65.5	138	6	US-10-467-657-2052	Sequence 2052, Ap
19	65.5	141	6	US-10-667-295-42	Sequence 42, Appl
19	65.5	141	6	US-10-467-657-5544	Sequence 5544, Ap
19	65.5	150	6	US-11-109-156-32	Sequence 32, Appl
19	65.5	153	6	US-10-467-657-7674	Sequence 7674, Ap
19	65.5	153	6	US-10-467-657-8432	Sequence 8432, Ap
19	65.5	157	7	US-11-116-144-167	Sequence 167, App

ALIGNMENTS

```

RESULT 1
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.

```

```

; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match          100.0%; Score 29; DB 7; Length 660;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536
        |||||

RESULT 2
US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match          100.0%; Score 29; DB 6; Length 708;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      579 KAVFFA 584
        |||||

RESULT 3
US-10-467-657-6318
; Sequence 6318, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```



```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match      82.8%; Score 24; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      4 KLVFFA 9

RESULT 8
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US2005024334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 9
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
```

```
;
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 10
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 11
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1
```

```
Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 12
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match      82.8%; Score 24; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 13
US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match      82.8%; Score 24; DB 6; Length 43;

Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 14
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 15
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 16
US-10-467-657-1272
; Sequence 1272, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1272
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1272

Query Match 82.8%; Score 24; DB 6; Length 288;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 44 AVFFA 48

RESULT 17
US-10-525-710-44
; Sequence 44, Application US/10525710
; Publication No. US20050260721A1
; GENERAL INFORMATION:
; APPLICANT: Kroger, Burkhard
; APPLICANT: Zelder, Oskar
; APPLICANT: Kolprogge, Corinna
; APPLICANT: Schroder, Hartwig
; APPLICANT: Hafner, Stefan
; TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
; TITLE OF INVENTION: Sulphur (metyl)
; FILE REFERENCE: 13111-00006-US
; CURRENT APPLICATION NUMBER: US/10/525,710
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: DE 102 39 082.7
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-525-710-44

Query Match 82.8%; Score 24; DB 6; Length 423;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 146 KAIFF 150

RESULT 18
US-10-467-657-7846
; Sequence 7846, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7846
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7846

Query Match 82.8%; Score 24; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 28 AVFFA 32

RESULT 19
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-NI), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE

```
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; US-10-982-545-15

Query Match      82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KAVFFA 6
Db 687 KLVFFA 692
```

```
RESULT 20
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
```

```
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-789-273-38
```

```
Query Match      82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KAVFFA 6
Db 687 KLVFFA 692
```

```
RESULT 21
US-10-982-891-44
; Sequence 44, Application US/10982891
; Publication No. US20050244844A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, ALPHONSE
; APPLICANT: CAYLA, XAVIER
; APPLICANT: REBOLLO, ANGELITA
; TITLE OF INVENTION: METHODS OF SCREENING OF PPI-INTERACTING POLYPEPTIDES OR PROTEINS,
; TITLE OF INVENTION: PEPTIDES INHIBITING PPIC BINDING TO Bcl-2 PROTEINS, BCL-XL AND
; TITLE OF INVENTION: BCL-W, AND USES THEREOF
; FILE REFERENCE: 260990USOCONT
; CURRENT APPLICATION NUMBER: US/10/982,891
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: PCT/EP03/05453
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: EP 02291170
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: MAMMALIAN
; US-10-982-891-44
```

```
Query Match      79.3%; Score 23; DB 6; Length 9;
Best Local Similarity 83.3%; Pred No. 4.4e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KAVFFA 6
Db 3 KAVMFA 8
```

```
RESULT 22
US-10-467-657-5012
; Sequence 5012, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5012
; LENGTH: 114
; TYPE: PRT
```

```

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5012

Query Match          79.3%; Score 23; DB 6; Length 114;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 34 RAVFFS 39

RESULT 23
US-11-082-389-252
; Sequence 252, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US 11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 252
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-254

Query Match          79.3%; Score 23; DB 7; Length 283;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
DB 264 AIFFA 268

RESULT 25
US-10-454-437-328
; Sequence 328, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5012

Query Match          79.3%; Score 23; DB 7; Length 283;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
DB 264 AIFFA 268

RESULT 24
US-11-082-389-254
; Sequence 254, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig

```

```
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 328
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-328

Query Match          79.3%; Score 23; DB 6; Length 310;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
   |:|
Db 63 AIFFA 67

RESULT 26
US-10-793-626-2080
; Sequence 2080, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2080
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2080

Query Match          79.3%; Score 23; DB 6; Length 411;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
   |:|
Db 304 AIFFA 308

RESULT 27
US-10-467-657-5540
; Sequence 5540, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
```

```
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5540
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5540

Query Match          79.3%; Score 23; DB 6; Length 557;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   |:|
Db 166 KAVNFA 171

RESULT 28
US-10-995-561-895
; Sequence 895, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 895
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-895

Query Match          79.3%; Score 23; DB 6; Length 974;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   |:|
Db 497 KAVLFA 502

RESULT 29
US-10-995-561-896
; Sequence 896, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-896

Query Match          79.3%; Score 23; DB 6; Length 997;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   |:|
Db 520 KAVLFA 525
```


RESULT 30
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436

Query Match 75.9%; Score 22; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | |
DB 46 KTVFFA 51

RESULT 31
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372

Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | |
DB 33 KTVFFA 38

RESULT 32
US-10-467-657-5976
; Sequence 5976, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5976
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5976

Query Match 75.9%; Score 22; DB 6; Length 216;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
| | | |
DB 8 KSVFF 12

RESULT 33
US-11-179-977-11
; Sequence 11, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GCS11-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-11

Query Match 75.9%; Score 22; DB 7; Length 269;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | |
DB 193 KAAFFS 198

RESULT 34
US-11-092-353-2
; Sequence 2, Application US/11092353
; Publication No. US20050272653A1
; GENERAL INFORMATION:
; APPLICANT: Knopf, John
; APPLICANT: Seehra, Jaabir
; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PHPH-P01-002
; CURRENT APPLICATION NUMBER: US/11/092,353
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US 60/557,100
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-092-353-2

Query Match 75.9%; Score 22; DB 7; Length 335;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPF 5
|||:|
Db 79 KAVPF 83

RESULT 35
US-10-131-826A-256
; Sequence 256, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 256
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-256

Query Match 75.9%; Score 22; DB 6; Length 341;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPF 5
|||:|
Db 102 KALPF 106

RESULT 36
US-11-099-691-6
; Sequence 6, Application US/11099691
; Publication No. US20050260644A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YANG, Junning
; TITLE OF INVENTION: CELL SIGNALING PROTEINS
; FILE REFERENCE: PF-0521 PCT
; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 2472655
US-11-099-691-6

Query Match 75.9%; Score 22; DB 7; Length 341;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPF 5
|||:|
Db 102 KALPF 106

RESULT 37
US-10-467-657-2684
; Sequence 2684, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2684
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2684

Query Match 75.9%; Score 22; DB 6; Length 397;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 KAVFFA 6
Db      309 KADFFA 314

RESULT 38
US-11-092-353-4
; Sequence 4, Application US/11092353
; Publication No. US20050272653A1
; GENERAL INFORMATION:
; APPLICANT: Knopf, John
; APPLICANT: Seehra, Jabir
; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PHPH-P01-002
; CURRENT APPLICATION NUMBER: US/11/092,353
; PRIOR FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US 60/557,100
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-092-353-4

Query Match      75.9%; Score 22; DB 7; Length 478;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      112 KAVFF 116

RESULT 39
US-10-467-657-234
; Sequence 234, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 234
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-234

Query Match      75.9%; Score 22; DB 6; Length 550;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      176 RAVFF 180

RESULT 40
US-10-467-657-924
; Sequence 924, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 924
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-924

Query Match      75.9%; Score 22; DB 6; Length 550;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      176 RAVFF 180

RESULT 41
US-10-510-386-32
; Sequence 32, Application US/10510386
; Publication No. US2005024922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-32

Query Match      75.9%; Score 22; DB 6; Length 645;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      123 KGLFFA 128

RESULT 42
US-10-821-234-975
; Sequence 975, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
```

```
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 975
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975
```

```
Query Match          75.9%; Score 22; DB 6; Length 989;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFFA 6
   :|||||
Db 312 ESVFFA 317
```

RESULT 43

```
US/11/062
; Sequence 4, Application US/11062471A
; Publication No. US20050255093A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: SUTTON, John Mark
; APPLICANT: HALLIS, Bassam
; APPLICANT: SILMAN, Nigel
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
; FILE REFERENCE: 1581.0800001
; CURRENT APPLICATION NUMBER: US/11/062,471A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 09/831,050
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker.
US/11/062,471A-4
```

```
Query Match          75.9%; Score 22; DB 7; Length 1070;
Best Local Similarity 80.0%; Pred. No. 9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFF 5
   :|||||
Db 762 KSVFF 766
```

RESULT 44

```
US/11/062
; Sequence 7, Application US/11062471A
; Publication No. US20050255093A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: SUTTON, John Mark
; APPLICANT: HALLIS, Bassam
; APPLICANT: SILMAN, Nigel
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
; FILE REFERENCE: 1581.0800001
; CURRENT APPLICATION NUMBER: US/11/062,471A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 09/831,050
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05
```

```
; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M.
US/11/062,471A-7
```

```
Query Match          75.9%; Score 22; DB 7; Length 1095;
Best Local Similarity 80.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFF 5
   :|||||
Db 787 KSVFF 791
```

RESULT 45

```
US-11-077-550-20
; Sequence 20, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-11-077-550-20
```

```
Query Match          75.9%; Score 22; DB 7; Length 1169;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFF 5
   :|||||
Db 983 KSVFF 987
```

RESULT 46

```
US-10-250-581-14
; Sequence 14, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
```

; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
| | | |
Db 16 KXVFF 20

RESULT 47
US-10-250-581-17
; Sequence 17, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
| | | |
Db 16 KXVFF 20

RESULT 48
US-10-250-581-14
; Sequence 14, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
| | | |
Db 16 KXVFF 20

RESULT 49
US-10-250-581-17
; Sequence 17, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
| | | |
Db 16 KXVFF 20

RESULT 50
US-10-250-581-15
; Sequence 15, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 51
US-10-250-581-18
; Sequence 18, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 52
US-10-250-581-15
; Sequence 15, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 53
US-10-250-581-18
; Sequence 18, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 54
US-10-250-581-16
; Sequence 16, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 55
US-10-250-581-19
; Sequence 19, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 19
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 56
US-10-250-581-16
; Sequence 16, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 57
US-10-250-581-19
; Sequence 19, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 19
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 58
US-10-467-657-4978
; Sequence 4978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:

```

; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4978
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4978

Query Match          72.4%; Score 21; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVFFA 6
      :|||
Db      41 SVFFA 45

RESULT 59
US-11-123-896-344
; Sequence 344, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-344

Query Match          72.4%; Score 21; DB 7; Length 71;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      :|||
Db      3 RAIFF 7

RESULT 60
US-11-123-896-335
; Sequence 335, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James

; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-344

Query Match          72.4%; Score 21; DB 7; Length 71;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      :|||
Db      3 RAIFF 7

RESULT 61
US-10-467-657-9209
; Sequence 9209, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9209
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9209

Query Match          72.4%; Score 21; DB 6; Length 105;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      :|||
Db      3 QTVFFA 8

RESULT 62
US-11-000-463-759
; Sequence 759, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping

```


; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIPACN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 759
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-759

Query Match 72.4%; Score 21; DB 7; Length 105;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 68 AVFFA 72

RESULT 63
US-10-793-626-1554
; Sequence 1554; Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1554
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1554

Query Match 72.4%; Score 21; DB 6; Length 115;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 23 SVFFA 27

RESULT 64
US-10-467-657-3152
; Sequence 3152; Application US/10467657
; Publication No. US20050260581A1

; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3152
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3152

Query Match 72.4%; Score 21; DB 6; Length 127;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 52 ALFFA 56

RESULT 65
US-10-467-657-6860
; Sequence 6860; Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6860
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6860

Query Match 72.4%; Score 21; DB 6; Length 134;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 78 ALFFA 82

RESULT 66
US-10-467-657-4112
; Sequence 4112; Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4112
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4112

Query Match          72.4%; Score 21; DB 6; Length 153;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVFFA 6
Db      111 AVYFA 115

RESULT 67
US-10-467-657-9046
; Sequence 9046, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9046
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9046

Query Match          72.4%; Score 21; DB 6; Length 162;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      87 RAYFFA 92

RESULT 68
US-10-467-657-5306
; Sequence 5306, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
```

```
; SEQ ID NO 5306
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5306

Query Match          72.4%; Score 21; DB 6; Length 167;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      159 KAVAF 164

RESULT 69
US-10-467-657-6854
; Sequence 6854, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6854
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6854

Query Match          72.4%; Score 21; DB 6; Length 189;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVFFA 6
Db      87 ALFFA 91

RESULT 70
US-10-467-657-7856
; Sequence 7856, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7856
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7856

Query Match          72.4%; Score 21; DB 6; Length 189;
```

Best Local Similarity 80.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

QY 2 AVFFA 6
|:|
Db 87 ALFFA 91

RESULT 71

US-10-467-657-818
; Sequence 818, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 818
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-818

Query Match 72.4%; Score 21; DB 6; Length 191;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|:|
Db 122 QAVFF 126

RESULT 72

US-10-981-873-40
; Sequence 40, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: US\$ THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-981-873-40

Query Match 72.4%; Score 21; DB 6; Length 213;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|:|
Db 203 KAAPP 207

RESULT 73

US-10-980-388-86
; Sequence 86, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-86

Query Match 72.4%; Score 21; DB 6; Length 227;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|:|
Db 81 KSIPP 85

RESULT 74

US-10-510-386-198
; Sequence 198, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3

```
; SEQ ID NO 198
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-198

Query Match      72.4%; Score 21; DB 6; Length 230;
Best Local Similarity 80.0%; Pred. NO. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      ||||
Db      94 KAAPF 98

RESULT 75
US-10-454-437-238
; Sequence 238, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habershauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 238
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-238

Query Match      72.4%; Score 21; DB 6; Length 244;
Best Local Similarity 83.3%; Pred. NO. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      |||||
Db      20 KAVFSA 25

Search completed: December 29, 2005, 18:50:20
Job time : 4.29032 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVFFPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:**

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:**

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:**

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:**

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:**

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	3	US-09-867-847-16
2	29	100.0	6	3	US-09-867-847-24
3	29	100.0	6	3	US-09-915-092-6
4	29	100.0	6	3	US-09-915-092-14
5	29	100.0	6	3	US-09-747-408-7
6	29	100.0	6	3	US-09-747-408-15
7	29	100.0	6	5	US-10-728-028-6
8	29	100.0	6	5	US-10-728-028-14
9	29	100.0	6	5	US-10-825-958-14
10	29	100.0	6	5	US-10-825-958-22
11	29	100.0	37	4	US-10-641-924-6
12	29	100.0	37	4	US-10-642-255-6
13	29	100.0	74	4	US-10-115-223-19
14	29	100.0	74	4	US-10-115-223-25
15	29	100.0	74	4	US-10-402-212-19
16	29	100.0	74	4	US-10-402-212-25
17	29	100.0	108	4	US-10-115-223-20
18	29	100.0	108	4	US-10-115-223-26
19	29	100.0	108	4	US-10-402-212-20
20	29	100.0	108	4	US-10-402-212-26
21	29	100.0	193	4	US-10-115-223-18
22	29	100.0	193	4	US-10-115-223-24
23	29	100.0	193	4	US-10-402-212-18
24	29	100.0	193	4	US-10-402-212-24
25	29	100.0	222	4	US-10-115-223-17
26	29	100.0	222	4	US-10-402-212-17
27	29	100.0	228	4	US-10-115-223-23

28	29	100.0	228	4	US-10-402-212-23	Sequence 23, Appl
29	29	100.0	261	5	US-10-795-159-697	Sequence 697, App
30	29	100.0	429	4	US-10-115-223-45	Sequence 45, Appl
31	29	100.0	429	4	US-10-402-212-45	Sequence 45, Appl
32	29	100.0	468	5	US-10-450-763-54360	Sequence 54360, A
33	29	100.0	660	3	US-09-391-104-19	Sequence 19, Appl
34	29	100.0	660	3	US-09-801-196-35	Sequence 35, Appl
35	29	100.0	660	3	US-09-918-715-208	Sequence 208, App
36	29	100.0	660	4	US-10-219-329-14	Sequence 14, Appl
37	29	100.0	660	4	US-10-301-822-125	Sequence 125, App
38	29	100.0	660	4	US-10-153-185-14	Sequence 14, Appl
39	29	100.0	660	4	US-10-219-561-14	Sequence 14, Appl
40	29	100.0	660	4	US-10-131-985-25	Sequence 25, Appl
41	29	100.0	660	4	US-10-447-315-3	Sequence 3, Appl
42	29	100.0	660	4	US-10-032-378A-14	Sequence 14, Appl
43	29	100.0	660	4	US-10-335-207-14	Sequence 14, Appl
44	29	100.0	660	4	US-10-480-621-1	Sequence 1, Appl
45	29	100.0	660	4	US-10-474-794-208	Sequence 208, App
46	29	100.0	660	5	US-10-601-059-14	Sequence 14, Appl
47	29	100.0	660	5	US-10-872-198-131	Sequence 131, App
48	29	100.0	660	5	US-10-901-417-25	Sequence 25, Appl
49	29	100.0	660	5	US-10-979-159-208	Sequence 208, App
50	29	100.0	660	5	US-10-287-436A-489	Sequence 489, App
51	29	100.0	660	5	US-10-287-436A-1185	Sequence 1185, Ap
52	29	100.0	660	6	US-11-021-951-131	Sequence 131, App
53	29	100.0	660	6	US-11-031-488-14	Sequence 14, Appl
54	29	100.0	663	4	US-10-115-223-30	Sequence 30, Appl
55	29	100.0	663	4	US-10-402-212-30	Sequence 30, Appl
56	29	100.0	718	4	US-10-369-493-4873	Sequence 4873, Ap
57	29	100.0	718	4	US-10-369-493-7633	Sequence 7633, Ap
58	29	100.0	770	4	US-10-437-963-138526	Sequence 138526, A
59	29	100.0	1330	5	US-10-450-763-54358	Sequence 54358, A
60	28	96.6	383	4	US-10-369-493-4941	Sequence 4941, Ap
61	28	96.6	383	4	US-10-369-493-7639	Sequence 7639, Ap
62	26	89.7	49	4	US-10-424-599-150066	Sequence 150066, A
63	26	89.7	61	4	US-10-424-599-150066	Sequence 150066, A
64	26	89.7	65	5	US-10-926-683-1595	Sequence 1595, Ap
65	26	89.7	89	4	US-10-425-115-35391	Sequence 35391, A
66	26	89.7	103	4	US-10-424-599-210814	Sequence 210814, A
67	26	89.7	108	4	US-10-437-963-114838	Sequence 114838, A
68	26	89.7	124	4	US-10-424-599-182643	Sequence 182643, A
69	26	89.7	131	4	US-10-767-701-41102	Sequence 41102, A
70	26	89.7	138	5	US-10-450-763-39449	Sequence 39449, A
71	26	89.7	172	4	US-10-437-963-172959	Sequence 172959, A
72	26	89.7	206	4	US-10-767-701-31699	Sequence 31699, A
73	26	89.7	208	5	US-10-450-763-39451	Sequence 39451, A
74	26	89.7	210	4	US-10-282-122A-61639	Sequence 61639, A
75	26	89.7	258	4	US-10-425-115-286732	Sequence 286732, A
76	26	89.7	270	4	US-10-437-963-176878	Sequence 176878, A
77	26	89.7	308	4	US-10-425-115-332957	Sequence 332957, A
78	26	89.7	314	4	US-10-425-115-286735	Sequence 286735, A
79	26	89.7	320	4	US-10-425-114-43310	Sequence 43310, A
80	26	89.7	320	4	US-10-425-114-64659	Sequence 64659, A
81	26	89.7	323	4	US-10-437-963-117099	Sequence 117099, A
82	26	89.7	334	3	US-09-933-767-348	Sequence 348, App
83	26	89.7	334	4	US-10-004-860-348	Sequence 348, App
84	26	89.7	334	4	US-10-023-282-348	Sequence 348, App
85	26	89.7	421	3	US-09-741-669-400	Sequence 400, App
86	26	89.7	421	4	US-10-282-122A-42751	Sequence 42751, A
87	26	89.7	441	5	US-10-821-273-34	Sequence 34, Appl
88	26	89.7	556	5	US-10-820-474A-119	Sequence 119, App
89	26	89.7	715	4	US-10-282-122A-75547	Sequence 75547, A
90	26	89.7	859	4	US-10-437-963-201533	Sequence 201533, A
91	26	89.7	1042	4	US-10-282-122A-61918	Sequence 61918, A
92	26	89.7	1166	4	US-10-437-963-128203	Sequence 128203, A
93	26	89.7	1172	5	US-10-450-763-36972	Sequence 36972, A
94	26	89.7	1749	4	US-10-437-963-142580	Sequence 142580, A
95	25	86.2	5	3	US-09-850-061A-40	Sequence 40, Appl
96	25	86.2	5	4	US-10-721-774-40	Sequence 40, Appl
97	25	86.2	6	3	US-09-867-847-18	Sequence 18, Appl
98	25	86.2	6	3	US-09-867-847-26	Sequence 26, Appl
99	25	86.2	6	3	US-09-915-092-8	Sequence 8, Appl
100	25	86.2	6	3	US-09-915-092-16	Sequence 16, Appl

101	25	86.2	6	3	US-09-747-408-9	Sequence 9, Appli	174	25	86.2	256	5	US-10-732-923-20752	Sequence 20752, A
102	25	86.2	6	3	US-09-747-408-17	Sequence 17, Appli	175	25	86.2	268	4	US-10-369-493-20071	Sequence 20071, A
103	25	86.2	6	5	US-10-728-028-8	Sequence 8, Appli	176	25	86.2	268	4	US-10-425-115-308997	Sequence 308997, A
104	25	86.2	6	5	US-10-728-028-16	Sequence 16, Appli	177	25	86.2	282	3	US-09-845-713A-2	Sequence 2, Appli
105	25	86.2	6	5	US-10-825-958-16	Sequence 16, Appli	178	25	86.2	282	4	US-10-435-696-35	Sequence 35, Appli
106	25	86.2	6	5	US-10-825-958-24	Sequence 24, Appli	179	25	86.2	289	4	US-10-425-115-215163	Sequence 215163, A
107	25	86.2	22	4	US-10-425-115-347015	Sequence 347015, A	180	25	86.2	297	4	US-10-425-114-73046	Sequence 73046, A
108	25	86.2	25	3	US-09-764-877-1260	Sequence 1260, Ap	181	25	86.2	303	5	US-10-491-0067A-5	Sequence 5, Appli
109	25	86.2	25	4	US-10-742-515-1260	Sequence 1260, Ap	182	25	86.2	314	3	US-09-908-0067A-16	Sequence 16, Appli
110	25	86.2	34	5	US-10-499-352A-444	Sequence 444, App	183	25	86.2	317	4	US-10-425-115-225676	Sequence 225676, A
111	25	86.2	37	4	US-10-641-924-7	Sequence 7, Appli	184	25	86.2	322	3	US-09-816-028A-48	Sequence 48, Appli
112	25	86.2	37	4	US-10-642-255-7	Sequence 7, Appli	185	25	86.2	322	3	US-09-886-035-253	Sequence 253, App
113	25	86.2	39	4	US-10-424-599-220682	Sequence 220682, A	186	25	86.2	322	3	US-09-804-291-253	Sequence 253, App
114	25	86.2	55	4	US-10-424-599-171652	Sequence 171652, A	187	25	86.2	322	4	US-10-017-161-156	Sequence 156, App
115	25	86.2	60	4	US-10-437-963-173619	Sequence 173619, A	188	25	86.2	322	4	US-10-303-161-48	Sequence 48, Appli
116	25	86.2	62	4	US-10-424-599-197144	Sequence 197144, A	189	25	86.2	322	4	US-10-303-118-48	Sequence 48, Appli
117	25	86.2	62	4	US-10-424-599-212719	Sequence 212719, A	190	25	86.2	322	4	US-10-303-128-48	Sequence 48, Appli
118	25	86.2	63	4	US-10-424-599-217238	Sequence 217238, A	191	25	86.2	322	4	US-10-303-134-48	Sequence 48, Appli
119	25	86.2	65	4	US-10-029-386-28659	Sequence 28659, A	192	25	86.2	322	4	US-10-303-162-48	Sequence 48, Appli
120	25	86.2	66	4	US-10-425-115-367811	Sequence 367811, A	193	25	86.2	322	4	US-10-387-629-76	Sequence 76, Appli
121	25	86.2	69	4	US-10-424-599-201270	Sequence 201270, A	194	25	86.2	322	4	US-10-292-798-134	Sequence 134, App
122	25	86.2	70	4	US-10-425-115-292851	Sequence 292851, A	195	25	86.2	322	4	US-10-343-650A-582	Sequence 582, App
123	25	86.2	71	4	US-10-424-599-170927	Sequence 170927, A	196	25	86.2	322	4	US-10-473-518-2	Sequence 2, Appli
124	25	86.2	75	4	US-10-425-115-239056	Sequence 239056, A	197	25	86.2	322	4	US-10-820-536-48	Sequence 48, Appli
125	25	86.2	80	4	US-10-243-552-570	Sequence 570, App	198	25	86.2	322	4	US-10-845-408-48	Sequence 48, Appli
126	25	86.2	80	4	US-10-437-963-111335	Sequence 111335, A	199	25	86.2	322	4	US-10-845-412-48	Sequence 48, Appli
127	25	86.2	81	4	US-10-425-115-299931	Sequence 299931, A	200	25	86.2	322	4	US-10-846-219-48	Sequence 48, Appli
128	25	86.2	84	4	US-10-424-599-245453	Sequence 245453, A	201	25	86.2	322	5	US-10-821-604-48	Sequence 48, Appli
129	25	86.2	87	4	US-10-437-963-133986	Sequence 133986, A	202	25	86.2	322	5	US-10-847-983-48	Sequence 48, Appli
130	25	86.2	89	4	US-10-425-115-302836	Sequence 302836, A	203	25	86.2	322	5	US-10-821-573-48	Sequence 48, Appli
131	25	86.2	90	4	US-10-424-599-147666	Sequence 147666, A	204	25	86.2	322	5	US-10-850-807-48	Sequence 48, Appli
132	25	86.2	90	4	US-10-425-115-236215	Sequence 236215, A	205	25	86.2	322	5	US-10-850-125-48	Sequence 48, Appli
133	25	86.2	95	4	US-10-437-963-197590	Sequence 197590, A	206	25	86.2	322	5	US-10-830-825-48	Sequence 48, Appli
134	25	86.2	98	4	US-10-425-115-364147	Sequence 364147, A	207	25	86.2	322	5	US-10-962-334-48	Sequence 48, Appli
135	25	86.2	99	4	US-10-437-963-150181	Sequence 150181, A	208	25	86.2	322	5	US-10-830-997-48	Sequence 48, Appli
136	25	86.2	109	4	US-10-437-963-105773	Sequence 105773, A	209	25	86.2	322	5	US-10-962-235-48	Sequence 48, Appli
137	25	86.2	109	4	US-10-425-115-226514	Sequence 226514, A	210	25	86.2	322	5	US-10-961-882-48	Sequence 48, Appli
138	25	86.2	117	3	US-09-864-761-37128	Sequence 37128, A	211	25	86.2	322	5	US-10-819-316-253	Sequence 253, App
139	25	86.2	127	4	US-10-425-115-362628	Sequence 362628, A	212	25	86.2	322	5	US-10-819-316-531	Sequence 531, App
140	25	86.2	127	4	US-10-767-701-47243	Sequence 47243, A	213	25	86.2	327	4	US-10-437-963-109308	Sequence 109308, A
141	25	86.2	128	4	US-10-425-115-192450	Sequence 192450, A	214	25	86.2	332	4	US-10-274-694-2	Sequence 2, Appli
142	25	86.2	129	4	US-10-424-599-278483	Sequence 278483, A	215	25	86.2	332	4	US-10-369-493-11167	Sequence 11167, A
143	25	86.2	130	4	US-10-424-599-170319	Sequence 170319, A	216	25	86.2	332	4	US-10-369-493-22884	Sequence 22884, A
144	25	86.2	132	4	US-10-029-386-28941	Sequence 28941, A	217	25	86.2	332	5	US-10-332-448-2	Sequence 2, Appli
145	25	86.2	133	4	US-10-424-599-270652	Sequence 270652, A	218	25	86.2	332	5	US-09-939-484-6	Sequence 6, Appli
146	25	86.2	133	4	US-10-425-115-305393	Sequence 305393, A	219	25	86.2	347	3	US-09-939-483-6	Sequence 6, Appli
147	25	86.2	135	4	US-10-437-963-141578	Sequence 141578, A	220	25	86.2	354	6	US-11-037-143-6189	Sequence 6189, Ap
148	25	86.2	140	4	US-10-424-599-151465	Sequence 151465, A	221	25	86.2	366	4	US-10-424-599-278238	Sequence 278238, A
149	25	86.2	150	4	US-10-335-977-6540	Sequence 6540, Ap	222	25	86.2	373	4	US-10-437-963-167534	Sequence 167534, A
150	25	86.2	155	4	US-10-424-599-200083	Sequence 200083, A	223	25	86.2	380	4	US-10-369-493-7986	Sequence 7986, Ap
151	25	86.2	171	4	US-10-424-599-229782	Sequence 229782, A	224	25	86.2	382	4	US-10-369-493-11163	Sequence 11163, A
152	25	86.2	175	4	US-10-437-963-123124	Sequence 123124, A	225	25	86.2	411	4	US-10-282-122A-77801	Sequence 77801, A
153	25	86.2	180	4	US-10-424-599-232237	Sequence 232237, A	226	25	86.2	415	4	US-10-282-122A-68770	Sequence 68770, A
154	25	86.2	186	5	US-10-481-032A-214	Sequence 214, App	227	25	86.2	416	4	US-10-055-475-14	Sequence 14, Appli
155	25	86.2	186	5	US-10-481-032A-228	Sequence 228, App	228	25	86.2	416	6	US-11-042-922-14	Sequence 14, Appli
156	25	86.2	188	4	US-10-437-963-172476	Sequence 172476, A	229	25	86.2	430	4	US-10-058-636-2	Sequence 2, Appli
157	25	86.2	190	4	US-10-437-963-137998	Sequence 137998, A	230	25	86.2	430	4	US-10-799-016-2	Sequence 2, Appli
158	25	86.2	198	4	US-10-437-963-172452	Sequence 172452, A	231	25	86.2	454	3	US-09-939-811-12	Sequence 12, Appli
159	25	86.2	201	4	US-10-425-114-67850	Sequence 67850, A	232	25	86.2	472	5	US-10-472-928-4158	Sequence 4158, Ap
160	25	86.2	202	5	US-10-732-923-19034	Sequence 19034, A	233	25	86.2	473	5	US-10-617-320-3273	Sequence 3273, Ap
161	25	86.2	209	4	US-10-424-599-280085	Sequence 280085, A	234	25	86.2	481	6	US-11-037-143-3162	Sequence 3162, Ap
162	25	86.2	210	4	US-10-282-122A-65447	Sequence 65447, A	235	25	86.2	507	4	US-10-223-070-9	Sequence 9, Appli
163	25	86.2	210	4	US-10-283-122A-66099	Sequence 66099, A	236	25	86.2	514	4	US-10-055-475-13	Sequence 13, Appli
164	25	86.2	224	4	US-10-424-599-246461	Sequence 246461, A	237	25	86.2	514	6	US-11-042-922-13	Sequence 13, Appli
165	25	86.2	224	4	US-10-424-599-257424	Sequence 257424, A	238	25	86.2	530	3	US-09-804-014A-28	Sequence 28, Appli
166	25	86.2	246	6	US-11-097-143-2748	Sequence 2748, Ap	239	25	86.2	532	3	US-09-939-811-6	Sequence 6, Appli
167	25	86.2	247	4	US-10-335-977-6541	Sequence 6541, Ap	240	25	86.2	532	3	US-09-875-321-13	Sequence 13, Appli
168	25	86.2	247	4	US-10-335-977-6542	Sequence 6542, Ap	241	25	86.2	532	3	US-09-804-014A-31	Sequence 31, Appli
169	25	86.2	247	5	US-10-732-923-19035	Sequence 19035, A	242	25	86.2	532	4	US-10-162-012-13	Sequence 13, Appli
170	25	86.2	249	4	US-10-369-493-10584	Sequence 10584, A	243	25	86.2	532	4	US-10-254-010-2	Sequence 2, Appli
171	25	86.2	254	4	US-10-369-493-18714	Sequence 18714, A	244	25	86.2	532	4	US-10-162-102-13	Sequence 13, Appli
172	25	86.2	255	5	US-10-732-923-20940	Sequence 20940, A	245	25	86.2	532	5	US-10-916-061-13	Sequence 13, Appli
173	25	86.2	255	6	US-11-097-143-29655	Sequence 29655, A	246	25	86.2	539	4	US-10-282-122A-48163	Sequence 48163, A

```

247 25 86.2 4 US-10-282-122A-49134 Sequence 49134, A
248 25 86.2 4 US-10-282-122A-50632 Sequence 50632, A
249 25 86.2 3 US-09-735-705-225 Sequence 225, App
250 25 86.2 3 US-09-850-716A-225 Sequence 225, App
251 25 86.2 3 US-09-897-778-225 Sequence 225, App
252 25 86.2 3 US-09-943-075A-6 Sequence 6, Appli
253 25 86.2 3 US-09-738-626-5465 Sequence 5465, Ap
254 25 86.2 3 US-10-039-272-2 Sequence 2, Appli
255 25 86.2 4 US-10-007-700-225 Sequence 225, App
256 25 86.2 4 US-10-117-982-225 Sequence 225, App
257 25 86.2 4 US-10-463-106-2 Sequence 2, Appli
258 25 86.2 4 US-10-295-027-1258 Sequence 1258, Ap
259 25 86.2 4 US-10-313-986-225 Sequence 225, App
260 25 86.2 4 US-10-309-290-152 Sequence 152, App
261 25 86.2 4 US-10-408-765A-466 Sequence 466, App
262 25 86.2 5 US-10-775-972-225 Sequence 225, App
263 25 86.2 5 US-10-723-860-1128 Sequence 1128, Ap
264 25 86.2 5 US-10-922-124-225 Sequence 225, App
265 25 86.2 5 US-10-978-758-6 Sequence 6, Appli
266 25 86.2 5 US-10-631-467-821 Sequence 821, App
267 25 86.2 5 US-10-450-763-39378 Sequence 39378, A
268 25 86.2 5 US-10-282-122A-50907 Sequence 50907, A
269 25 86.2 4 US-10-227-884-42 Sequence 42, Appl
270 25 86.2 4 US-10-230-163-42 Sequence 42, Appl
271 25 86.2 4 US-10-230-338-42 Sequence 42, Appl
272 25 86.2 4 US-10-218-631-42 Sequence 42, Appl
273 25 86.2 4 US-10-230-414-42 Sequence 42, Appl
274 25 86.2 4 US-10-232-224-42 Sequence 42, Appl
275 25 86.2 4 US-10-216-159A-42 Sequence 42, Appl
276 25 86.2 4 US-10-218-849-42 Sequence 42, Appl
277 25 86.2 4 US-10-227-873-42 Sequence 42, Appl
278 25 86.2 4 US-10-227-883-42 Sequence 42, Appl
279 25 86.2 4 US-10-219-076-42 Sequence 42, Appl
280 25 86.2 4 US-10-230-434-42 Sequence 42, Appl
281 25 86.2 4 US-10-219-003-42 Sequence 42, Appl
282 25 86.2 4 US-10-219-075-42 Sequence 42, Appl
283 25 86.2 4 US-10-219-464-42 Sequence 42, Appl
284 25 86.2 4 US-10-219-466-42 Sequence 42, Appl
285 25 86.2 4 US-10-219-479-42 Sequence 42, Appl
286 25 86.2 4 US-10-219-481-42 Sequence 42, Appl
287 25 86.2 4 US-10-230-260-42 Sequence 42, Appl
288 25 86.2 4 US-10-232-231-42 Sequence 42, Appl
289 25 86.2 4 US-10-232-233-42 Sequence 42, Appl
290 25 86.2 4 US-10-216-165-42 Sequence 42, Appl
291 25 86.2 4 US-10-218-956-42 Sequence 42, Appl
292 25 86.2 4 US-10-219-468-42 Sequence 42, Appl
293 25 86.2 4 US-10-219-478-42 Sequence 42, Appl
294 25 86.2 4 US-10-219-536-42 Sequence 42, Appl
295 25 86.2 4 US-10-233-205-42 Sequence 42, Appl
296 25 86.2 4 US-10-219-072-42 Sequence 42, Appl
297 25 86.2 4 US-10-219-470-42 Sequence 42, Appl
298 25 86.2 4 US-10-219-474-42 Sequence 42, Appl
299 25 86.2 4 US-10-219-524-42 Sequence 42, Appl
300 25 86.2 4 US-10-219-528-42 Sequence 42, Appl

```

ALIGNMENTS

```

RESULT 1
US-09-867-847-16
; Sequence 16, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

```

```

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-16

```

```

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KAVFFA 6
Db 1 KAVFFA 6

```

RESULT 2

```

US-09-867-847-24
; Sequence 24, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-24

```

```

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KAVFFA 6
Db 1 KAVFFA 6

```

RESULT 3

```

US-09-915-092-6
; Sequence 6, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalfour, Robert

```

RESULT 6
US-09-747-408-15
: Sequence 15. Application US/09747408

; PUBLICATION NO. US20
 ; GENERAL INFORMATION:
 ; APPLICANT: Green, A
 ; APPLICANT: Gervais

```

; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-15

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

```

0: Gaps 0:

APPLICANT: GERVAS,
; APPLICANT: KONG, X
; APPLICANT: CHALIFO
; APPLICANT: MIGNEAU

```

; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

```



```
;
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-6

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 8
US-10-728-028-14
; Sequence 14, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 9
US-10-825-958-14
; Sequence 14, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 10
US-10-825-958-22
; Sequence 22, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-22

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 11
US-10-641-924-6
; Sequence 6, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kausner, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 53035AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
```

```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-641-924-6

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 12
US-10-642-255-6
; Sequence 6, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kausser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubany1, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: cNOS
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-642-255-6

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 13
US-10-115-223-19
; Sequence 19, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 14
US-10-115-223-25
; Sequence 25, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-25

Query Match      100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 15
US-10-402-212-19
; Sequence 19, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
```

; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-19

Query Match 100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 16

US-10-402-212-25
; Sequence 25, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-25

Query Match 100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 17

US-10-115-223-20
; Sequence 20, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-20

Query Match 100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 18

US-10-115-223-26
; Sequence 26, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-26

Query Match 100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 19

US-10-402-212-20
; Sequence 20, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223

```
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-20

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 20
US-10-402-212-26
; Sequence 26, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-26

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 21
US-10-115-223-18
; Sequence 18, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-24

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 22
US-10-115-223-24
; Sequence 24, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-24

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 23
US-10-402-212-18
; Sequence 18, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
```

; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-18

Query Match 100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
Db 64 KAVFFA 69

RESULT 24
US-10-402-212-24
; Sequence 24, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-24

Query Match 100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
Db 64 KAVFFA 69

RESULT 25
US-10-115-223-17
; Sequence 17, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-17

Query Match 100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
Db 93 KAVFFA 98

RESULT 26
US-10-402-212-17
; Sequence 17, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-17

Query Match 100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 93 KAVFFA 98

RESULT 27
US-10-115-223-23
; Sequence 23, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-23

Query Match 100.0%; Score 29; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 99 KAVFFA 104

RESULT 28
US-10-402-212-23
; Sequence 23, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-23

Query Match 100.0%; Score 29; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 99 KAVFFA 104

RESULT 29
US-10-795-159-697
; Sequence 697, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 28335/38815A
; CURRENT APPLICATION NUMBER: US/10/795,159
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 697
; LENGTH: 261
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-795-159-697

Query Match 100.0%; Score 29; DB 5; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 205 KAVFFA 210

RESULT 30
US-10-115-223-45
; Sequence 45, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-45

Query Match 100.0%; Score 29; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 300 KAVFFA 305

OTHER INFORMATION: Fibronectin type II domain identified by Pfam, accession name
OTHER INFORMATION: fn2, E-value=4.4e-55, Pfam score of 147.1

FEATURES:

NAME/KEY: misc_feature
LOCATION: (1)...(468)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-54360

Query Match 100.0%; Score 29; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 KAVFFA 6

DB

361 KAVFFA 366

RESULT 33

US-09-391-104-19
Sequence 19, Application US/09391104
Publication No. US20020031817A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
FILE REFERENCE: 6073.US.P1
CURRENT APPLICATION NUMBER: US/09/391,104
PRIOR FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-09-391-104-19

Query Match

100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 KAVFFA 6

DB

531 KAVFFA 536

RESULT 34

US-09-801-196-35
Sequence 35, Application US/09801196
Patent No. US20020037827A1
GENERAL INFORMATION:
APPLICANT: Wang, Kai
APPLICANT: Smith, Ryan
APPLICANT: Fajardo, Mark
APPLICANT: Moss, Patrick
TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
FILE REFERENCE: 240083.509
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-196-35

RESULT 31

US-10-402-212-45
Sequence 45, Application US/10402212
Publication No. US20040063790A1
GENERAL INFORMATION:
APPLICANT: Brooks, Peter C.
APPLICANT: Cheresch, David A.
APPLICANT: Silletti, Steven A.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
FILE REFERENCE: TSRI-419.3
CURRENT APPLICATION NUMBER: US/10/402,212
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: 10/115,223
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/194,468
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: PCT/US97/09158
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/018,773
PRIOR FILING DATE: 1996-05-31
PRIOR APPLICATION NUMBER: 60/015,869
PRIOR FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 429
TYPE: PRT
ORGANISM: Homo sapiens
US-10-402-212-45

Query Match 100.0%; Score 29; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 KAVFFA 6

DB

300 KAVFFA 305

RESULT 32

US-10-450-763-54360
Sequence 54360, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 54360
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (221)...(258)
OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00023, p-value=4.682e-3
OTHER INFORMATION: raw score of 24.31
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (167)...(264)

Query Match 100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 35
US-09-918-715-208
; Sequence 208, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Bert Vogelstein
; APPLICANT: Brad St. Croix
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-208

Query Match 100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 36
US-10-219-329-14
; Sequence 14, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035W01
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 37
US-10-301-822-125
; Sequence 125, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burtart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-125

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 38
US-10-153-185-14
; Sequence 14, Application US/10153185
; Publication No. US20030148959A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6


```
Db          531 KAVFFA 536
|||||
RESULT 39
US-10-219-561-14
; Sequence 14, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-14
Query Match          100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KAVFFA 6
|||||
Db          531 KAVFFA 536
|||||
RESULT 40
US-10-131-985-25
; Sequence 25, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-25
Query Match          100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KAVFFA 6
|||||
Db          531 KAVFFA 536
|||||
RESULT 41
US-10-447-315-3
; Sequence 3, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heisig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-3
Query Match          100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KAVFFA 6
|||||
Db          531 KAVFFA 536
|||||
RESULT 42
US-10-032-376A-14
; Sequence 14, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-14
Query Match          100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KAVFFA 6
|||||
Db          531 KAVFFA 536
|||||
RESULT 43
US-10-335-207-14
; Sequence 14, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
```

```
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 44
US-10-480-621-1
; Sequence 1, Application US/10480621
; Publication No. US20040175817A1
; GENERAL INFORMATION:
; APPLICANT: Jepson, Holly
; APPLICANT: Minshull, Claire
; APPLICANT: Paupitt, Richard
; APPLICANT: Rowsell, Sian
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN
; TITLE OF INVENTION: MMP9 MODULATORS
; FILE REFERENCE: 06275-377US1
; CURRENT APPLICATION NUMBER: US/10/480,621
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/SE02/01266
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: SE 0102298-7
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-621-1

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 45
US-10-474-794-208
; Sequence 208, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-208

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 46
US-10-601-059-14
; Sequence 14, Application US/10601059
; Publication No. US20040259802A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shu-Ping
; APPLICANT: Quirk, Stephen
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: Anti-Chondrosarcoma Compounds
; FILE REFERENCE: 1443.064US1
; CURRENT APPLICATION NUMBER: US/10/601,059
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 10/335,207
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/219,329
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US02/26319
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-059-14

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 47
US-10-872-198-131
; Sequence 131, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
```

```
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 0403058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-131

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 48
US-10-901-417-25
; Sequence 25, Application US/10901417
; Publication No. US20050026836A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/901,417
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-417-25

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 49
US-10-979-159-208
; Sequence 208, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler

; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-208

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 50
US-10-287-436A-489
; Sequence 489, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 489
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-489

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 51
US-10-287-436A-1185
; Sequence 1185, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
```

CURRENT APPLICATION NUMBER: US/11/031,488

; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PstSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-30

Query Match 100.0%; Score 29; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 534 KAVFFA 539

RESULT 56

US-10-369-493-4873
; Sequence 4873, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4873
; LENGTH: 718
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4873

Query Match 100.0%; Score 29; DB 4; Length 718;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 576 KAVFFA 581

RESULT 57

US-10-369-493-7633
; Sequence 7633, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7633
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7633

Query Match 100.0%; Score 29; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 576 KAVFFA 581

RESULT 58

US-10-437-963-138526
; Sequence 138526, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138526
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39906C.1.pep
US-10-437-963-138526

Query Match 100.0%; Score 29; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 555 KAVFFA 560

RESULT 59

US-10-450-763-54358
; Sequence 54358, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23

```
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54358
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (579)..(616)
; OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00023, p-value=4.682e-3
; OTHER INFORMATION: raw score of 24.31
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (271)..(451)
; OTHER INFORMATION: Matrixin domain identified by Pfam, accession name
; OTHER INFORMATION: Peptidase_M10, E-value=3.7e-109, Pfam score of 376.1
US-10-450-763-54358

Query Match      100.0%; Score 29; DB 5; Length 1330;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      768 KAVFFA 773

RESULT 60
US-10-369-493-4941
; Sequence 4941, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4941
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4941

Query Match      96.6%; Score 28; DB 4; Length 383;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      167 KAVFFA 172

RESULT 61
US-10-369-493-7699
; Sequence 7699, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 150066
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
```

```
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7699
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7699

Query Match      96.6%; Score 28; DB 4; Length 383;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      164 KAVFFA 169

RESULT 62
US-10-424-599-278606
; Sequence 278606, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278606
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93603C.1.pep
US-10-424-599-278606

Query Match      89.7%; Score 26; DB 4; Length 49;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      15 KAVFFA 20

RESULT 63
US-10-424-599-150066
; Sequence 150066, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 150066
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
```

; OTHER INFORMATION: Clone ID: PAT_MRT3847_106530C.1.pep
US-10-424-599-150066

Query Match 89.7%; Score 26; DB 4; Length 61;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 53 KSVFFA 58

RESULT 64

US-10-926-683-1595
; Sequence 1595, Application US/10926683
; Publication No. US20050106595A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/10/926,683
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/09/471,276
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/057,719
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 09/069,047
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: PCT/IB99/00712
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1595
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-683-1595

Query Match 89.7%; Score 26; DB 5; Length 65;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 54 KAVFFS 59

RESULT 65

US-10-425-115-359391
; Sequence 359391, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 359391
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_90934C.1.pep
US-10-425-115-359391

Query Match 89.7%; Score 26; DB 4; Length 89;

Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 54 KAVFFS 59

RESULT 66

US-10-424-599-210814
; Sequence 210814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210814
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32392C.1.pep
US-10-424-599-210814

Query Match 89.7%; Score 26; DB 4; Length 103;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 44 KALFFA 49

RESULT 67

US-10-437-963-114838
; Sequence 114838, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114838
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(108)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18490C.1.pep
US-10-437-963-114838

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

||||:|
Db 48 KAVFYA 53

RESULT 68

US-10-424-599-182643
; Sequence 182643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182643
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(124)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13593C.1.pep
US-10-424-599-182643

Query Match

89.7%; Score 26; DB 4; Length 124;

Best Local Similarity 83.3%; Pred. No. 6.1e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

||||:
Db 65 KAVFFS 70

RESULT 69

US-10-767-701-41102
; Sequence 41102, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41102
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1929_1.pep
US-10-767-701-41102

Query Match

89.7%; Score 26; DB 4; Length 131;

Best Local Similarity 83.3%; Pred. No. 6.4e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

||||:
Db 42 KAVFFA 47

RESULT 70

US-10-450-763-39449
; Sequence 39449, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39449
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-39449

Query Match

89.7%; Score 26; DB 5; Length 138;

Best Local Similarity 83.3%; Pred. No. 6.7e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

||||:
Db 49 RAVFFA 54

RESULT 71

US-10-437-963-172959
; Sequence 172959, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172959
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71044C.1.pep
US-10-437-963-172959

Query Match

89.7%; Score 26; DB 4; Length 172;

Best Local Similarity 83.3%; Pred. No. 8.4e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

||||:
Db 145 RAVFFA 150

RESULT 72

US-10-767-701-31699
; Sequence 31699, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 31699
LENGTH: 206
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C102839_1.pep
US-10-767-701-31699

Query Match 89.7%; Score 26; DB 4; Length 206;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 6 KAVFFS 11

RESULT 73

US-10-450-763-39451
Sequence 39451, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 39451
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
LOCATION: (1)-(208)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-39451

Query Match 89.7%; Score 26; DB 5; Length 208;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 37 RAVFFA 42

RESULT 74

US-10-282-122A-61639
Sequence 61639, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl

APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61639
LENGTH: 210
TYPE: PRT
ORGANISM: Mycobacterium avium
US-10-282-122A-61639

Query Match 89.7%; Score 26; DB 4; Length 210;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 54 RAVFFA 59

RESULT 75

US-10-425-115-286732
Sequence 286732, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 286732
LENGTH: 258
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_24595C.1.pep
US-10-425-115-286732

Query Match 89.7%; Score 26; DB 4; Length 258;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
||:||||
Db 212 KAMFFA 217

Search completed: December 29, 2005, 18:49:47
Job time : 67.2903 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUTS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-7
2	29	100.0	6	2	US-09-747-408-15
3	29	100.0	74	2	US-09-194-468A-19
4	29	100.0	74	2	US-09-194-468A-20
5	29	100.0	108	2	US-09-194-468A-25
6	29	100.0	108	2	US-09-194-468A-26
7	29	100.0	193	2	US-09-194-468A-18
8	29	100.0	193	2	US-09-194-468A-24
9	29	100.0	222	2	US-09-194-468A-17
10	29	100.0	228	2	US-09-194-468A-23
11	29	100.0	429	2	US-09-194-468A-45
12	29	100.0	631	2	US-08-448-489-17
13	29	100.0	631	2	US-09-689-730-17
14	29	100.0	660	2	US-08-704-711A-18
15	29	100.0	660	2	US-09-521-220-18
16	29	100.0	660	2	US-09-391-104-19
17	29	100.0	660	2	US-09-917-254-89
18	29	100.0	660	2	US-09-949-016-6512
19	29	100.0	660	2	US-09-949-016-7937
20	29	100.0	660	2	US-10-153-185-14
21	29	100.0	663	2	US-09-194-468A-30
22	26	89.7	65	2	US-09-471-276-1595
23	26	89.7	128	2	US-09-540-236-2808
24	26	89.7	295	2	US-09-248-796A-18333
25	26	89.7	334	2	US-09-205-258-348
26	26	89.7	334	2	US-10-004-860-348
27	26	89.7	494	2	US-09-328-352-7729

28	26	89.7	535	2	US-09-902-540-10002	Sequence 10002, A
29	26	89.7	1507	2	US-08-929-329-5	Sequence 5, Appli
30	25	86.2		2	US-09-095-106A-40	Sequence 40, Appl
31	25	86.2	6	2	US-09-747-408-9	Sequence 9, Appli
32	25	86.2	6	2	US-09-747-408-17	Sequence 17, Appl
33	25	86.2	28	1	US-08-461-216-4	Sequence 4, Appli
34	25	86.2	77	2	US-09-513-999C-6921	Sequence 6921, Ap
35	25	86.2	80	2	US-09-248-796A-27785	Sequence 27785, A
36	25	86.2	77	2	US-09-270-767-33756	Sequence 33756, A
37	25	86.2	142	2	US-09-270-767-33756	Sequence 33756, A
38	25	86.2	142	2	US-09-270-767-48973	Sequence 48973, A
39	25	86.2	261	2	US-09-270-767-43456	Sequence 43456, A
40	25	86.2	281	2	US-09-252-991A-29199	Sequence 29199, A
41	25	86.2	282	2	US-09-845-713A-2	Sequence 2, Appli
42	25	86.2	306	2	US-09-303-518D-676	Sequence 676, App
43	25	86.2	306	2	US-09-303-518D-678	Sequence 678, App
44	25	86.2	307	2	US-09-303-518D-680	Sequence 680, App
45	25	86.2	322	2	US-09-495-406-34	Sequence 34, Appl
46	25	86.2	322	2	US-09-816-028A-48	Sequence 48, Appl
47	25	86.2	322	2	US-10-303-162-48	Sequence 48, Appl
48	25	86.2	322	2	US-10-303-134-48	Sequence 48, Appl
49	25	86.2	322	2	US-10-303-118-48	Sequence 48, Appl
50	25	86.2	334	2	US-09-270-767-43522	Sequence 43522, A
51	25	86.2	337	2	US-09-438-185A-960	Sequence 960, App
52	25	86.2	347	2	US-08-749-816-3	Sequence 3, Appli
53	25	86.2	347	2	US-09-144-914-6	Sequence 6, Appli
54	25	86.2	375	2	US-09-489-039A-11261	Sequence 11261, A
55	25	86.2	421	2	US-09-543-681A-5731	Sequence 5731, Ap
56	25	86.2	430	2	US-09-272-960-2	Sequence 2, Appli
57	25	86.2	430	2	US-10-058-636-2	Sequence 2, Appli
58	25	86.2	462	2	US-09-583-110-3587	Sequence 3587, Ap
59	25	86.2	473	2	US-09-107-433-3273	Sequence 3273, Ap
60	25	86.2	474	2	US-09-489-039A-13140	Sequence 13140, A
61	25	86.2	532	1	US-08-288-405A-10	Sequence 10, Appl
62	25	86.2	532	2	US-10-162-012-13	Sequence 13, Appl
63	25	86.2	547	2	US-09-605-703B-2398	Sequence 2398, Ap
64	25	86.2	560	1	US-08-594-031-90	Sequence 90, Appl
65	25	86.2	560	2	US-09-643-597-225	Sequence 225, App
66	25	86.2	560	2	US-09-480-884A-225	Sequence 225, App
67	25	86.2	560	2	US-09-542-615A-225	Sequence 225, App
68	25	86.2	560	2	US-09-606-421B-225	Sequence 225, App
69	25	86.2	560	2	US-09-476-496A-225	Sequence 225, App
70	25	86.2	560	2	US-09-630-940B-225	Sequence 225, App
71	25	86.2	560	2	US-09-943-075A-6	Sequence 6, Appli
72	25	86.2	560	2	US-10-039-272A-2	Sequence 2, Appli
73	25	86.2	560	2	US-10-007-700-225	Sequence 225, App
74	25	86.2	560	5	US-09-985-799-90	Sequence 90, Appl
75	25	86.2	560	5	US-09-977-371-90	Sequence 90, Appl
76	25	86.2	591	2	US-09-489-039A-12837	Sequence 12837, A
77	25	86.2	605	2	US-08-693-214-8	Sequence 8, Appli
78	25	86.2	945	2	US-09-198-452A-1030	Sequence 1030, Ap
79	25	86.2	1144	1	US-08-147-812-5	Sequence 5, Appli
80	25	86.2	1144	1	US-08-319-866-12	Sequence 12, Appl
81	25	86.2	1144	2	US-09-123-708-2	Sequence 2, Appli
82	25	86.2	1144	2	US-09-123-624-2	Sequence 2, Appli
83	25	86.2	1144	2	US-09-661-258-5	Sequence 5, Appli
84	25	86.2	1144	2	US-08-809-917-12	Sequence 12, Appl
85	25	86.2	1144	2	US-09-419-371-12	Sequence 12, Appl
86	25	86.2	2343	2	US-09-324-867-2	Sequence 2, Appli
87	24	82.8	5	1	US-08-612-785B-25	Sequence 25, Appl
88	24	82.8	5	2	US-08-703-675C-38	Sequence 38, Appl
89	24	82.8	5	2	US-08-617-267C-25	Sequence 25, Appl
90	24	82.8	6	1	US-08-612-785B-9	Sequence 9, Appli
91	24	82.8	6	2	US-08-703-675C-32	Sequence 32, Appl
92	24	82.8	6	2	US-08-617-267C-9	Sequence 9, Appli
93	24	82.8	6	2	US-09-747-408-1	Sequence 1, Appli
94	24	82.8	6	2	US-09-747-408-3	Sequence 3, Appli
95	24	82.8	6	2	US-09-747-408-10	Sequence 10, Appl
96	24	82.8	6	2	US-09-747-408-11	Sequence 11, Appl
97	24	82.8	7	1	US-08-127-904-14	Sequence 14, Appl
98	24	82.8	7	1	US-08-612-785B-7	Sequence 7, Appli
99	24	82.8	7	2	US-08-703-675C-30	Sequence 30, Appl
100	24	82.8	7	2	US-08-617-267C-7	Sequence 7, Appli

101	24	82.8	7	2	US-09-264-709A-13	Sequence 13, Appl	174	24	82.8	19	2	US-10-815-353-5	Sequence 5, Appl
102	24	82.8	7	2	US-09-747-408-2	Sequence 2, Appl	175	24	82.8	19	2	US-10-816-529-5	Sequence 5, Appl
103	24	82.8	7	2	US-09-747-408-18	Sequence 18, Appl	176	24	82.8	19	2	US-10-815-391-5	Sequence 5, Appl
104	24	82.8	7	2	US-09-747-408-19	Sequence 19, Appl	177	24	82.8	19	2	US-10-816-022-5	Sequence 5, Appl
105	24	82.8	7	4	PCT-US94-10475-14	Sequence 14, Appl	178	24	82.8	19	2	US-09-724-940-75	Sequence 75, Appl
106	24	82.8	8	1	US-08-612-785B-5	Sequence 5, Appl	179	24	82.8	19	2	US-10-934-609-5	Sequence 5, Appl
107	24	82.8	8	1	US-08-630-645-1	Sequence 1, Appl	180	24	82.8	19	2	US-10-884-892-5	Sequence 5, Appl
108	24	82.8	8	2	US-08-703-675C-28	Sequence 28, Appl	181	24	82.8	20	2	US-08-970-833-10	Sequence 10, Appl
109	24	82.8	8	2	US-08-617-267C-5	Sequence 5, Appl	182	24	82.8	20	2	US-09-724-953-33	Sequence 33, Appl
110	24	82.8	8	2	US-09-095-106A-44	Sequence 44, Appl	183	24	82.8	20	2	US-09-724-567-33	Sequence 33, Appl
111	24	82.8	8	2	US-08-766-596A-1	Sequence 1, Appl	184	24	82.8	20	2	US-09-729-952-33	Sequence 33, Appl
112	24	82.8	8	2	US-09-668-314C-73	Sequence 73, Appl	185	24	82.8	20	2	US-09-585-817-33	Sequence 33, Appl
113	24	82.8	8	4	PCT-US96-10220-1	Sequence 1, Appl	186	24	82.8	26	1	US-08-304-585-7	Sequence 7, Appl
114	24	82.8	9	2	US-08-766-596A-50	Sequence 50, Appl	187	24	82.8	26	1	US-08-346-849-4	Sequence 4, Appl
115	24	82.8	9	2	US-08-766-596A-64	Sequence 64, Appl	188	24	82.8	28	1	US-08-302-080-7	Sequence 7, Appl
116	24	82.8	9	2	US-09-747-408-20	Sequence 20, Appl	189	24	82.8	28	1	US-08-609-090-2	Sequence 2, Appl
117	24	82.8	9	2	US-10-014-658-15	Sequence 15, Appl	190	24	82.8	28	1	US-08-986-948-7	Sequence 7, Appl
118	24	82.8	10	2	US-08-970-833-3	Sequence 3, Appl	191	24	82.8	28	1	US-08-233-284A-4	Sequence 4, Appl
119	24	82.8	10	2	US-09-724-961-20	Sequence 20, Appl	192	24	82.8	28	1	US-08-461-216-2	Sequence 2, Appl
120	24	82.8	10	2	US-09-724-961-21	Sequence 21, Appl	193	24	82.8	28	2	US-09-388-890-2	Sequence 2, Appl
121	24	82.8	10	2	US-09-724-961-22	Sequence 22, Appl	194	24	82.8	28	2	US-09-388-890-3	Sequence 3, Appl
122	24	82.8	10	2	US-09-724-961-23	Sequence 23, Appl	195	24	82.8	28	2	US-09-388-890-4	Sequence 4, Appl
123	24	82.8	10	2	US-09-724-961-24	Sequence 24, Appl	196	24	82.8	28	2	US-09-388-890-5	Sequence 5, Appl
124	24	82.8	10	2	US-09-580-018-20	Sequence 20, Appl	197	24	82.8	28	2	US-09-388-890-6	Sequence 6, Appl
125	24	82.8	10	2	US-09-580-018-21	Sequence 21, Appl	198	24	82.8	28	2	US-09-388-890-7	Sequence 7, Appl
126	24	82.8	10	2	US-09-580-018-22	Sequence 22, Appl	199	24	82.8	28	2	US-09-388-890-8	Sequence 8, Appl
127	24	82.8	10	2	US-09-580-018-23	Sequence 23, Appl	200	24	82.8	28	2	US-09-388-890-9	Sequence 9, Appl
128	24	82.8	10	2	US-09-580-018-24	Sequence 24, Appl	201	24	82.8	28	2	US-09-388-890-10	Sequence 10, Appl
129	24	82.8	10	2	US-09-724-551-20	Sequence 20, Appl	202	24	82.8	28	2	US-09-388-890-12	Sequence 12, Appl
130	24	82.8	10	2	US-09-724-551-21	Sequence 21, Appl	203	24	82.8	28	2	US-09-388-890-13	Sequence 13, Appl
131	24	82.8	10	2	US-09-724-551-22	Sequence 22, Appl	204	24	82.8	28	2	US-09-388-890-14	Sequence 14, Appl
132	24	82.8	10	2	US-09-724-551-23	Sequence 23, Appl	205	24	82.8	28	2	US-09-264-709A-1	Sequence 1, Appl
133	24	82.8	10	2	US-09-724-551-24	Sequence 24, Appl	206	24	82.8	28	2	US-08-723-661B-2	Sequence 2, Appl
134	24	82.8	10	2	US-09-724-940-20	Sequence 20, Appl	207	24	82.8	28	2	US-09-660-954-2	Sequence 2, Appl
135	24	82.8	10	2	US-09-724-940-21	Sequence 21, Appl	208	24	82.8	28	2	US-09-660-954-3	Sequence 3, Appl
136	24	82.8	10	2	US-09-724-940-22	Sequence 22, Appl	209	24	82.8	28	2	US-09-660-954-4	Sequence 4, Appl
137	24	82.8	10	2	US-09-724-940-23	Sequence 23, Appl	210	24	82.8	28	2	US-09-660-954-5	Sequence 5, Appl
138	24	82.8	10	2	US-09-724-940-24	Sequence 24, Appl	211	24	82.8	28	2	US-09-660-954-6	Sequence 6, Appl
139	24	82.8	11	1	US-08-630-645-14	Sequence 14, Appl	212	24	82.8	28	2	US-09-660-954-7	Sequence 7, Appl
140	24	82.8	11	2	US-08-766-596A-14	Sequence 14, Appl	213	24	82.8	28	2	US-09-660-954-8	Sequence 8, Appl
141	24	82.8	11	2	US-09-988-842-9	Sequence 9, Appl	214	24	82.8	28	2	US-09-660-954-9	Sequence 9, Appl
142	24	82.8	11	4	PCT-US96-10220-14	Sequence 14, Appl	215	24	82.8	28	2	US-09-660-954-10	Sequence 10, Appl
143	24	82.8	11	4	PCT-US96-10220-14	Sequence 14, Appl	216	24	82.8	28	2	US-09-660-954-12	Sequence 12, Appl
144	24	82.8	14	2	US-09-594-366-5	Sequence 5, Appl	217	24	82.8	28	2	US-09-660-954-13	Sequence 13, Appl
145	24	82.8	14	2	US-09-992-800-5	Sequence 5, Appl	218	24	82.8	28	2	US-09-660-954-14	Sequence 14, Appl
146	24	82.8	15	1	US-08-612-785B-14	Sequence 14, Appl	219	24	82.8	28	2	US-08-898-300-4	Sequence 4, Appl
147	24	82.8	15	1	US-08-612-785B-37	Sequence 37, Appl	220	24	82.8	28	2	US-08-824-513-4	Sequence 4, Appl
148	24	82.8	15	2	US-08-617-267C-14	Sequence 14, Appl	221	24	82.8	28	2	US-09-623-548A-959	Sequence 959, App
149	24	82.8	15	2	US-08-766-596A-56	Sequence 56, Appl	222	24	82.8	28	2	US-09-623-548A-965	Sequence 965, App
150	24	82.8	15	2	US-08-766-596A-57	Sequence 57, Appl	223	24	82.8	28	2	US-09-623-548A-976	Sequence 976, App
151	24	82.8	15	2	US-08-766-596A-58	Sequence 58, Appl	224	24	82.8	28	2	US-09-623-548A-992	Sequence 992, App
152	24	82.8	15	2	US-08-766-596A-60	Sequence 60, Appl	225	24	82.8	28	2	US-09-623-548A-1003	Sequence 1003, App
153	24	82.8	15	2	US-08-766-596A-61	Sequence 61, Appl	226	24	82.8	28	2	US-09-657-276-959	Sequence 959, App
154	24	82.8	15	2	US-08-766-596A-63	Sequence 63, Appl	227	24	82.8	28	2	US-09-657-276-965	Sequence 965, App
155	24	82.8	15	2	US-08-766-596A-65	Sequence 65, Appl	228	24	82.8	28	2	US-09-657-276-976	Sequence 976, App
156	24	82.8	17	2	US-09-264-709A-2	Sequence 2, Appl	229	24	82.8	28	2	US-09-657-276-992	Sequence 992, App
157	24	82.8	17	2	US-09-594-366-3	Sequence 3, Appl	230	24	82.8	28	2	US-09-657-276-1003	Sequence 1003, App
158	24	82.8	17	2	US-09-623-548A-950	Sequence 950, App	231	24	82.8	28	2	US-09-865-294A-66	Sequence 66, Appl
159	24	82.8	17	2	US-09-623-548A-983	Sequence 983, App	232	24	82.8	30	1	US-08-609-090-3	Sequence 3, Appl
160	24	82.8	17	2	US-09-992-800-3	Sequence 3, Appl	233	24	82.8	30	2	US-09-861-847A-1	Sequence 1, Appl
161	24	82.8	17	2	US-09-657-276-950	Sequence 950, App	234	24	82.8	33	1	US-08-609-090-4	Sequence 4, Appl
162	24	82.8	17	2	US-09-657-276-983	Sequence 983, App	235	24	82.8	34	1	US-08-475-579A-4	Sequence 4, Appl
163	24	82.8	19	2	US-08-970-833-11	Sequence 11, Appl	236	24	82.8	35	1	US-08-304-585-6	Sequence 6, Appl
164	24	82.8	19	2	US-09-723-384-5	Sequence 5, Appl	237	24	82.8	35	1	US-08-612-785B-16	Sequence 16, Appl
165	24	82.8	19	2	US-09-724-961-75	Sequence 75, Appl	238	24	82.8	35	1	US-08-612-785B-36	Sequence 36, Appl
166	24	82.8	19	2	US-09-724-552-5	Sequence 5, Appl	239	24	82.8	35	1	US-08-612-785B-38	Sequence 38, Appl
167	24	82.8	19	2	US-09-580-018-75	Sequence 75, Appl	240	24	82.8	35	1	US-08-612-785B-40	Sequence 40, Appl
168	24	82.8	19	2	US-09-724-927-5	Sequence 5, Appl	241	24	82.8	35	2	US-08-617-267C-16	Sequence 16, Appl
169	24	82.8	19	2	US-09-724-489-5	Sequence 5, Appl	242	24	82.8	35	2	US-09-623-548A-979	Sequence 979, App
170	24	82.8	19	2	US-09-724-477-5	Sequence 5, Appl	243	24	82.8	35	2	US-09-623-548A-1006	Sequence 1006, App
171	24	82.8	19	2	US-09-723-762-5	Sequence 5, Appl	244	24	82.8	35	2	US-09-657-276-979	Sequence 979, App
172	24	82.8	19	2	US-09-201-430-5	Sequence 5, Appl	245	24	82.8	35	2	US-09-657-276-1006	Sequence 1006, App
173	24	82.8	19	2	US-09-724-551-75	Sequence 75, Appl	246	24	82.8	36	1	US-08-609-090-6	Sequence 6, Appl

247 24 82.8 36 2 US-09-861-847A-6
248 24 82.8 36 2 US-09-861-847A-11
249 24 82.8 38 1 US-08-302-808-1
250 24 82.8 38 1 US-07-737-371B-68
251 24 82.8 38 1 US-08-986-948-1
252 24 82.8 38 2 US-09-623-548A-975
253 24 82.8 38 2 US-09-623-548A-1002
254 24 82.8 38 2 US-09-657-276-975
255 24 82.8 38 2 US-09-657-276-1002
256 24 82.8 39 1 US-08-304-585-5
257 24 82.8 39 1 US-08-302-808-2
258 24 82.8 39 1 US-08-609-090-7
259 24 82.8 39 1 US-08-682-245A-1
260 24 82.8 39 1 US-08-986-948-2
261 24 82.8 40 1 US-07-744-767A-1
262 24 82.8 40 1 US-08-235-400-2
263 24 82.8 40 1 US-08-476-464A-2
264 24 82.8 40 1 US-08-304-585-1
265 24 82.8 40 1 US-08-304-585-8
266 24 82.8 40 1 US-08-302-808-3
267 24 82.8 40 1 US-08-433-734-1
268 24 82.8 40 1 US-08-609-090-8
269 24 82.8 40 1 US-07-737-371B-69
270 24 82.8 40 1 US-08-682-245A-2
271 24 82.8 40 1 US-08-986-948-3
272 24 82.8 40 1 US-08-461-216-1
273 24 82.8 40 2 US-08-959-148-1
274 24 82.8 40 2 US-09-242-724-22
275 24 82.8 40 2 US-08-723-661B-1
276 24 82.8 40 2 US-09-062-365-3
277 24 82.8 40 2 US-09-133-866-1
278 24 82.8 40 2 US-09-861-847A-7
279 24 82.8 40 2 US-09-861-847A-8
280 24 82.8 40 2 US-09-988-842-3
281 24 82.8 40 2 US-10-455-218-1
282 24 82.8 40 2 US-10-151-614-1
283 24 82.8 40 2 US-09-623-548A-956
284 24 82.8 40 2 US-09-623-548A-962
285 24 82.8 40 2 US-09-623-548A-968
286 24 82.8 40 2 US-09-623-548A-978
287 24 82.8 40 2 US-09-623-548A-989
288 24 82.8 40 2 US-09-623-548A-995
289 24 82.8 40 2 US-09-623-548A-1005
290 24 82.8 40 2 US-09-657-276-956
291 24 82.8 40 2 US-09-657-276-962
292 24 82.8 40 2 US-09-657-276-968
293 24 82.8 40 2 US-09-657-276-978
294 24 82.8 40 2 US-09-657-276-989
295 24 82.8 40 2 US-09-657-276-995
296 24 82.8 40 2 US-09-657-276-1005
297 24 82.8 40 2 PCT-US92-955D-36
298 24 82.8 40 4 PCT-US92-06700-1
299 24 82.8 41 1 US-07-819-361-1
300 24 82.8 41 1 US-08-302-808-4

ALIGNMENTS

RESULT 1
US-09-747-408-7
; Sequence 7, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-7

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 2
US-09-747-408-15
; Sequence 15, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-15

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 3
US-09-194-468A-19
; Sequence 19, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chersesh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-19

Query Match 100.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 4
US-09-194-468A-25
; Sequence 25, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-25

Query Match 100.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 5
US-09-194-468A-20
; Sequence 20, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-20

Query Match 100.0%; Score 29; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 38;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 6
US-09-194-468A-26
; Sequence 26, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-26

Query Match 100.0%; Score 29; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 7
US-09-194-468A-18
; Sequence 18, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-18

Query Match 100.0%; Score 29; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 8
US-09-194-468A-24
; Sequence 24, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-24

Query Match 100.0%; Score 29; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 9
US-09-194-468A-17
; Sequence 17, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-17

Query Match 100.0%; Score 29; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 93 KAVFFA 98

RESULT 10
US-09-194-468A-23
; Sequence 23, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-23

Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 99 KAVFFA 104

RESULT 11
US-09-194-468A-45
; Sequence 45, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-45

Query Match 100.0%; Score 29; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 300 KAVFFA 305

RESULT 12

US-08-448-489-17

```
; Sequence 17, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-17

Query Match          100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 502 KAVFFA 507

RESULT 13
US-09-689-730-17
; Sequence 17, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-17

Query Match          100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 502 KAVFFA 507

RESULT 14
US-08-704-711A-18
; Sequence 18, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
```

```
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-18

Query Match          100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 15
US-09-521-220-18
; Sequence 18, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```


;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/521,220
;; FILING DATE: 08-Mar-2000
;; CLASSIFICATION: <Unknown>
;; 21-OCT-1994
;; 17-MAR-1994
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/704,711
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: DE 4438838.1
;; FILING DATE: 21-OCT-1994
;; APPLICATION NUMBER: DE 4409663.1
;; FILING DATE: 17-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GRANADOS, Patricia D.
;; REGISTRATION NUMBER: 33,683
;; REFERENCE/DOCKET NUMBER: 26083/124
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;;
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 660 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-521-220-18

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 16
US-09-391-104-19
; Sequence 19, Application US/09391104
; Patent No. 639371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT FILING DATE: 1999-09-07
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-19

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 17
US-09-917-254-89
; Sequence 89, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-89

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 18
US-09-949-016-6512
; Sequence 6512, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6512
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6512

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 19
US-09-949-016-7937
; Sequence 7937, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7937
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7937

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 20
US-10-153-185-14
; Sequence 14, Application US/10153185
; Patent No. 6906036
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 21
US-09-194-468A-30
; Sequence 30, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-30

Query Match 100.0%; Score 29; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 534 KAVFFA 539

RESULT 22
US-09-471-276-1595
; Sequence 1595, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1595
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1595

Query Match 89.7%; Score 26; DB 2; Length 65;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 54 KAVFFS 59

RESULT 23
US-09-540-236-2808
; Sequence 2808, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2808
; LENGTH: 128
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2808

```
Query Match      89.7%; Score 26; DB 2; Length 128;
Best Local Similarity 83.3%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY      1 KAVFFA 6
Db      55 KAVFYA 60

RESULT 24
US-09-248-796A-18333
; Sequence 18333, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18333
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18333

Query Match      89.7%; Score 26; DB 2; Length 295;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      31 KAVFYA 36

RESULT 25
US-09-205-258-348
; Sequence 348, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,372
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 348
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (334)
; OTHER INFORMATION: Xaa equals stop translation
;
US-09-205-258-348
```

```
Query Match      89.7%; Score 26; DB 2; Length 334;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      273 KAVFYA 278

RESULT 26
US-10-004-860-348
; Sequence 348, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007PI
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 348
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;
; NAME/KEY: SITE
; LOCATION: (334)
; OTHER INFORMATION: Xaa equals stop translation
US-10-004-860-348

Query Match      89.7%; Score 26; DB 2; Length 334;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      273 KAVFYA 278

RESULT 27
US-09-328-352-7729
; Sequence 7729, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7729
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7729

Query Match      89.7%; Score 26; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      79 KSVFFA 84

RESULT 28
```

```
US-09-902-540-10002
; Sequence 10002, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10002
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10002

Query Match      89.7%; Score 26; DB 2; Length 535;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      131 KALFFA 136

RESULT 29
US-08-929-329-5
; Sequence 5, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1507 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

```
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoelii
US-08-929-329-5

Query Match      89.7%; Score 26; DB 2; Length 1507;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 1454 KAVYFA 1459

RESULT 30
US-09-095-106A-40
; Sequence 40, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERNIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVPF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-40

Query Match      86.2%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 1 KAVFF 5

RESULT 31
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match      86.2%; Score 25; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KAVFFA 6
Db 1 KVVFFA 6

RESULT 32
US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match      86.2%; Score 25; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 1 KVVFFA 6

RESULT 33
US-08-461-216-4
; Sequence 4, Application US/08461216
; Patent No. 5958883
; GENERAL INFORMATION:
; APPLICANT: Snow, A.D.
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,734
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: September 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: UOFW-1-6707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
; TELEFAX: 1-206-224-0779
```

```
/
/
/ TELEX: 4938023
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ DESCRIPTION: {SYMBOL 98 \f "Symbol"}A4(1-28) mutant;
/ DESCRIPTION: page 83, lines 27-28
US-08-461-216-4

Query Match      86.2%; Score 25; DB 1; Length 28;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      16 KGVFFA 21

RESULT 34
US-09-513-999C-6921
; Sequence 6921, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6921

Query Match      86.2%; Score 25; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      38 KGVFFA 43

RESULT 35
US-09-248-796A-27785
; Sequence 27785, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27785
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
```

```
US-09-248-796A-27785

Query Match      86.2%; Score 25; DB 2; Length 80;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      31 RA1FFA 36

RESULT 36
US-09-270-767-33756
; Sequence 33756, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33756
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33756

Query Match      86.2%; Score 25; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      99 KGVFFA 104

RESULT 37
US-09-270-767-48973
; Sequence 48973, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48973
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48973

Query Match      86.2%; Score 25; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      99 KGVFFA 104

RESULT 38
US-09-270-767-43456
; Sequence 43456, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
```

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43456
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43456

Query Match 86.2%; Score 25; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
| | | | |
Db 184 KAVFF 188

RESULT 39
US-09-252-991A-29199
; Sequence 29199, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29199
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29199

Query Match 86.2%; Score 25; DB 2; Length 281;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 6
: | | | | |
Db 257 EAVFF 262

RESULT 40
US-09-845-713A-2
; Sequence 2, Application US/09845713A
; Patent No. 6660476
; GENERAL INFORMATION:
; APPLICANT: Comings, David E.
; APPLICANT: MacMurray, James P.
; TITLE OF INVENTION: Polymorphisms in the PNMT Gene
; FILE REFERENCE: 1954-327-II
; CURRENT APPLICATION NUMBER: US/09/845,713A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,310
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-713A-2

Query Match 86.2%; Score 25; DB 2; Length 282;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 6
| | | | |
Db 270 KGVFF 275

RESULT 41
US-09-303-518D-676
; Sequence 676, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 676
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-676

Query Match 86.2%; Score 25; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
| | | | |
Db 155 KAVFF 159

RESULT 42
US-09-303-518D-678
; Sequence 678, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 678
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (203)..(203)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (208)..(208)
; OTHER INFORMATION: Xaa= any amino acid

```
; NAME/KEY: misc_feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: Xaa= any amino acid
US-09-303-518D-678

Query Match      86.2%; Score 25; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 155 KAVFF 159

RESULT 43
US-09-303-518D-680
; Sequence 680, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-303-518D-680

Query Match      86.2%; Score 25; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 155 KAVFF 159

RESULT 44
US-09-495-406-34
; Sequence 34, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (cstI)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-495-406-34

; NAME/KEY: misc_feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: Xaa= any amino acid
US-09-303-518D-678

Query Match      86.2%; Score 25; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 155 KAVFF 159

RESULT 43
US-09-303-518D-680
; Sequence 680, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-303-518D-680

Query Match      86.2%; Score 25; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 155 KAVFF 159

RESULT 44
US-09-495-406-34
; Sequence 34, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (cstI)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-495-406-34

; NAME/KEY: misc_feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: Xaa= any amino acid
US-09-303-518D-678

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 61 KAVFF 65

RESULT 45
US-09-816-028A-48
; Sequence 48, Application US/09816028A
; Patent No. 6699705
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-816-028A-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 61 KAVFF 65

RESULT 46
US-10-303-162-48
; Sequence 48, Application US/10303162
; Patent No. 6723545
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,162
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
```



```
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-162-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFP 5
        |||||
Db      61 KAVFP 65

RESULT 47
US-10-303-134-48
; Sequence 48, Application US/10303134
; Patent No. 6825019
; GENERAL INFORMATION:
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,134
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-134-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFP 5
        |||||
Db      61 KAVFP 65

RESULT 48
US-10-303-118-48
; Sequence 48, Application US/10303118
; Patent No. 6905867
; GENERAL INFORMATION:
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
```

```
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-118-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFP 5
        |||||
Db      61 KAVFP 65

RESULT 49
US-10-303-128-48
; Sequence 48, Application US/10303128
; Patent No. 6911337
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-128-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFP 5
        |||||
Db      61 KAVFP 65

RESULT 50
US-09-270-767-43522
; Sequence 43522, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43522
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
```

US-09-270-767-43522

Query Match 86.2%; Score 25; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||]
Db 282 KSIFPA 287

RESULT 51

US-09-438-185A-960
; Sequence 960, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 960
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0958
US-09-438-185A-960

Query Match 86.2%; Score 25; DB 2; Length 337;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||]
Db 284 RAIFPA 289

RESULT 52

US-08-749-816-3
; Sequence 3, Application US/08749816
; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemare, Eric
; APPLICANT: Fink, Michel
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunki, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; TITLE OF INVENTION: OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-816-3

Query Match 86.2%; Score 25; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||]
Db 111 KAIFFS 116

RESULT 53

US-09-144-914-6
; Sequence 6, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunki, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
US-09-144-914-6

Query Match 86.2%; Score 25; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||]
Db 111 KAIFFS 116

RESULT 54

US-09-489-039A-11261

; Sequence 11261, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Berton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11261
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11261

Query Match 86.2%; Score 25; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 KAVFF 5
Db 19 KAVFF 23

RESULT 55
US-09-543-681A-5731
; Sequence 5731, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BERTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5731
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5731

Query Match 86.2%; Score 25; DB 2; Length 421;
Best Local Similarity 66.7%; Pred. No. 9.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

Qy 1 KAVFFA 6
Db 334 RA1FFA 339

RESULT 56
US-09-272-960-2
; Sequence 2, Application US/09272960
; Patent No. 6689604
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and Its Uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/09/272,960
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 60/078,891
; EARLIER FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: US 09/272,960
; EARLIER FILING DATE: 1999-03-18

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-09-272-960-2

Query Match 86.2%; Score 25; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 KAVFF 5
Db 61 KAVFF 65

RESULT 57
US-10-058-636-2
; Sequence 2, Application US/10058636
; Patent No. 6709834
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and Its Uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/10/058,636
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/272,960
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/078,891
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/272,960
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-058-636-2

Query Match 86.2%; Score 25; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 KAVFF 5
Db 61 KAVFF 65

RESULT 58
US-09-583-110-3587
; Sequence 3587, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3587
; LENGTH: 462

;
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3587

Query Match 86.2%; Score 25; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
|
Db 4 KAVFF 8

RESULT 59

US-09-107-433-3273
; Sequence 3273, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESS: GENE THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3273:

SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...473
SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

US-09-107-433-3273

Query Match 86.2%; Score 25; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
|
Db 15 KAVFF 19

RESULT 60

US-09-489-039A-13140
; Sequence 13140, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13140

LENGTH: 474

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13140

Query Match 86.2%; Score 25; DB 2; Length 474;

Best Local Similarity 100.0%; Pred. No. 1.e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5

|
|
|
|
|
Db 362 KAVFF 366

RESULT 61

US-08-288-405A-10
; Sequence 10, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:

APPLICANT: Chandoy, Kanianthara G.
APPLICANT: Kalman, Katalin
APPLICANT: Chandoy, Grischa

APPLICANT: Gutman, George A.

TITLE OF INVENTION: A No. 5559009e1 Voltage-Gated Potassium Channel

TITLE OF INVENTION: Gene

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,
ATTN: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,405A

FILING DATE: 10-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,431

FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-59844-1/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-405A-10

Query Match 86.2%; Score 25; DB 1; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||
DB 310 KAVFF 314

RESULT 62

US-10-162-012-13
; Sequence 13, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-162-012-13

Query Match 86.2%; Score 25; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||
DB 310 KAVFF 314

RESULT 63

US-09-605-703B-2398
; Sequence 2398, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 2398
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-2398

Query Match 86.2%; Score 25; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||
DB 454 KAVFF 458

RESULT 64

US-08-594-031-90
; Sequence 90, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-594-031-90

Query Match      86.2%; Score 25; DB 1; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 65
US-09-643-597-225
; Sequence 225, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, AiJun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-643-597-225

Query Match      86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 66
US-09-480-884A-225
; Sequence 225, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, AiJun
; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-480-884A-225

Query Match      86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 67
US-09-542-615A-225
; Sequence 225, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-542-615A-225

Query Match      86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 68
US-09-606-421B-225
; Sequence 225, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, AiJun
; APPLICANT: Skeiky, Yasir A.W.
```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-606-421B-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 537 KAVFP 541

RESULT 69

US-09-476-496A-225
; Sequence 225, Application US/09476496A
; Patent No. 6706262
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C5
; CURRENT APPLICATION NUMBER: US/09/476,496A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-476-496A-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 537 KAVFP 541

RESULT 70

US-09-630-940B-225
; Sequence 225, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B

; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-630-940B-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 537 KAVFP 541

RESULT 71

US-09-943-075A-6
; Sequence 6, Application US/09943075A
; Patent No. 6812002
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Ravez F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same, Compositions and Methods of Stimulating Bone Differentiation
; FILE REFERENCE: 71369.262
; CURRENT APPLICATION NUMBER: US/09/943,075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Human
US-09-943-075A-6

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 537 KAVFP 541

RESULT 72

US-10-039-272A-2
; Sequence 2, Application US/10039272A
; Patent No. 6939955
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE 1 RECEPTOR AGONISTS
; FILE REFERENCE: 267/033 (UMD-0055)
; CURRENT APPLICATION NUMBER: US/10/039,272A
; CURRENT FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-272A-2

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;


```

;
; TELEFAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 90:
;
US-09-977-371-90

```

```

Query Match      86.2%; Score 25; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      |||||
Db      537 KAVFF 541

```

Search completed: December 29, 2005, 17:52:38
Job time : 20.1323 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-15
Perfect score: 29
Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum Match 100%
Maximum DB seq length: 2000000000
Listing first 300 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4 AAB48480	Aab48480 Antifibri
2	29	100.0	6	4 AAB48488	Aab48488 Antifibri
3	29	100.0	6	4 AAB82636	Aab82636 All-D pep
4	29	100.0	6	4 AAB82628	Aab82628 All-D pep
5	29	100.0	6	5 AAU96824	Aau96824 Amyloid t
6	29	100.0	6	5 AAU96816	Aau96816 Amyloid t
7	29	100.0	6	5 AAU11662	Aau11662 Peptide #
8	29	100.0	6	5 AAU11654	Aau11654 Peptide #
9	29	100.0	6	6 AAE35450	Aae35450 Abeta pep
10	29	100.0	6	6 AAE35443	Aae35443 Abeta pep
11	29	100.0	6	8 ADQ37275	Adq37275 Vaccine a
12	29	100.0	6	8 ADQ37267	Adq37267 Vaccine a
13	29	100.0	6	8 ADQ37319	Adq37319 Antifibri
14	29	100.0	6	8 ADQ37327	Adq37327 Antifibri
15	29	100.0	6	9 ADY37934	Ady37934 Amyloid-t
16	29	100.0	6	9 ADY37926	Ady37926 Amyloid-t
17	29	100.0	37	3 AAB05909	Aab05909 Rat induc
18	29	100.0	37	8 ADK34079	Adk34079 Mouse iNO
19	29	100.0	37	8 ADL70726	Adl70726 Rat iNOS
20	29	100.0	42	8 ADG17617	Adg17617 Modified
21	29	100.0	42	8 ADG17612	Adg17612 Modified
22	29	100.0	74	2 AAW41091	Aaw41091 Chicken m
23	29	100.0	74	2 AAW41085	Aaw41085 Human mat
24	29	100.0	74	2 AAW41230	Aaw41230 Alpha-v-b

25	29	100.0	74	8 ADT05998	Adt05998 Modified
26	29	100.0	74	8 ADT05965	Adt05965 Human mat
27	29	100.0	74	8 ADT05971	Adt05971 Chicken m
28	29	100.0	108	2 AAW41086	Aaw41086 Human mat
29	29	100.0	108	2 AAW41092	Aaw41092 Chicken m
30	29	100.0	108	2 AAW41231	Aaw41231 Alpha-v-b
31	29	100.0	108	2 AAW41237	Aaw41237 Alpha-v-b
32	29	100.0	108	8 ADT05972	Adt05972 Chicken m
33	29	100.0	108	8 ADT05966	Adt05966 Human mat
34	29	100.0	108	8 ADT05999	Adt05999 Modified
35	29	100.0	122	2 AAW41238	Aaw41238 Alpha-v-b
36	29	100.0	152	2 AAW41232	Aaw41232 Alpha-v-b
37	29	100.0	193	2 AAW41090	Aaw41090 Chicken m
38	29	100.0	193	2 AAW41084	Aaw41084 Human mat
39	29	100.0	193	2 AAW41229	Aaw41229 Alpha-v-b
40	29	100.0	193	2 AAW41235	Aaw41235 Alpha-v-b
41	29	100.0	193	8 ADT05964	Adt05964 Human mat
42	29	100.0	193	8 ADT05970	Adt05970 Chicken m
43	29	100.0	222	2 AAW41083	Aaw41083 Human mat
44	29	100.0	222	2 AAW41228	Aaw41228 Alpha-v-b
45	29	100.0	222	8 ADT05963	Adt05963 Human mat
46	29	100.0	228	2 AAW41089	Aaw41089 Chicken m
47	29	100.0	228	2 AAW41234	Aaw41234 Alpha-v-b
48	29	100.0	228	8 ADT05969	Adt05969 Chicken m
49	29	100.0	261	8 ADT05661	Adt05661 Haemophil
50	29	100.0	429	2 AAW41112	Aaw41112 Human mat
51	29	100.0	429	8 ADT05991	Adt05991 Human mat
52	29	100.0	468	4 ABG24001	Abg24001 Novel hum
53	29	100.0	623	8 ABM84057	Abm84057 Human dia
54	29	100.0	626	8 ADG17622	Adg17622 Modified
55	29	100.0	631	1 ADG17627	Adg17627 Modified
56	29	100.0	631	1 AAP96143	Aap96143 Sequence
57	29	100.0	631	1 AAP91139	Aap91139 Human typ
58	29	100.0	631	2 AAR07969	Aar07969 Complete
59	29	100.0	631	2 AAY07350	Aay07350 Human typ
60	29	100.0	631	2 AAW41226	Aaw41226 Human mat
61	29	100.0	631	7 ADM48668	Adm48668 Human mat
62	29	100.0	631	8 ADT05996	Adt05996 Human mat
63	29	100.0	633	8 ADT05997	Adt05997 Mouse mat
64	29	100.0	644	4 AAB20490	Aab20490 Human mat
65	29	100.0	660	2 AAR06420	Aar06420 Type IV c
66	29	100.0	660	4 AAB84607	Aab84607 Amino aci
67	29	100.0	660	4 AAE10431	Aae10431 Human mat
68	29	100.0	660	5 ABB79413	Abb79413 Human mat
69	29	100.0	660	5 ABB90738	Abb90738 Human Tum
70	29	100.0	660	5 AAB84348	Aab84348 Protein M
71	29	100.0	660	6 ABUS4445	Abu54445 Human tum
72	29	100.0	660	6 ABP97136	Abp97136 Human mat
73	29	100.0	660	6 AAO16608	Aao16608 Human mat
74	29	100.0	660	6 ABG76322	Abg76322 Human mat
75	29	100.0	660	7 ADD18578	Add18578 Human dis
76	29	100.0	660	7 ADP65244	Adp65244 Human mat
77	29	100.0	660	8 ADN07697	Adn07697 Human mat
78	29	100.0	660	8 ADQ17087	Adq17087 Human mat
79	29	100.0	660	9 ADV90301	Adv90301 Protease-
80	29	100.0	660	9 ADV68478	Adv68478 Human mat
81	29	100.0	662	7 ADE62857	Ad62857 Rat Prote
82	29	100.0	662	7 ADD46270	Add46270 Rat Prote
83	29	100.0	663	2 AAW41111	Aaw41111 Chicken m
84	29	100.0	663	2 AAW41227	Aaw41227 Chicken m
85	29	100.0	663	8 ADT05976	Adt05976 Chicken m
86	29	100.0	663	8 ADT05995	Adt05995 Chicken m
87	29	100.0	708	7 ADF60554	Adf60554 Human con
88	29	100.0	708	9 AEA20970	Aea20970 Novel hum
89	29	100.0	718	8 ADN22220	Adn22220 Bacterial
90	29	100.0	737	8 ADN24980	Adn24980 Bacterial
91	29	100.0	1147	2 AAW02571	Aaw02571 Rat induc
92	29	100.0	1330	4 ABG23999	Abg23999 Novel hum
93	28	96.6	383	8 ADN25046	Adn25046 Bacterial
94	28	96.6	383	8 ADN22288	Adn22288 Bacterial
95	26	89.7	65	3 AAY65434	Aay65434 Human 5'
96	26	89.7	65	8 ADU72998	Adu72998 Non-819a
97	26	89.7	65	9 ADZ73989	Adz73989 Human com

98	26	89.7	128	8	ADJ05122	AdJ05122 M. catarr	171	25	86.2	117	4	AAW17468	Aaw17468 Peptide #
99	26	89.7	138	4	ABG09090	Abg09090 Novel hum	172	25	86.2	117	4	ABB36488	Abb36488 Peptide #
100	26	89.7	149	9	AEB41486	Aeb41486 L. pneumo	173	25	86.2	117	4	AAM29987	Aam29987 Peptide #
101	26	89.7	166	9	AEB38197	Aeb38197 L. pneumo	174	25	86.2	117	4	ABB31282	Abb31282 Peptide #
102	26	89.7	208	4	ABG09092	Abg09092 Novel hum	175	25	86.2	117	4	ABB21830	Abb21830 Protein #
103	26	89.7	210	6	ABU33715	Abu33715 Protein e	176	25	86.2	117	4	AAM69653	Aam69653 Human bon
104	26	89.7	238	4	AAU31660	Aau31660 Novel hum	177	25	86.2	117	4	AAM57251	Aam57251 Human bra
105	26	89.7	292	3	AAW42075	Aaw42075 Human pol	178	25	86.2	117	4	ABG51335	Abg51335 Human liv
106	26	89.7	296	3	AAE43372	Aae43372 Human ORF	179	25	86.2	117	4	AAW05146	Aaw05146 Peptide #
107	26	89.7	320	8	ADY08844	Ady08844 Plant ful	180	25	86.2	117	5	ABG39273	Abg39273 Human pep
108	26	89.7	320	8	ADX73944	Adx73944 Plant ful	181	25	86.2	132	8	ABO55307	AbO55307 Human gen
109	26	89.7	322	5	ABR06658	AbR06658 G protein	182	25	86.2	141	7	ADL06701	AdL06701 Carassius
110	26	89.7	329	4	AAW40289	Aaw40289 Human pol	183	25	86.2	150	2	AAW20912	Aaw20912 H. pylori
111	26	89.7	334	2	AAW88633	Aaw88633 Secreted	184	25	86.2	160	4	AAU60292	Aau60292 Propionib
112	26	89.7	334	6	ABO44657	AbO44657 Human sec	185	25	86.2	160	6	ABM56811	Abm56811 Propionib
113	26	89.7	334	6	ABO44657	AbO44657 Human sec	186	25	86.2	170	3	ABG23502	Abg23502 Arabidops
114	26	89.7	334	7	ABO26137	AbO26137 Human pro	187	25	86.2	174	3	ABG39522	Abg39522 Arabidops
115	26	89.7	352	8	ADP29738	Adp29738 Human sec	188	25	86.2	175	4	AAO11219	Aao11219 Human pol
116	26	89.7	358	8	ADQ96208	Adq96208 T cell ac	189	25	86.2	186	7	ADC07962	Adc07962 Rice prot
117	26	89.7	358	8	ADQ96210	Adq96210 T cell ac	190	25	86.2	186	7	ADC07948	Adc07948 Rice prot
118	26	89.7	421	4	AGS98352	Ags98352 Escherich	191	25	86.2	190	4	AAW83792	Aaw83792 Human imm
119	26	89.7	421	6	ABU14827	Abu14827 Protein e	192	25	86.2	200	7	ABM89622	Abm89622 Rice abio
120	26	89.7	441	3	AY53014	Ay53014 Human sec	193	25	86.2	201	8	ADY12035	Ady12035 Plant ful
121	26	89.7	494	6	ADA36442	Ada36442 Acinetoba	194	25	86.2	202	8	ADU05630	Adu05630 H. pylori
122	26	89.7	535	9	ABM90803	Abm90803 M. xanthu	195	25	86.2	206	3	AAW39521	Aaw39521 Arabidops
123	26	89.7	555	4	AAW93388	Aaw93388 Human pol	196	25	86.2	207	3	AAW23501	Aaw23501 Arabidops
124	26	89.7	555	8	AAW66641	Aaw66641 Human maj	197	25	86.2	210	6	ABP79894	Abp79894 N. gonorr
125	26	89.7	555	8	ADL30943	Adl30943 Human pro	198	25	86.2	210	6	ABU37523	Abu37523 Protein e
126	26	89.7	555	8	ADQ96132	Adq96132 T cell ac	199	25	86.2	210	6	ABU38175	Abu38175 Protein e
127	26	89.7	555	9	ADX07709	Adx07709 Cyclin-de	200	25	86.2	213	3	AAW51077	Aaw51077 Arabidops
128	26	89.7	556	3	AY87342	Ay87342 Human sig	201	25	86.2	239	8	ADN46479	Adn46479 Thermococ
129	26	89.7	564	4	AAW88362	Aaw88362 Human mem	202	25	86.2	242	3	AAW51076	Aaw51076 Arabidops
130	26	89.7	564	8	ADQ96212	Adq96212 T cell ac	203	25	86.2	243	3	AAW12759	Aaw12759 Arabidops
131	26	89.7	564	9	ADY63089	Ady63089 Human clo	204	25	86.2	246	3	AAW51075	Aaw51075 Arabidops
132	26	89.7	715	6	ABU47623	Abu47623 Protein e	205	25	86.2	246	4	ABW58652	Abw58652 Drosophil
133	26	89.7	1042	6	ABU33994	Abu33994 Protein e	206	25	86.2	247	2	AAW20248	Aaw20248 H. pylori
134	26	89.7	1172	4	ABG06613	Abg06613 Novel hum	207	25	86.2	249	8	ADS21551	Ads21551 Bacterial
135	26	89.7	1507	3	AAW44128	Aaw44128 Plasmodiu	208	25	86.2	254	8	ADS27681	Ads27681 Bacterial
136	25	86.2	5	2	AAW45963	Aaw45963 Peptide d	209	25	86.2	255	4	ABW67621	Abw67621 Drosophil
137	25	86.2	5	4	ABW48482	Abw48482 Antifibri	210	25	86.2	255	6	ABM68528	Abm68528 Phototrab
138	25	86.2	6	4	ABW48490	Abw48490 Antifibri	211	25	86.2	256	6	ABW68528	Abw68528 Phototrab
139	25	86.2	6	4	ABW48490	Abw48490 Antifibri	212	25	86.2	256	6	ABW68528	Abw68528 Phototrab
140	25	86.2	6	4	ABW48490	Abw48490 Antifibri	213	25	86.2	256	6	ABW68528	Abw68528 Phototrab
141	25	86.2	6	4	ABW48490	Abw48490 Antifibri	214	25	86.2	256	6	ABW68528	Abw68528 Phototrab
142	25	86.2	6	5	AAU96826	Aau96826 Amyloid t	215	25	86.2	281	7	ABO80453	AbO80453 Pseudomon
143	25	86.2	6	5	AAU96826	Aau96826 Amyloid t	216	25	86.2	282	1	AAU90422	Aau90422 Human phe
144	25	86.2	6	5	AAU11664	Aau11664 Peptide #	217	25	86.2	282	6	ABU09405	Abu09405 Human phe
145	25	86.2	6	5	AAU11656	Aau11656 Peptide #	218	25	86.2	282	8	ADH13186	Adh13186 Human mal
146	25	86.2	6	6	AAW35452	Aaw35452 Abeta pep	219	25	86.2	282	9	AEA15073	Aea15073 Human pol
147	25	86.2	6	8	ADQ37277	Adq37277 Vaccine a	220	25	86.2	282	9	AEA08357	Aea08357 Human phe
148	25	86.2	6	8	ADQ37321	Adq37321 Antifibri	221	25	86.2	285	4	AAW39174	Aaw39174 Human pol
149	25	86.2	6	9	ADQ37329	Adq37329 Antifibri	222	25	86.2	297	8	ADY25262	Ady25262 Plant ful
150	25	86.2	6	9	ADY37928	Ady37928 Amyloid-t	223	25	86.2	303	6	ABR40195	AbR40195 alpha-2,3
151	25	86.2	6	9	ADY37936	Ady37936 Amyloid-t	224	25	86.2	306	2	AAW38837	Aaw38837 Neisseria
152	25	86.2	22	8	ADQ09761	Adq09761 Rice 26kD	225	25	86.2	306	2	AAW38836	Aaw38836 Neisseria
153	25	86.2	22	8	ADY93984	Ady93984 Rice 26 k	226	25	86.2	306	4	AAW71923	Aaw71923 Human Olf
154	25	86.2	25	4	ABW03313	Abw03313 Human mus	227	25	86.2	306	9	ABW49486	Abw49486 N. mening
155	25	86.2	25	6	ABU12607	Abu12607 Novel hum	228	25	86.2	306	9	ABW49484	Abw49484 N. mening
156	25	86.2	28	8	ADJ28633	Adj28633 Human mus	229	25	86.2	307	9	ABW49488	Abw49488 N. gonorr
157	25	86.2	28	8	ADJ28633	Adj28633 Human mus	230	25	86.2	307	9	ABW49488	Abw49488 N. gonorr
158	25	86.2	34	7	ADW72404	Adw72404 Human end	231	25	86.2	309	5	ABW06659	Abw06659 G protein
159	25	86.2	37	3	AAW05910	Aaw05910 Mouse ind	232	25	86.2	314	5	AAU83579	Aau83579 Human nov
160	25	86.2	37	3	ADK34080	Adk34080 Human nNO	233	25	86.2	314	7	ADM29640	Adm29640 Novel hum
161	25	86.2	37	3	ADL70727	Adl70727 Mouse iNO	234	25	86.2	319	7	ABW87620	Abw87620 Rice abio
162	25	86.2	42	8	AGQ04347	Agq04347 Arabidops	235	25	86.2	322	5	ABW06657	Abw06657 G protein
163	25	86.2	50	3	AGQ04346	Agq04346 Arabidops	236	25	86.2	322	5	ABW06657	Abw06657 G protein
164	25	86.2	69	3	ABW05025	Abw05025 Human gen	237	25	86.2	322	5	ABW05597	Abw05597 Human GPC
165	25	86.2	69	3	AGW24897	Agw24897 Arabidops	238	25	86.2	322	5	AAU85262	Aau85262 G-coupled
166	25	86.2	77	3	ABG02840	Abg02840 Human sec	239	25	86.2	322	5	AAU85262	Aau85262 G-coupled
167	25	86.2	80	6	ABO00562	AbO00562 Novel hum	240	25	86.2	322	7	ADW85681	Adw85681 Human GPC
168	25	86.2	83	4	AAW92860	Aaw92860 Human dig	241	25	86.2	322	7	ADW85681	Adw85681 Human GPC
169	25	86.2	90	4	AAU47327	Aau47327 Propionib	242	25	86.2	332	5	ABW07514	Abw07514 Human Olf
170	25	86.2	105	4	AAW00117	Aaw00117 Human pol	243	25	86.2	332	8	ADS44454	Ads44454 Bacterial

KW	cytoprotection; amyloid deposit degradation; amyloidosis disorder; Alzheimer's disease.
KW	Homo sapiens.
OS	WO200068263-A2.
PN	16-NOV-2000.
XX	04-MAY-2000; 2000WO-CA000515.
XX	05-MAY-1999; 99US-0132592P.
XX	(NEUR-) NEUROCHEM INC.
XX	Chalifour R, Gervais F, Gupta A;
DR	WPI; 2001-031852/04.
XX	Antifibrillogenic agent useful for inhibiting amyloidosis and/or for cytoprotection for treating amyloidosis disorders, comprises a peptide, its isomer or peptidomimetic.
XX	Claim 7; Page 25; 46pp; English.
XX	Peptides AAB48474-B48496 are antifibrillogenic agents that can be used for inhibiting amyloidosis and/or for cytoprotection. The peptides of AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore useful for treating amyloidosis disorders such as Alzheimer's disease.
XX	Peptides AAB48474-B48496 were identified from the glycosaminoglycan binding region and the prot-prot interaction region of the human amyloid protein
SQ	Sequence 6 AA;
QV	Query Match 100.0%; Score 29; DB 4; Length 6;
DB	Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QV	1 KAVFFA 6
DB	1 KAVFFA 6
RESULT 2	
ID	AAB48488 standard; peptide; 6 AA.
XX	AAB48488;
XX	02-MAR-2001 (first entry)
XX	Antifibrillogenic peptide #15.
XX	Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition; cytoprotection; amyloid deposit degradation; amyloidosis disorder; Alzheimer's disease.
OS	Homo sapiens.
XX	Key Location/Qualifiers
FT	Modified-site 6
FT	/note= "C-terminal amide"
XX	WO200068263-A2.
XX	16-NOV-2000.
XX	04-MAY-2000; 2000WO-CA000515.
XX	05-MAY-1999; 99US-0132592P.
XX	(NEUR-) NEUROCHEM INC.

XX
PI Chalifour R, Gervais F, Gupta A;
XX WPI; 2001-031852/04.
DR
XX
XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
FT its isomer or peptidomimetic.
XX
XX Claim 7; Page 25; 46pp; English.
XX
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
Db |||||
1 KAVFFA 6
RESULT 3
ID AAB82636 standard; peptide; 6 AA.
XX
AC AAB82636;
XX
DT 02-OCT-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
KW therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "all D-form residues"
FT Modified-site 6 /note= "C-terminal amide"
FT
XX WO200139796-A2.
XX
XX 07-JUN-2001.
XX
XX 29-NOV-2000; 2000WO-CA001413.
XX
XX 29-NOV-1999; 99US-0168594P.
PR 28-NOV-2000; 2000US-00724842.
XX
XX (NEUR-) NEUROCHEM INC.
PA
XX Chalifour R, Hebert L, Kong X, Gervais F;
XX WPI; 2001-441458/47.
XX
XX Preventing/treating amyloid-related disease, especially Alzheimer's
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
PT which elicits production of antibodies to prevent fibrillogenesis and
PT associated cellular toxicity.
XX
XX Disclosure; Page 11; 3lpp; English.
PS
XX

CC The present sequence is that of an all-D peptide suitable for use in
CC preparing vaccines for preventing or treating Alzheimer's disease and
CC other amyloid related disorders in humans. It is based on a portion of
CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
CC inserting 1 or more amino acid residues, or by substituting 1 or more
CC amino acid residues with other amino acid residues or non-amino acid
CC fragments. Vaccines of the invention are produced using 'non-self'
CC peptides synthesised from the unnatural D-configuration amino acids to
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
CC aggregated to be operative or immunogenic. They preferably interact with
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
CC fragments, protein conjugates, immunogenic derivative peptides and
CC immunogenic peptidomimetics. Examples include all-D peptides
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
CC related diseases may be localised amyloidosis, e.g. diabetes type II,
CC neurodegenerative diseases, e.g. bovine spongiform encephalopathy,
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
CC prion protein related disorders, or systemic amyloidosis associated with
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
CC amyloidosis found in long-term haemodialysis patients
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
Db |||||
1 KAVFFA 6
RESULT 4
ID AAB82628 standard; peptide; 6 AA.
XX
AC AAB82628;
XX
DT 02-OCT-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
KW therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "all D-form residues"
FT
XX WO200139796-A2.
XX
XX 07-JUN-2001.
XX
XX 29-NOV-2000; 2000WO-CA001413.
XX
XX 29-NOV-1999; 99US-0168594P.
PR 28-NOV-2000; 2000US-00724842.
XX
XX (NEUR-) NEUROCHEM INC.
PA
XX Chalifour R, Hebert L, Kong X, Gervais F;
XX WPI; 2001-441458/47.
XX
XX Preventing/treating amyloid-related disease, especially Alzheimer's
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
PT

PT which elicits production of antibodies to prevent fibrillogenesis and
 XX associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AA882622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AA882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 Db 1 KAVFFPA 6

RESULT 5
 AAU96824
 ID AAU96824 standard; peptide; 6 AA.

XX

AC AAU96824;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #14.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1. .6

FT Modified-site 6 /note= "Preferably D-form residue"

FT /note= "Ala is amidated"

XX WO200207781-A2.

XX 31-JAN-2002.

XX

PF 25-JUL-2001; 2001WO-CA001071.
 XX
 PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 XX
 PA (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A t-(A 1 n k) z-A 1 a b (I) where z = 0 - 1;
 CC A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 Db 1 KAVFFPA 6

RESULT 6

AAU96816

ID AAU96816 standard; peptide; 6 AA.

XX

AC AAU96816;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #6.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX

```

FH Key Location/Qualifiers
FT Misc-difference 1..6
XX /note= "Preferably D-form residue"
XX WO200207781-A2.
XX 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
XX
XX 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A_t-(A_1)_n_k z-A_1 a_b (t) where z = 0 - 1;
XX A_t = an amyloid targeting moiety; A_1_n_k = a linker moiety; and A_1 a_b
XX = a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (I) to the patient, and ultrasound imaging (I) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (I), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidoses (transmissible virus dementias), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
DB 1 KAVFFFA 6
RESULT 7
AAU11662
ID AAU11662 standard; peptide; 6 AA.
XX
XX AAU11662;
XX
XX 09-APR-2002 (first entry)
XX
XX Peptide #15, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX Synthetic.
XX
XX WO200185093-A2.
XX
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
DB 1 KAVFFFA 6
RESULT 8
AAU11654
ID AAU11654 standard; peptide; 6 AA.
XX
XX AAU11654;
XX
XX 09-APR-2002 (first entry)
XX
XX Peptide #7, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX Synthetic.
XX
XX WO200185093-A2.
XX
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX

```


XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX PT WPI; 2002-075222/10.
 XX DR
 XX XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX PS Disclosure; Page 10; 68pp; English.
 XX XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX CC
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 |||||
 Db 1 KAVFFPA 6
 RESULT 9
 AAE35450
 ID AAE35450 standard; peptide; 6 AA.
 XX AC AAE35450;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #21.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX XX
 XX FH Key Location/Qualifiers
 FT Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT FT
 XX XX WO200296937-A2.
 XX XX
 XX PD 05-DEC-2002.
 XX XX
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX XX
 XX PR 29-MAY-2001; 2001US-00867847.
 XX XX
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX DR Prevention and/or treatment of an amyloid-related disease e.g.
 XX PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX PT
 XX XX Claim 1; Page 59; 44pp; English.
 XX XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX CC
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 |||||
 Db 1 KAVFFPA 6
 RESULT 10
 AAE35443
 ID AAE35443 standard; peptide; 6 AA.
 XX AC AAE35443;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #14.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX XX
 XX FH Key Location/Qualifiers
 FT Misc-difference 1. .6 /note= "D-form residues"
 FT FT
 XX XX WO200296937-A2.
 XX XX
 XX PD 05-DEC-2002.
 XX XX
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX XX
 XX PR 29-MAY-2001; 2001US-00867847.
 XX XX
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 PS Claim 1; Page 59; 44pp; English.
 XX
 CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an A-beta peptide used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 1 KAVFFA 6
 RESULT 11
 ADQ37275
 ID ADQ37275 standard; peptide; 6 AA.
 XX
 AC ADQ37275;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antihypertic; vasotropic; cardiovascular; tranquilliser; uteratic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT /note= "D-form residues"
 FT Modified-site 6
 FT /note= "amidated"

XX WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini F;
 WPI; 2004-543342/52.
 Composition for treating e.g. Alzheimer's disease comprises first agent
 that prevents or treats amyloid-beta related disease and second agent
 that is either a peptide or peptidomimetic or an immune system modulator.
 Disclosure; Page 67; 143pp; English.
 The present invention describes compositions (C) comprising: (a) a first
 agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 a second agent (a2) that is: (i) a peptide or peptidomimetic that
 modulates amyloid-beta fibril formation or induces a prophylactic or
 therapeutic immune response against amyloid-beta fibril formation; or
 (ii) an immune system modulator that prevents or inhibits amyloid-beta
 fibril formation. Also described is a kit comprising (C) (C) have
 nootropic, neuroprotective, cerebroprotective, haemostatic,
 ophthalmological, antihypertic, vasotropic, cardiovascular, tranquilliser,
 uteratic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 and can be used as amyloid-beta fibril formation modulators, and as
 immune system modulators. (C) can be used for preventing or treating an
 amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 mild-to-moderate cognitive impairment, vascular dementia, cerebral
 amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 Down's syndrome, inclusion body myositis, age-related macular
 degeneration, or a condition associated with Alzheimer's disease
 (including hypothyroidism, cerebrovascular disease, cardiovascular
 disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 aggression, or incontinence), a neurological condition (e.g. Huntington's
 disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 field deficits, incoordination, gait disturbance, transient ischaemic
 attack or stroke, transient alertness, attention deficit, frequent falls,
 syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 damage), or a psychological condition (e.g. depression, delusions,
 illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 excessive guilt)) in a subject e.g. human having a genomic mutation in an
 amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 having amyloid-beta deposits. The present sequence represents a peptide
 that can be used as a vaccine antigen in the exemplification of the
 present invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 1 KAVFFA 6
 RESULT 12

ADQ37267
 ID ADQ37267 standard; peptide; 6 AA.
 AC ADQ37267;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT /note= "D-form residues"
 XX
 PN WO2004058239-A1.
 XX
 PD 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 PR 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 PA Gervais P, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 67; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 DB 1 KAVFFPA 6

RESULT 13
 ADQ37319
 ID ADQ37319 standard; peptide; 6 AA.
 XX
 AC ADQ37319;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Antifibrillogenic amyloidosis inhibiting peptide.
 XX

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

Synthetic.

OS
 XX WO2004058239-A1.
 XX
 PD 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 PA Gervais P, Bellini F;
 PI WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent

PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 PS Disclosure; Page 69; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAVFFA 6

Db 1 KAVFFA 6

RESULT 14

ADQ37327

ID ADQ37327 standard; peptide; 6 AA.

XX ADQ37327;

AC ADQ37327;

DT 07-OCT-2004 (first entry)

DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
 XX amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.

Key Location/Qualifiers
 Modified-site 6 /note= "amidated"

WO2004058239-A1.

15-JUL-2004.

24-DEC-2003; 2003WO-CA002021.

24-DEC-2002; 2002US-0436379P.

23-JUN-2003; 2003US-0482214P.

(NEUR-) NEUROCHEM INT LTD.

Gervais F, Bellini F;

WPI; 2004-543342/52.

Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 70; 143pp; English.

CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.
XX
XX
SQ Sequence 6 AA;

Query Match	100.0%;	Score 29;	DB 9;	Length 6;
Best Local Similarity	100.0%;	Pred. No. 2e+06;		
Matches	6;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0

QY 1 KAVFFFA 6
| | | | |
DB 1 KAVFFFA 6

RESULT 16
ADY37926
ID ADY37926 standard; peptide; 6 AA.
XX
AC ADY37926;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:6, for use in imaging agent.
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
XX US2005048000-A1.
XX
XX 03-MAR-2005.
XX
XX 03-DEC-2003; 2003US-00728028.
XX
XX 25-JUL-2000; 2000US-0220808P.
XX
XX 24-JUL-2001; 2001US-00915092.
XX
XX 29-JAN-2003; 2003US-0443291P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX
XX WPI; 2005-212201/22.
XX
XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
XX related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
XX encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 6; 34pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent. The imaging
XX agent comprises an amyloid targeting moiety (such as a peptide) joined to
XX a labeling moiety via a linking moiety, and is preferably able to cross
XX the blood-brain barrier. The invention also relates to a kit for
XX preparing a radiopharmaceutical preparation from the imaging agent of the
XX invention, a method for imaging amyloid deposition in a patient and a
XX method for diagnosing an amyloid-related condition in a patient. The
XX amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
XX related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
XX transmissible cerebral amyloidoses (also known as transmissible virus
XX dementias), familial CJD, scrapie, transmissible mink encephalopathy,
XX bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
XX type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
XX non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
XX mediated diseases, dialysis-related amyloidosis, light chain-related
XX amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
XX patient. The agent does not exhibit excessive toxicity or irritation,
XX does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 1 KAVFFA 6

RESULT 17

AAB05909
 ID AAB05909 standard; peptide; 37 AA.

XX AC AAB05909;

XX 16-OCT-2000 (first entry)

DE Rat inducible nitric oxide synthase calmodulin-binding region.

XX Rat; inducible nitric oxide synthase; iNOS;
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
 KW AMP-activated protein kinase; AMPK; calmodulin; CaM;
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
 KW obstructive airways disease.

XX Rattus sp.

XX WO200028076-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-AU000968.

XX 06-NOV-1998; 98AU-00006976.

XX (SVIN-) ST VINCENTS INST MEDICAL RES.

XX Stapleton DI, Chen Z, Michell BU, Kemp BE, Mitchellhill KI;

XX WPI; 2000-376583/32.

XX Identifying modulators of AMP-activated protein kinase-mediated
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
 PT disease, comprises testing for the increase or decrease in
 PT phosphorylation of NOS.

XX Example 4; Fig 5; 41pp; English.

XX The present sequence is the calmodulin (CaM)-binding region of rat
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric
 CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease

XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 18

ADK34079
 ID ADK34079 standard; peptide; 37 AA.

XX AC ADK34079;

XX 20-MAY-2004 (first entry)

DE Mouse iNOS calmodulin binding domain peptide seqid 6.

XX vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;
 KW microvascular dysfunction; mouse; calmodulin binding domain;
 KW inducible nitric oxide; iNOS.

XX Mus musculus.

XX WO2004016761-A2.

XX 26-FEB-2004.

XX 15-AUG-2003; 2003WO-US025626.

XX 16-AUG-2002; 2002US-0403637P.

XX (SCHD) SCHERING AG.

XX Dole WP, Kauser K, Qian HS, Rubanyi G;

XX WPI; 2004-203789/19.

XX Treating critical limb ischemia (CLI), or angiogenesis comprises
 PT administering to a patient a polynucleotide encoding a mammalian
 PT endothelial nitric oxide synthase (eNOS) polypeptide.

XX Example 1; SEQ ID NO 6; 82pp; English.

XX The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a mouse inducible nitric synthase
 CC (iNOS) calmodulin binding domain peptide.

XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 19

ADL70726
 ID ADL70726 standard; peptide; 37 AA.

XX AC ADL70726;

XX 20-MAY-2004 (first entry)

XX DE Rat iNOS calmodulin-binding site amino acid sequence SEQ ID NO:6.
 XX rat; endothelial nitric oxide synthase; eNOS; enzyme; mutant;
 KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;
 KW antidiabetic; vulnary; antilipemic; anorectic;
 KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;
 KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;
 KW obesity; iNOS.
 XX Rattus rattus.
 XX WO2004016764-A2.
 XX 26-FEB-2004.
 XX 15-AUG-2003; 2003WO-US025745.
 XX 16-AUG-2002; 2002US-0403638P.
 XX (SCHD) SCHERING AG.
 XX Blasko E, Kauser K, Parkinson J;
 XX WPI; 2004-203792/19.
 XX New isolated endothelial nitric oxide synthase polypeptide mutant, useful
 PT for diagnosing or treating ischemia, atherosclerosis, hypertension,
 PT diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
 PT obesity.
 XX Example 1; SEQ ID NO 6; 57pp; English.

XX The present sequence represents the calmodulin-binding site of rat iNOS
 CC amino acid sequence. The present invention describes endothelial nitric
 CC oxide synthase (eNOS) mutants having one or more mutations in an amino
 CC acid sequence corresponding to a functional domain of a mammalian eNOS.
 CC At least one of the mutations is at a position corresponding to an amino
 CC acid residue in a calmodulin-binding domain that is phosphorylated in
 CC mammalian cells, and not an amino acid substitution to Ala or Asp. Also
 CC described: (1) an isolated eNOS polypeptide mutant that is substantially
 CC homologous, or has a 95-99% sequence identity to the amino acid sequence
 CC of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
 CC encoding the polypeptide mutant; (3) a recombinant vector comprising the
 CC polynucleotide operably linked to at least one regulatory sequence; (4) a
 CC pharmaceutical composition comprising the polypeptide mutant or the
 CC polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
 CC modulating eNOS activity in a cell by administering to the cell the
 CC polypeptide mutant; (7) modulating eNOS activity in a cell by
 CC administering the polypeptide mutant or the polynucleotide to the cell,
 CC such that the polypeptide mutant is expressed in the cell; (8) diagnosing
 CC a condition associated with aberrant eNOS activity by contacting a cell
 CC of a patient with the polynucleotide, and detecting a level of eNOS
 CC activity indicative of the medical condition; and (9) prophylactic and
 CC therapeutic methods of treating a condition associated with aberrant eNOS
 CC activity by administering the polypeptide mutant or polynucleotide to the
 CC patient. The eNOS mutant has vasotropic, antiarteriosclerotic,
 CC hypotensive, antidiabetic, vulnary, antilipemic and anorectic
 CC activities, and has reduced calcium dependence and increased activity.
 CC The polypeptide mutant, polynucleotide and methods are useful for
 CC diagnosing or treating a condition associated with aberrant eNOS
 CC activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
 CC Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.

XX Sequence 37 AA;
 Query Match 100.0%; Score 29; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 DB 18 KAVFFA 23

RESULT 20
 ADG17617
 ID ADG17617 standard; protein; 42 AA.
 XX AC ADG17617;
 XX DT 26-FEB-2004 (first entry)
 XX Modified amyloid beta precursor protein-related partial protein SeqID8.
 DE amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX OS Unidentified.
 XX WO2003102177-A1.
 XX 11-DEC-2003.
 XX 21-MAY-2003; 2003WO-JP006319.
 XX 31-MAY-2002; 2002JP-00159472.
 XX (SAXA) OTSUKA PHARM CO LTD.
 XX Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 XX WPI; 2004-053473/05.
 XX Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 PT for screening for treatments for Alzheimers disease.
 XX Claim 14; SEQ ID NO 8; 89pp; Japanese.
 CC This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX Sequence 42 AA;
 Query Match 100.0%; Score 29; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 18 KAVFFA 23
 RESULT 21
 ADG17612
 ID ADG17612 standard; protein; 42 AA.
 XX AC ADG17612;
 XX DT 26-FEB-2004 (first entry)
 XX Modified amyloid beta precursor protein-related partial protein SeqID3.
 DE amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX OS Unidentified.
 XX WO2003102177-A1.
 XX 11-DEC-2003.

PF 21-MAY-2003; 2003WO-JP006319.
 PR 31-MAY-2002; 2002JP-00159472.
 XX (SAKA) OTSUKA PHARM CO LTD.
 PA Shinabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 PI WPI; 2004-053473/05.
 DR Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 XX for screening for treatments for Alzheimers disease.
 PT Claim 13; SEQ ID NO 3; 89pp; Japanese.
 XX This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 29; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 18 KAVFFA 23
 RESULT 22
 AAW41091
 ID AAW41091 standard; protein; 74 AA.
 AC AAW41091;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Chicken matrix metalloproteinase chMMP-2 (aa445-518).
 XX
 KW Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.
 XX
 OS Gallus sp.
 XX
 PN WO9745137-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009158.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 XX
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA;
 XX
 DR WPI; 1998-032334/03.
 XX
 PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX
 PS Claim 2; Page 159-160; 234pp; English.
 XX
 CC This polypeptide comprises amino acid residues 445-518 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by

CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders
 CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity
 XX
 SQ Sequence 74 AA;
 Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 64 KAVFFA 69
 RESULT 23
 AAW41085
 ID AAW41085 standard; protein; 74 AA.
 XX
 AC AAW41085;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Human matrix metalloproteinase huMMP-2 (aa439-512).
 XX
 KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9745137-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009158.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 XX
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA;
 XX
 DR WPI; 1998-032334/03.
 XX
 PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX
 PS Claim 2; Page 153; 234pp; English.
 XX
 CC This polypeptide comprises amino acid residues 439-512 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification of huMMP-2 coding sequence and cloning
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein

CC with glutathione-S-transferase. The invention relates to the discovery
 CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
 CC fragments (see AAW41093-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce regression or to inhibit growth of
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular
 CC degeneration (all claimed). They can also be used to treat restenosis
 CC caused by migration of smooth muscle cells following angioplasty and to
 CC reduce blood supply to selected tissues (claimed). The new antagonists
 CC are highly selective for angiogenesis. Only new blood vessels express
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
 CC should be of low toxicity

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 24

AAW41230
 ID AAW41230 standard; protein; 74 AA.

AC AAW41230;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

KW Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.

OS Homo sapiens.

XX WO9745447-A1.

PD 04-DEC-1997.

PP 30-MAY-1997; 97WO-US009099.

PR 31-MAY-1996; 96US-0015859P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIpps RES INST.

XX Brooks P, Cheresch DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-512. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an

CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 25

ADT05998

ID ADT05998 standard; protein; 74 AA.

XX ADT05998;

DT 30-DEC-2004 (first-entry)

DE Modified chicken MMP-2 Y517C, residues 445-518.

XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloproteinase 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken;
 KW mutant; mutein; cyclic.

XX Gallus gallus.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 2..73

FT Misc-difference 73

FT /note= "Cys replaces wild-type Tyr. This residue
 corresponds to residue 517 of the mature MMP-2 protein"

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI) SCRIpps RES INST.

XX Brooks PC, Cheresch DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v
 CC beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX

PS Example 2; Page; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05998-ADT06001 represent C-terminal (hemopexin
CC domain) fragments of chicken matrix metalloprotease 2 (MMP-2, gelatinase)
CC containing the amino acid substitutions Y517C and/or W551C which are
CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used
CC in an example of the invention. Note: The present sequence is not shown
CC in the specification, but was derived from the wild-type chicken MMP-2 C-
CC terminal fragment ADT05971 and the information given on page 49.

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 64 KAVFFA 69

RESULT 26

ADT05965
ID ADT05965 standard; protein; 74 AA.

XX AC ADT05965;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloprotease (MMP-2) residues 439-512, SEQ ID NO:19.

XX KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cyostatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX OS Homo sapiens.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX

PS Example 1A; SEQ ID NO 19; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
CC receptor binding.

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 64 KAVFFA 69

RESULT 27

ADT05971
ID ADT05971 standard; protein; 74 AA.

XX AC ADT05971;

XX DT 30-DEC-2004 (first entry)

XX DE Chicken matrix metalloprotease (MMP-2) residues 445-518, SEQ ID NO:25.

XX KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cyostatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.

OS Gallus gallus.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

PS Example 1A; SEQ ID NO 25; 184pp; English.

CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to inhibit the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloproteinase 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 Db 64 KAVFFFA 69

RESULT 28

AAW41086
 ID AAW41086 standard; protein; 108 AA.

XX AC AAW41086;

DT 08-JUN-1998 (first entry)

XX Human matrix metalloproteinase hMMP-2 (aa439-546).

XX Matrix metalloproteinase; MMP-2; hMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.

OS Homo sapiens.

XX WO9745137-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresch DA;

XX WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page 154; 234pp; English.

XX This polypeptide comprises amino acid residues 439-546 of human mature
 CC matrix metalloproteinase 2 (hMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification of hMMP-2 coding sequence and cloning
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein
 CC with glutathione-S-transferase. The invention relates to the discovery

CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
 CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce regression or to inhibit growth of
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular
 CC degeneration (all claimed). They can also be used to treat restenosis
 CC caused by migration of smooth muscle cells following angioplasty and to
 CC reduce blood supply to selected tissues (claimed). The new antagonists
 CC are highly selective for angiogenesis. Only new blood vessels express
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
 CC should be of low toxicity

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||

Db 64 KAVFFFA 69

RESULT 29

AAW41092

ID AAW41092 standard; protein; 108 AA.

XX AC AAW41092;

XX 08-JUN-1998 (first entry)

XX Chicken matrix metalloproteinase chMMP-2 (aa445-552).

XX Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.

OS Gallus sp.

XX WO9745137-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresch DA;

XX WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page 160; 234pp; English.

XX This polypeptide comprises amino acid residues 445-552 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of

CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders
 CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 30

AAW41231
 ID AAW41231 standard; protein; 108 AA.

XX AC AAW41231;
 XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX KW Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 XX vitronectin receptor; inhibition; angiogenesis; tumour growth;
 XX restenosis; neovascularisation.

XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9745447-A1.
 XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.
 XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;
 XX WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, beta5
 XX integrin - used for inhibition of angiogenesis, and for treating tumours,
 XX inflammation, eye diseases etc.
 XX Claim 2; Page; 117pp; English.

XX CC Peptides AAW41228-33 are derived from the mature protein of human matrix
 XX metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 XX amino acids 439-546. The peptides are able to act as alpha-v-beta-5
 XX antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 XX alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 XX novel labelled package that contains an inhibitor of angiogenesis i.e. an
 XX alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 XX beta-5 and includes a part of the C-terminal domain of MMP-2. The
 XX antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 31

AAW41237
 ID AAW41237 standard; protein; 108 AA.

XX AC AAW41237;
 XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX KW Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 XX vitronectin receptor; inhibition; angiogenesis; tumour growth;
 XX restenosis; neovascularisation.

XX OS Synthetic.
 XX OS Gallus sp.

XX PN WO9745447-A1.
 XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.
 XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;
 XX WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, beta5
 XX integrin - used for inhibition of angiogenesis, and for treating tumours,
 XX inflammation, eye diseases etc.
 XX Claim 2; Page; 117pp; English.

XX CC Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
 XX 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
 XX acids 445-552. The peptides are able to act as alpha-v-beta-5
 XX antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 XX alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 XX novel labelled package that contains an inhibitor of angiogenesis i.e. an
 XX alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 XX beta-5 and includes a part of the C-terminal domain of MMP-2. The
 XX antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 XX tumours or metastases, and in a wide range of ocular disorders (e.g.
 XX diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 XX transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX
 SQ Sequence 108 AA;
 Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 90 KAVFFA 95

RESULT 32

ADT05972
 ID ADT05972 standard; protein; 108 AA.

XX
 AC ADT05972;

XX
 DT 30-DEC-2004 (first entry)

XX
 DE Chicken matrix metalloprotease (MMP-2) residues 445-552, SEQ ID NO:26.

XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.

XX
 OS Gallus gallus.

XX
 PN WO2004087057-A2.

XX
 PD 14-OCT-2004.

XX
 PF 26-MAR-2004; 2004WO-US009321.

XX
 PR 28-MAR-2003; 2003US-00402212.

XX
 PA (SCRI) SCRIPPS RES INST.

XX
 PI Brooks PC, Cheresh DA;

XX
 DR WPI; 2004-737508/72.

XX
 PT Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX
 PS Example 1A; SEQ ID NO 26; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to

CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 33

ADT05966
 ID ADT05966 standard; protein; 108 AA.

XX
 AC ADT05966;

XX
 DT 30-DEC-2004 (first entry)

XX
 DE Human matrix metalloprotease (MMP-2) residues 439-546, SEQ ID NO:20.

XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX
 OS Homo sapiens.

XX
 PN WO2004087057-A2.

XX
 PD 14-OCT-2004.

XX
 PF 26-MAR-2004; 2004WO-US009321.

XX
 PR 28-MAR-2003; 2003US-00402212.

XX
 PA (SCRI) SCRIPPS RES INST.

XX
 PI Brooks PC, Cheresh DA;

XX
 DR WPI; 2004-737508/72.

XX
 PT Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX
 PS Example 1A; SEQ ID NO 20; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

CC domain) fragments of human and chicken matrix metalloproteinase 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 34

ADT05999
 ID ADT05999 standard; protein; 108 AA.

AC ADT05999;

DT 30-DEC-2004 (first entry)

DE Modified chicken MMP-2 Y517C/W551C, residues 445-552.

XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytostatic; antiinflammatory; antiarthritic; antineumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloproteinase 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken;
 KW mutant; mutein.

XX Gallus gallus.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 73

FT /note= "Cys replaces wild-type Tyr. This residue
 corresponds to residue 517 of the mature MMP-2 protein"

FT Misc-difference 107

FT /note= "Cys replaces wild-type Trp. This residue
 corresponds to residue 551 of the mature MMP-2 protein"

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI) SCRIPPS RES INST.

XX Brooks PC, Cheresch DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v
 FT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX Example 2; Page; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression

CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05998-ADT06001 represent C-terminal (hemopexin
 CC domain) fragments of chicken matrix metalloproteinase 2 (MMP-2, gelatinase)
 CC containing the amino acid substitutions Y517C and/or W551C which are
 CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used
 CC in an example of the invention. Note: The present sequence is not shown
 CC in the specification, but was derived from the wild-type chicken MMP-2 C-
 CC terminal fragment ADT05971 and the information given on page 49.

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 35

AAW41238

ID AAW41238 standard; protein; 122 AA.

AC AAW41238;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

OS Synthetic.

XX Gallus sp.

XX WO9745447-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US0090999.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresch DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 FT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

PS Claim 2; Page; 117pp; English.

XX Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
 CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
 CC acids 516-637. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 122 AA;
 SQ

Query Match 100.0%; Score 29; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 Db 19 KAVFFPA 24

RESULT 36

AAW41232
 ID AAW41232 standard; protein; 152 AA.

AC AAW41232;
 DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.
 DE Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.
 OS Homo sapiens.

XX WO9745447-A1.
 PN 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.
 PF 31-MAY-1996; 96US-0015869P.
 PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresh DA, Friedlander M;
 PI WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, betas
 FT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 510-631. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 152 AA;
 SQ

Query Match 100.0%; Score 29; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 Db 23 KAVFFPA 28

RESULT 37

AAW41090
 ID AAW41090 standard; protein; 193 AA.

AC AAW41090;
 XX 08-JUN-1998 (first entry)

XX Chicken matrix metalloproteinase chMMP-2 (aa445-637).
 DE Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.

XX Gallus sp.
 OS WO9745137-A1.

XX 04-DEC-1997.
 PN 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.
 PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresh DA;
 PI WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, betas
 FT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page 158-159; 234pp; English.

XX This polypeptide comprises amino acid residues 445-637 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW1083-94) of human
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders

CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity

XX Sequence 193 AA;
 SQ
 Query Match 100.0%; Score 29; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 38
 AAW41084
 ID AAW41084 standard; protein; 193 AA.
 AC
 XX AAW41084;
 DT 08-JUN-1998 (first entry)
 DE Human matrix metalloproteinase huMMP-2 (aa439-631).
 KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.

OS Homo sapiens.
 PN WO9745137-A1.
 XX

PD 04-DEC-1997.

PF 30-MAY-1997; 97WO-US009158.

PR 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

PA Brooks P, Chereah DA;
 PI
 XX

DR WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

PS Claim 2; Page 152-153; 234pp; English.

XX This polypeptide comprises amino acid residues 439-631 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification (see AAV12510) of huMMP-2 coding
 CC sequence and cloning into e.g. pGEX-3X vector for expression in E. coli
 CC as a glutathione-S-transferase fusion protein. The invention relates to
 CC the discovery that angiogenesis is mediated by the specific vitronectin
 CC receptor alpha-v beta-3, and that inhibition of alpha-v beta-3 function
 CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-
 CC terminal fragments (see AAW41083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce tumour regression or inhibit growth
 CC of tumours; and in ocular disorders such as diabetic retinopathy or
 CC macular degeneration (all claimed). They can also be used to treat
 CC restenosis caused by migration of smooth muscle cells following

CC angioplasty and to reduce blood supply to selected tissues (claimed). The
 CC new antagonists are highly selective for angiogenesis. Only new blood
 CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the
 CC antagonists should be of low toxicity

XX Sequence 193 AA;
 SQ

Query Match 100.0%; Score 29; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 39
 AAW41229
 ID AAW41229 standard; protein; 193 AA.

AC AAW41229;

XX 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

OS Synthetic.

OS Homo sapiens.

XX WO9745447-A1.

PN 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

PR 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Chereah DA, Friedlander M;
 PI
 XX

DR WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

PS Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-631. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using

CC Information provided

XX Sequence 193 AA;

SQ Query Match 100.0%; Score 29; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 40

AAW41235 ID AAW41235 standard; protein; 193 AA.

XX AC AAW41235;

XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;

XX KW vitronectin receptor; inhibition; angiogenesis; tumour growth;

XX KW restenosis; neovascularisation.

XX OS Synthetic.

XX OS Gallus sp.

XX PN WQ9745447-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;

XX DR WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, betas

XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,

XX PT inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX CC Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-

XX CC 2 (MMP-2) protein (AAW41237). The present peptide is derived from amino

XX CC acids 445-637. The peptides are able to act as alpha-v-beta-5

XX CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of

XX CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a

XX CC novel labelled package that contains an inhibitor of angiogenesis i.e. an

XX CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-

XX CC beta-5 and includes a part of the C-terminal domain of MMP-2. The

XX CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

XX CC tumours or metastases, and in a wide range of ocular disorders (e.g.

XX CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal

XX CC transplants). They are particularly used to induce regression or to

XX CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX CC used to treat restenosis caused by migration of smooth muscle cells

XX CC following angioplasty and to reduce blood supply to selected tissues. The

XX CC antagonists particularly inhibit neovascularisation where this is induced

XX CC by cytokines, e.g. transforming growth factor alpha, epidermal growth

XX CC factor or especially vascular endothelial growth factor. note: this

XX CC sequence does not appear in the specification; it was created using

XX CC information provided

XX SQ Sequence 193 AA;

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 193;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 90 KAVFFA 95

RESULT 41

ADT05964 ID ADT05964 standard; protein; 193 AA.

XX AC ADT05964;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloprotease (MMP-2) residues 439-631, SEQ ID NO:18.

XX KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;

XX KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;

XX KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;

XX KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;

XX KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;

XX KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;

XX KW peptidomimetic; matrix metalloprotease 2; MMP-2; Gelatinase;

XX KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX OS Homo sapiens.

XX PN WQ2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v

XX PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue

XX PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX PS Example 1A; SEQ ID NO 18; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue

XX CC by the administration of a composition comprising an organic

XX CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin

XX CC receptor). The integrin alpha-v beta-3 antagonist and compositions

XX CC containing it are useful for inhibiting angiogenesis in a variety of

XX CC medical conditions. The antagonist may be used to induce the regression

XX CC of solid tumours or solid tumour metastases; to inhibit the growth of

XX CC solid tumours undergoing neovascularisation; to treat inflamed tissue in

XX CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to

XX CC treat neovascularisation in retinal tissue (e.g., in diabetic

XX CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle

XX CC cell migration (such as that which occurs following angioplasty); and to

XX CC reduce the blood supply to a tissue required to support new growth of the

XX CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

XX CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,

XX CC gelatinase) used in an example of the invention in assays of inhibition

XX CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-

XX CC receptor binding.

XX SQ Sequence 193 AA;

Query Match

100.0%; Score 29; DB 8; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KAVFFA 6
|||||
Db 64 KAVFFA 69

RESULT 42
ADT05970
ID ADT05970 standard; protein; 193 AA.

XX AC ADT05970;
XX DT 30-DEC-2004 (first entry)
XX DE Chicken matrix metalloproteinase (MMP-2) residues 445-637, SEQ ID NO:24.
XX KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytosatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.
XX OS Gallus gallus.
XX PF WO2004087057-A2.
XX PN 14-OCT-2004.
XX PD 26-MAR-2004; 2004WO-US009321.
XX PR 28-MAR-2003; 2003US-00402212.
XX PS (SCRI) SCRIPPS RES INST.
XX PI Brooks PC, Cheresh DA;
XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX PS Example 1A; SEQ ID NO 24; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
CC receptor binding.

XX SQ Sequence 193 AA;
Query Match 100.0%; Score 29; DB 8; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0;
Matches 6; Conservative 0;

QY 1 KAVFFA 6
|||||
Db 64 KAVFFA 69

RESULT 43
AAW41083
ID AAW41083 standard; protein; 222 AA.

XX AC AAW41083;
XX DT 08-JUN-1998 (first entry)
XX DE Human matrix metalloproteinase huMMP-2 (aa410-631).
XX KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
KW macular degeneration; restenosis; therapy.
XX OS Homo sapiens.
XX PN WO9745137-A1.
XX PD 04-DEC-1997.
XX PF 30-MAY-1997; 97WO-US009158.
XX PR 31-MAY-1996; 96US-0015869P.
XX PR 31-MAY-1996; 96US-0018733P.
XX PA (SCRI) SCRIPPS RES INST.
XX PI Brooks P, Cheresh DA;
XX DR WPI; 1998-032334/03.

XX PT Packaging material containing polypeptide antagonist of alphav, beta3
PT integrin - used for inhibition of angiogenesis, and for treating tumours,
PT inflammation, eye diseases etc.

XX PS Claim 2; Page 150-151; 234pp; English.

XX CC This polypeptide comprises amino acid residues 410-631 of human mature
CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
CC methods such as PCR amplification of huMMP-2 coding sequence and cloning
CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein
CC with glutathione-S-transferase. The invention relates to the discovery
CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion
CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
CC derivatised polypeptides, a monoclonal antibody or organic mimetic
CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
CC or metastases, particularly to induce regression or to inhibit growth of
CC tumours; and in ocular disorders such as diabetic retinopathy or macular
CC degeneration (all claimed). They can also be used to treat restenosis
CC caused by migration of smooth muscle cells following angioplasty and to
CC reduce blood supply to selected tissues (claimed). The new antagonists
CC are highly selective for angiogenesis. Only new blood vessels express
CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
CC should be of low toxicity

XX SQ Sequence 222 AA;

Query Match 100.0%; Score 29; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0;
Matches 6; Conservative 0;

QY 1 KAVFFA 6

Db 93 KAVFFA 98

RESULT 44
AAW41228
ID AAW41228 standard; protein; 222 AA.

XX AC
XX DT 09-JUN-1998 (first entry)
XX DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
XX KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
XX KW restenosis; neovascularisation.

OS Synthetic.
OS Homo sapiens.

XX WO9745447-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;

XX DR WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, beta5
XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,
XX PT inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX CC Peptides AAW41228-33 are derived from the mature protein of human matrix
XX CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from
XX CC amino acids 410-631. The peptides are able to act as alpha-v-beta-5
XX CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
XX CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
XX CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
XX CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
XX CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
XX CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
XX CC tumours or metastases, and in a wide range of ocular disorders (e.g.
XX CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
XX CC transplants). They are particularly used to induce regression or to
XX CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
XX CC used to treat restenosis caused by migration of smooth muscle cells
XX CC following angioplasty and to reduce blood supply to selected tissues. The
XX CC antagonists particularly inhibit neovascularisation where this is induced
XX CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
XX CC factor or especially vascular endothelial growth factor. note: this
XX CC information does not appear in the specification; it was created using
XX CC information provided

XX SQ Sequence 222 AA;

Query Match 100.0%; Score 29; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 93 KAVFFA 98

RESULT 45
ADT05963
ID ADT05963 standard; protein; 222 AA.

XX AC ADT05963;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloprotease (MMP-2) residues 410-631, SEQ ID NO:17.

XX KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
XX KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
XX KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
XX KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
XX KW cystostatic; antiinflammatory; antiarthritic; antineumatic;
XX KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
XX KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
XX KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX OS Homo sapiens.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v
XX PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
XX PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX PS Example 1A; SEQ ID NO 17; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue
XX CC by the administration of a composition comprising an organic
XX CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
XX CC receptor). The integrin alpha-v beta-3 antagonist and compositions
XX CC containing it are useful for inhibiting angiogenesis in a variety of
XX CC medical conditions. The antagonist may be used to induce the regression
XX CC of solid tumours or solid tumour metastases; to inhibit the growth of
XX CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
XX CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
XX CC treat neovascularisation in retinal tissue (e.g., in diabetic
XX CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
XX CC cell migration (such as that which occurs following angioplasty); and to
XX CC reduce the blood supply to a tissue required to support new growth of the
XX CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
XX CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
XX CC gelatinase) used in an example of the invention in assays of inhibition
XX CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
XX CC receptor binding.

XX SQ Sequence 222 AA;

Query Match 100.0%; Score 29; DB 8; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 93 KAVFFA 98

RESULT-46

```

AAW41089
ID AAW41089 standard; protein; 228 AA.
XX AC AAW41089;
XX DT 08-JUN-1998 (first entry)
XX DE
XX DE Chicken matrix metalloproteinase chMMP-2 (aa410-637).
XX DE Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
XX KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
XX KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
XX KW diabetic retinopathy; macular degeneration; restenosis; therapy.
XX OS Gallus sp.
XX PN WO9745137-A1.
XX PD 04-DEC-1997.
XX PF 30-MAY-1997; 97WO-US009158.
XX PR 31-MAY-1996; 96US-0015869P.
XX PR 31-MAY-1996; 96US-0018733P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Brooks P, Cheres DA;
XX PI WPI; 1998-032334/03.
XX DR
XX DR Packaging material containing polypeptide antagonist of alphav, beta3
XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,
XX PT inflammation, eye diseases etc.
XX PS Claim 2; Page 157-158; 234pp; English.
XX CC This polypeptide comprises amino acid residues 410-637 of chicken mature
XX CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
XX CC recombinant methods such as PCR amplification (see AAV12501) of chMMP-2
XX CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
XX CC expression in E. coli as a fusion protein with glutathione-S-transferase.
XX CC The invention relates to the discovery that angiogenesis is mediated by
XX CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
XX CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
XX CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
XX CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
XX CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
XX CC organic mimetic compound. The antagonists are used to inhibit
XX CC angiogenesis in: inflamed tissue for treatment of arthritis or
XX CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
XX CC tumour regression or inhibit growth of tumours; and in ocular disorders
XX CC such as diabetic retinopathy or macular degeneration (all claimed). They
XX CC can also be used to treat restenosis caused by migration of smooth muscle
XX CC cells following angioplasty and to reduce blood supply to selected
XX CC tissues (claimed). The new antagonists are highly selective for
XX CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
XX CC vessels are unaffected, and the antagonists should be of low toxicity
XX SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 99 KAVFFA 104
RESULT 47
AAW41234
ID AAW41234 standard; protein; 228 AA.
XX AC AAW41234;
XX DT 09-JUN-1998 (first entry)
XX DE
XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.
XX DE Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
XX KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
XX KW restenosis; neovascularisation.
XX OS Synthetic.
XX OS Gallus sp.
XX PN WO9745447-A1.
XX PD 04-DEC-1997.
XX PF 30-MAY-1997; 97WO-US009099.
XX PR 31-MAY-1996; 96US-0015869P.
XX PR 31-MAY-1996; 96US-0018733P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Brooks P, Cheres DA, Friedlander M;
XX PI WPI; 1998-041758/04.
XX DR
XX DR Packaging material containing polypeptide antagonist of alphav, beta5
XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,
XX PT inflammation, eye diseases etc.
XX PS Claim 2; Page; 117pp; English.
XX CC Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
XX CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
XX CC acids 410-637. The peptides are able to act as alpha-v-beta-5
XX CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
XX CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
XX CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
XX CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
XX CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
XX CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
XX CC tumours or metastases, and in a wide range of ocular disorders (e.g.
XX CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
XX CC transplants). They are particularly used to induce regression or to
XX CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
XX CC used to treat restenosis caused by migration of smooth muscle cells
XX CC following angioplasty and to reduce blood supply to selected tissues. The
XX CC antagonists particularly inhibit neovascularisation where this is induced
XX CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
XX CC factor or especially vascular endothelial growth factor. note: this
XX CC sequence does not appear in the specification; it was created using
XX CC information provided
XX SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 125 KAVFFA 130
RESULT 48
ADT05969
ID ADT05969 standard; protein; 228 AA.
XX AC ADT05969;
XX XX

```

DT 30-DEC-2004 (first entry)
 XX
 DE Chicken matrix metalloprotease (MMP-2) residues 410-637, SEQ ID NO:23.
 KW
 XX
 KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytostatic; anti-inflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; Gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.
 XX
 OS Gallus gallus.
 XX
 XX WO2004087057-A2.
 PN
 XX
 XX 14-OCT-2004.
 PD
 XX
 XX 26-MAR-2004; 2004WO-US009321.
 PF
 XX
 XX 28-MAR-2003; 2003US-00402212.
 PR
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Brooks FC, Cheresch DA;
 PI
 XX
 XX WPI; 2004-737508/72.
 DR
 XX
 XX Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
 XX
 XX Example 1A; SEQ ID NO 23; 184pp; English.
 PS
 XX
 CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
 CC receptor). The integrin alpha-V beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
 CC receptor binding.
 XX
 XX Sequence 228 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 228;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVEFA 6
 |||||
 Db 99 KAVEFA 104
 RESULT 49
 ADT05661
 ID ADT05661 standard; protein; 261 AA.
 XX
 XX ADT05661;
 AC
 XX 02-DEC-2004 (first entry)
 DT
 XX

DE Haemophilus influenzae (NTHi) protein - SEQ ID 697.
 XX
 KW middle ear bacterial infection; nasopharynx bacterial infection.
 XX
 OS Haemophilus influenzae.
 XX
 XX WO2004078949-A2.
 PN
 XX 16-SEP-2004.
 PD
 XX 05-MAR-2004; 2004WO-US007001.
 PF
 XX 06-MAR-2003; 2003US-0453134P.
 PR
 XX (CHIL-) CHILDRENS HOSPITAL INC.
 PA
 XX Bakaletz LO, Munson RS, Dyer DW;
 PI
 XX WPI; 2004-662422/64.
 DR
 XX N-PSDB; ADT05660.
 XX
 XX New polynucleotides of nontypeable strain of Haemophilus influenzae,
 PT useful for treating or preventing NTHi bacterial infections of the middle
 PT ear and/or nasopharynx.
 XX
 XX Claim 3; SEQ ID NO 697; 88pp; English.
 PS
 XX
 CC The invention comprises nucleotide sequences (genes) from the genome of a
 CC nontypeable strain of Haemophilus influenzae (NTHi). The NTHi DNA
 CC sequences of the invention are useful for treating or preventing NTHi
 CC bacterial infections of the middle ear and/or nasopharynx. The present
 CC amino acid sequence represents an NTHi protein of the invention.
 XX
 XX Sequence 261 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 261;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVEFA 6
 |||||
 Db 205 KAVEFA 210
 RESULT 50
 AAW41112
 ID AAW41112 standard; protein; 429 AA.
 XX
 XX AAW41112;
 AC
 XX 08-JUN-1998 (first entry)
 DT
 XX Human matrix metalloproteinase huMMP-2 (aa203-631).
 DE
 XX Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.
 XX
 XX Homo sapiens.
 OS
 XX WO9745137-A1.
 PN
 XX 04-DEC-1997.
 PD
 XX 30-MAY-1997; 97WO-US009158.
 PF
 XX 31-MAY-1996; 96US-0015869P.
 PR
 XX 31-MAY-1996; 96US-0018733P.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Brooks P, Cheresch DA;
 PI

XX
DR WPI; 1998-032334/03.
XX
PT Packaging material containing polypeptide antagonist of alphav, beta3
PT integrin - used for inhibition of angiogenesis, and for treating tumours,
PT inflammation, eye diseases etc.
XX
PS Example 4; Page 177-179; 234pp; English.
XX
CC This polypeptide comprises amino acid residues 203-631 of human mature
CC matrix metalloproteinase 2 (hMMP-2). It was produced by recombinant
CC methods involving PCR amplification (see AAV12509) of hMMP-2 coding
CC sequence and cloning into e.g. pGEX-lambda vector for expression in E.
CC coli as a glutathione-S-transferase fusion protein. The invention relates
CC to the discovery that angiogenesis is mediated by the specific
CC vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v beta-
CC 3 function inhibits angiogenesis. Claimed antagonists of alpha-v beta-3
CC comprise C-terminal fragments (see AAW1083-94) of human or chicken MMP-
CC 2, fusion polypeptides, cyclic or linear polypeptides (see also AAW41098-
CC 110), derivatised polypeptides, a monoclonal antibody or organic mimetic
CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
CC or metastases, particularly to induce tumour regression or inhibit growth
CC of tumours; and in ocular disorders such as diabetic retinopathy or
CC macular degeneration (all claimed). They can also be used to treat
CC restenosis caused by migration of smooth muscle cells following
CC angioplasty and to reduce blood supply to selected tissues (claimed). The
CC new antagonists are highly selective for angiogenesis. Only new blood
CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the
CC antagonists should be of low toxicity
XX
SQ Sequence 429 AA;
Query Match 100.0%; Score 29; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
Db 300 KAVFFA 305
|||||
RESULT 51
ADT05991
ID ADT05991 standard; protein; 429 AA.
XX
AC ADT05991;
XX
DT 30-DEC-2004 (first entry)
DE Human matrix metalloprotease (MMP-2) residues 203-631, SEQ ID NO:45.
XX
KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmologic; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; progelatinase; human;
KW C-terminal fragment; glutathione-S-transferase; GST fusion protein.
XX
OS Homo sapiens.
XX
PN WO2004087057-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009321.
XX
PR 28-MAR-2003; 2003US-00402212.
XX
PA (Scripps) Scripps Res Inst.
XX

PI Brooks PC, Cheresch DA;
XX
DR WPI; 2004-737508/72.
XX
PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX
PS Example 2; SEQ ID NO 45; 184pp; English.
XX
CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
CC receptor). The integrin alpha-v beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. The present sequence represents residues 203-631 of human MMP-2
CC which is a component of a glutathione-S-transferase (GST)/MMP-2 fusion
CC protein produced in an example of the invention.
XX
SQ Sequence 429 AA;
Query Match 100.0%; Score 29; DB 8; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
Db 300 KAVFFA 305
|||||
RESULT 52
ABG24001
ID ABG24001 standard; protein; 468 AA.
XX
AC ABG24001;
XX
DT 18-FEB-2002 (first entry)
DE Novel human diagnostic protein #23992.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS88188.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 54360; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activities. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AEG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 468 AA;

Query Match 100.0%; Score 29; DB 4; Length 468;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||

DB 361 KAVFFPA 366

RESULT 53

ABM84057

ID ABM84057 standard; protein; 623 AA.

XX

AC ABM84057;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human diagnostic and therapeutic pproteins SEQ ID NO:4306.

XX

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX

OS Homo sapiens.

XX

PN WO2004023973-A2.

XX

PD 25-MAR-2004.

XX

PF 12-SEP-2003; 2003WO-US028227.

XX

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX

PA (INCY-) INCYTE CORP.

XX

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve JL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Patury S, Shi X, Suarez CJ;

XX

PI WPI; 2004-329368/30.

DR N-PSDB; ACN42709.

XX

XX

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

PT Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 623 AA;

Query Match 100.0%; Score 29; DB 8; Length 623;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||

DB 494 KAVFFPA 499

RESULT 54

ADG17622

ID ADG17622 standard; protein; 626 AA.

XX

AC ADG17622;

XX

DT 26-FEB-2004 (first entry)

XX

DE Modified amyloid beta precursor protein-related fusion protein SeqID13.

XX

KW amyloid beta precursor protein; APP; beta-selectase cleavage; alpha-selectase cleavage; Alzheimer's disease; dementia.

XX

OS Unidentified.

XX

PN WO2003102177-A1.

XX

PD 11-DEC-2003.

XX

PF 21-MAY-2003; 2003WO-JP006319.

XX

PR 31-MAY-2002; 2002JP-00159472.

XX

PA (SAKA) OTSUKA PHARM CO LTD.

XX

PI Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;

XX

DR WPI; 2004-053473/05.

XX

PT Amyloid beta precursor protein cleaved by beta- but not alpha-selectase for screening for treatments for Alzheimers disease.

PT Claim 15; SEQ ID NO 13; 89pp; Japanese.

XX This invention relates to a novel modified amyloid beta precursor protein (APP) which contains a beta-selectase cleavage site and a modification which prevents cleavage by alpha-selectase. The invention may be useful for screening for, treating and preventing Alzheimer's disease and

CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX
 SQ Sequence 626 AA;

Query Match 100.0%; Score 29; DB 8; Length 626;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 543 KAVFFA 548

RESULT 55
 ADG17627
 ID ADG17627 standard; protein; 626 AA.
 XX
 AC ADG17627;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Modified amyloid beta precursor protein-related fusion protein SeqID18.
 XX
 KW amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX
 OS Unidentified.
 XX
 PN WO2003102177-A1.
 XX
 PD 11-DEC-2003.
 XX
 PF 21-MAY-2003; 2003WO-JP006319.
 XX
 PR 31-MAY-2002; 2002JP-00159472.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 PI Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 XX
 DR WPI; 2004-053473/05.
 XX
 PT Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 PT for screening for treatments for Alzheimers disease.
 XX
 PS Claim 16; SEQ ID NO 18; 89pp; Japanese.
 XX

CC This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX
 SQ Sequence 626 AA;

Query Match 100.0%; Score 29; DB 8; Length 626;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 543 KAVFFA 548

RESULT 56
 AAP96143
 ID AAP96143 standard; protein; 631 AA.
 XX
 AC AAP96143;
 XX
 DT 25-MAR-2003 (revised)

DT 09-MAY-1991 (first entry)
 XX
 DE Sequence of human type IV collagenase (gelatinase) in pGEL 186.2.
 XX
 KW Hypertrophic scar; keloid; intervertebral disc disease; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN GB2209526-A.
 XX
 PD 17-MAY-1989.
 XX
 PF 02-SEP-1988; 88GB-00820803.
 XX
 PR 04-SEP-1987; 87US-00093421.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Eisen AZ, Goldberg GI;
 XX
 DR WPI; 1989-147011/20.
 DR N-PSDB; AAN91700.
 XX
 PT DNA encoding human type IV collagenase (gelatinase) - for use in the
 PT treatment of hypertrophic scars, keloids and intervertebral disc disease.
 XX
 PS Disclosure; Fig 3; 36pp; English.
 XX

CC The original source of the protein material was H-ras transformed human
 CC bronchial epithelial cells (TBE-1). The AA sequence was then used to
 CC develop oligonucleotide probes which were used to screen a cDNA library
 CC of human skin fibroblast mRNA. The longest clone, pGEL 186.2, represented
 CC almost the full gelatinase mRNA sequence except the leader sequence
 CC encoding the first few AA's of the signal peptide. (Updated on 25-MAR-
 CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 502 KAVFFA 507

RESULT 57
 AAP91139
 ID AAP91139 standard; protein; 631 AA.
 XX
 AC AAP91139;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-DEC-1989 (first entry)
 XX
 XX Human type IV collagenase (gelatinase).
 DE
 XX Human type IV collagenase; gelatinase; hypertrophic scars; keloids;
 KW intervertebral disc disease; extracellular matrix metalloprotease;
 KW bronchial epithelial cells; TBE-1 cells; pGel186.2; type II motif;
 KW fibonectin; collagen-binding domain.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH Domain 1..192
 FT Domain 193..367
 FT Duplication 197..254
 FT Duplication 255..312
 FT Duplication 313..368
 FT Domain 368..631

XX GB2209526-A.
 PN 17-MAY-1989.
 XX 02-SEP-1988; 88GB-00820803.
 XX 04-SEP-1987; 87US-00093421.
 PR (UNIW) UNIV WASHINGTON.
 PA Eisen AZ, Goldberg GI;
 XX WPI; 1989-147011/20.
 XX DNA encoding human type IV collagenase (gelatinase) - for use in the
 PT treatment of hypertrophic scars, keloids and intervertebral disc disease.
 PT Claim 2; Fig 6; 36pp; English.
 PS Human type IV collagenase (gelatinase). Protein source was H-ras
 XX transformed human bronchial epithelial cells (TBE-1). The sequence was
 CC determined from clone pGel 186.2 which represents almost the full mRNA
 CC sequence. Feature 1 is the N-terminal domain. I; feature 2 is a middle
 CC domain, II, which is organised into 3 x 58 amino acid long head to tail
 CC repeats (features 4,5, and 6). These show homology to the type II motif
 CC collagen binding domain of fibronectin. Feature 3 is the C-terminal
 CC domain. The enzyme could be used in the treatment of hypertrophic scars,
 CC keloids, and intervertebral disc disease. See also AAN91700. (Updated on
 CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

Qy 1 KAVFFA 6
 |||||
 Db 502 KAVFFA 507

RESULT 58
 AAR07969
 ID AAR07969 standard; protein; 631 AA.

XX AAR07969;
 XX 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 16-JAN-1991 (first entry)
 XX Complete type IV collagenase.

XX Type IV collagenase; peptide fragments; metalloproteinase detection;
 KW antibodies; metalloproteinase inhibition; angiogenesis; arthritis;
 KW tumour growth; metastasis; granulomatous inflammatory conditions;
 KW sarcoidosis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..18
 FT Peptide /label= 1
 FT Peptide 19..33
 FT Peptide /label= 2
 FT Peptide 26..42
 FT Peptide /label= 3
 FT Protein 34..50
 FT Peptide /label= 4
 FT Peptide 51..66
 FT Peptide /label= 5

FT Peptide 67..89
 FT Peptide /label= 7
 FT Peptide 67..80
 FT Peptide /label= 6
 FT Peptide 69..75
 FT Peptide /label= 8
 FT Peptide 75..94
 FT Peptide /label= 9
 FT Peptide 141..150
 FT Peptide /label= 10
 FT Peptide 299..307
 FT Peptide /label= 11
 FT Peptide 308..318
 FT Peptide /label= 12
 FT Peptide 344..368
 FT Peptide /label= 13
 FT Peptide 371..386
 FT Peptide /label= 14
 FT Peptide 372..375
 FT Peptide /label= 15
 FT Peptide 472..491
 FT Peptide /label= 16

USN7317407-N.

21-AUG-1990.

01-MAR-1989; 89US-00317407.

01-MAR-1989; 89US-00317407.

(USSH) US NAT CANCER INST.

(USDC) US SEC OF COMMERCE.

Liotta LA, Stetlerste W, Krutzsch H;

WPI; 1990-290093/38.

New type-IV collagenase peptide fragments - used for metallo-proteinase
 detection and inhibition and for producing antibodies for enzyme
 detection.

Disclosure; Fig 1; -pp; English.

Type IV procollagenase was purified from human A2058 melanoma cells. The
 complete amino acid sequence was determined (see also Hoyhtya, M. et al,
 (1988) FEBS Letters 233, 109-113). Based on this sequence, peptides were
 synthesised (see features) having homology with a histidine contg. domain
 at residues 371-386, a cysteine contg. domain at residues 200-370, the 80
 residue amino terminus or a region 159 residues from the carboxy
 terminus. These regions correspond to the domain of the enzyme involved
 in enzyme activation and interaction of the enzyme with the substrate.
 The peptides are useful in metalloproteinase detection and inhibition.
 They can be used in the treatment of inappropriate angiogenesis,
 arthritis, tumour growth, invasion and metastasis and granulomatous
 inflammatory conditions such as sarcoidosis. The peptides can be used to
 produce antibodies. Peptide 6, at concn. of 0.1 mM inhibited 80% of the
 enzyme activity. See also US7494796-A and WO9010228. (Note: Revised entry
 submitted to correct the patent number format of US Government-owned NTIS
 applications to prevent clashes with ongoing US granted patent numbers.
 For further information please visit the Derwent web site at
 www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
 correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

Sequence 631 AA;

Query Match 100.0%; Score 29; DB 2; Length 631;

Best Local Similarity 100.0%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

Qy 1 KAVFFA 6

|||||
 Db 502 KAVFFA 507

```

RESULT 59
AAW07350
ID AAW07350 standard; protein; 631 AA.
XX
AC AAW07350;
XX
XX 25-MAR-2003 (revised)
DT 16-JUL-1999 (first entry)
XX
XX Human type IV matrix metalloprotease protein.
XX
XX Matrix metalloprotease; inhibitor; tissue damage; angiogenesis; antibody;
KW arthritis; tumour growth; granulomatous inflammatory condition; enzyme;
KW metastasis; sarcoidosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 452
FT /note= "designated in specification as U"
XX
XX WO9010228-A.
XX
XX 07-SEP-1990.
XX
XX 01-MAR-1989; 89US-00317407.
XX
XX 01-MAR-1989; 89US-00317407.
XX
XX 26-FEB-1990; 90US-00488460.
XX
XX (USDC ) US SEC OF COMMERCE.
XX
XX (USSH ) NAT INST OF HEALTH.
XX
XX Liotta LA, Stetlerste W, Krutzsch H;
XX
XX WPI; 1990-290458/38.
XX
XX Matrix metalloproteinase peptide(s) - used to inhibit enzyme in treating
XX tissue damage caused by activated enzyme.
XX
XX Disclosure; Fig 1; 61pp; English.
XX
XX This sequence represents a human type IV matrix metalloprotease (MMP)
XX zymogen (precursor protein). The invention relates to MMP inhibitor
XX peptides which can be used to treat tissue damage caused by activated
XX MMPs, e.g. for treating inappropriate angiogenesis, arthritis, tumour
XX growth, invasion and metastasis and granulomatous inflammatory conditions
XX such as sarcoidosis. Antibodies to the peptides can be used to detect the
XX MMPs and can distinguish activated from latent enzyme. (Updated on 25-MAR
XX -2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 631 AA;
XX
XX Query Match 100.0%; Score 29; DB 2; Length 631;
XX Best Local Similarity 100.0%; Pred. No. 6.8e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KAVFFA 6
XX |||||
XX 502 KAVFFA 507
XX
XX RESULT 60
XX AAW41226
XX ID AAW41226 standard; protein; 631 AA.
XX
XX AAW41226;
XX
XX 09-JUN-1998 (first entry)
XX

```

```

DE Human mature matrix metalloprotease-2 (MMP-2) protein sequence.
XX
XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
KW vitronectin receptor; inhibition; angiogenesis; integrin; tumour growth;
KW restenosis; neovascularisation.
XX
XX Homo sapiens.
XX
XX WO9745447-A1.
XX
XX 04-DEC-1997.
XX
XX 30-MAY-1997; 97WO-US009099.
XX
XX 31-MAY-1996; 96US-0015869P.
XX
XX 31-MAY-1996; 96US-0018733P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Brooks P, Cheresch DA, Friedlander M;
XX
XX WPI; 1998-041758/04.
XX
XX Packaging material containing polypeptide antagonist of alphav, beta5
XX integrin - used for inhibition of angiogenesis, and for treating tumours,
XX inflammation, eye diseases etc.
XX
XX Disclosure; Fig 16; 117pp; English.
XX
XX The present sequence represents the mature protein of human matrix
XX metalloprotease-2 (MMP-2). Fragments of this protein (AAW41228-33) are
XX able to act as alpha-v-beta-5 antagonists. Alpha-v-beta-5 is a
XX vitronectin receptor. Inhibitors of alpha-v-beta-5 can inhibit
XX angiogenesis. The specification describes a novel labelled package that
XX contains an inhibitor of angiogenesis i.e. an alpha-v-beta-5 antagonising
XX polypeptide that binds to integrin alpha-v-beta-5 and includes a part of
XX the C-terminal domain of MMP. The antagonists are used to inhibit
XX angiogenesis in inflamed tissue, in solid tumours or metastases, and in a
XX wide range of ocular disorders (e.g. diabetic or other forms of
XX retinopathy, neovascular glaucoma, or corneal transplants). They are
XX particularly used to induce regression or to inhibit growth of tumours.
XX The alpha-v-beta-5 antagonists can also be used to treat restenosis
XX caused by migration of smooth muscle cells following angioplasty and to
XX reduce blood supply to selected tissues. The antagonists particularly
XX inhibit neovascularisation where this is induced by cytokines, e.g.
XX transforming growth factor alpha, epidermal growth factor or especially
XX vascular endothelial growth factor
XX
XX Sequence 631 AA;
XX
XX Query Match 100.0%; Score 29; DB 2; Length 631;
XX Best Local Similarity 100.0%; Pred. No. 6.8e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KAVFFA 6
XX |||||
XX 502 KAVFFA 507
XX
XX RESULT 61
XX ADM48668
XX ID ADM48668 standard; protein; 631 AA.
XX
XX AC ADM48668;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human matrix metalloproteinase-2 (MMP-2) protein.
XX
XX Cancer; metastasis; matrix metalloproteinase-2; MMP-2; vaccine;
KW immune response; gene therapy; cytostatic; enzyme; human.
XX
XX Homo sapiens.
XX

```

XX US2003139345-A1.
 XX 24-JUL-2003.
 XX 23-JAN-2003; 2003US-00350258.
 XX 23-JAN-2002; 2002US-035117P.
 XX (NETK/) NETKE S.
 XX (NIED/) NIEDZWIECKI A.
 XX (RATH/) RATH M.
 XX Netke S, Niedzwiecki A, Rath M;
 XX WPI; 2003-897356/82.
 XX New synthetic oligopeptide, useful for blocking or treating cancer
 XX invasion and metastases in a human patient, particularly as a vaccine for
 XX treating or preventing diagnosing brain cancer, lung cancer, skin cancer
 XX or breast cancer.
 XX Example 1; Fig 1; 11pp; English.
 XX The present invention relates to novel synthetic oligopeptides effective
 XX in blocking cancer invasion and metastasis. The invention relates to
 XX matrix metalloproteinase-2 (MMP-2) peptides. The synthetic oligopeptides
 XX are useful as pharmaceutical compositions for blocking or treating cancer
 XX invasion and metastases in a human patient. In particular, they are
 XX useful for treating brain cancer, lung cancer, skin cancer or breast
 XX cancer. The oligopeptides are also useful as vaccines for preventing
 XX these cancers, enhancing immune response or raising antibodies for assays
 XX used to diagnose diseases involving matrix metalloproteinases or clinical
 XX monitoring of the progression or regression of disease. They are also
 XX useful in gene therapy. The present sequence is the human MMP-2 protein.
 XX Sequence 631 AA;
 SQ Query Match 100.0%; Score 29; DB 7; Length 631;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 502 KAVFFA 507

RESULT 62
 ADT05996
 ID ADT05996 standard; protein; 631 AA.
 XX AC ADT05996;
 XX 30-DEC-2004 (first entry)
 XX Human mature matrix metalloprotease (MMP-2).
 XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
 XX vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 XX inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 XX restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 XX cytostatic; antiinflammatory; antiarthritic; antirheumatic;
 XX ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 XX peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase; human;
 XX enzyme.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX Region 410..631
 XX Domain /note= "Corresponds to SEQ ID NO:17"
 XX /label = Hemopexin_domain

FT FT Region /note = Corresponds to SEQ ID NO:18
 FT FT 439..546
 FT FT /note= "Corresponds to SEQ ID NO:20"
 FT FT 439..512
 FT FT /note= "Corresponds to SEQ ID NO:19"
 FT FT 510..631
 FT FT /note= "Corresponds to SEQ ID NO:21"
 FT FT 543..631
 FT FT /note= "Corresponds to SEQ ID NO:22"
 XX WO2004087057-A2.
 XX 14-OCT-2004.
 XX 26-MAR-2004; 2004WO-US009321.
 XX 28-MAR-2003; 2003US-00402212.
 XX (SCRI) SCRIPPS RES INST.
 XX Brooks PC, Chereesh DA;
 XX WPI; 2004-737508/72.
 XX Administration of composition comprising organic peptidomimetic alpha-v
 XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
 XX Example 2; Fig 7A-C; 184pp; English.
 XX The invention relates to a method of inhibiting angiogenesis in a tissue
 XX by the administration of a composition comprising an organic
 XX peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
 XX receptor). The integrin alpha-V beta-3 antagonist and compositions
 XX containing it are useful for inhibiting angiogenesis in a variety of
 XX medical conditions. The antagonist may be used to induce the regression
 XX of solid tumours or solid tumour metastases; to inhibit the growth of
 XX solid tumours undergoing neovascularisation; to treat inflamed tissue in
 XX which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 XX treat neovascularisation in retinal tissue (e.g., in diabetic
 XX retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 XX cell migration (such as that which occurs following angioplasty); and to
 XX reduce the blood supply to a tissue required to support new growth of the
 XX tissue. The present sequence represents human mature matrix
 XX metalloprotease 2 (MMP-2, gelatinase) used in an example of the
 XX invention.
 XX Sequence 631 AA;
 SQ Query Match 100.0%; Score 29; DB 8; Length 631;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 502 KAVFFA 507

RESULT 63
 ADT05997
 ID ADT05997 standard; protein; 633 AA.
 XX AC ADT05997;
 XX 30-DEC-2004 (first entry)
 XX Mouse mature matrix metalloprotease (MMP-2).
 XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
 XX vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 XX inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 XX restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 XX cytostatic; antiinflammatory; antiarthritic; antirheumatic;

KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase; mouse;
 KW murine; enzyme.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 441..633
 FT /label = Hemopexin_domain
 XX
 XX WO2004087057-A2.
 XX
 XX PD 14-OCT-2004.
 XX
 XX PF 26-MAR-2004; 2004WO-US009321.
 XX
 XX PR 28-MAR-2003; 2003US-00402212.
 XX
 XX PA (SCRI) SCHRIPS RES INST.
 XX
 XX PI Brooks PC, Cheresch DA;
 XX
 XX WPI; 2004-737508/72.
 XX
 XX Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
 XX
 XX Example 2; Fig 7A-C; 184pp; English.
 XX
 CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
 CC receptor). The integrin alpha-V beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. The present sequence represents mouse mature matrix
 CC metalloprotease 2 (MMP-2, gelatinase) used in an example of the
 CC invention.
 XX
 SQ Sequence 633 AA;
 Query Match 100.0%; Score 29; DB 8; Length 633;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 504 KAVFFA 509
 |||||
 RESULT 64
 AAB20490
 ID AAB20490 standard; protein; 644 AA.
 XX
 AC AAB20490;
 XX
 XX 21-JUN-2001 (first entry)
 DT
 DE Human matrix metalloproteinase-2 (MMP-2).
 XX
 KW Matrix metalloproteinase-2; MMP-2; human; pain; analgesic;
 KW nerve tissue damage; stroke; haemorrhage; reperfusion injury;
 KW cerebral ischaemia; cerebral infarction; narcotic tolerance;
 KW narcotic withdrawal.
 XX

OS Homo sapiens.
 XX WO200126671-A1.
 XX
 XX PD 19-APR-2001.
 XX
 XX PF 11-OCT-2000; 2000WO-US027949.
 XX
 XX PR 12-OCT-1999; 99US-0158787P.
 XX
 XX PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX PI Romanic Arnold A, Barone FC, Bingham S;
 XX
 XX WPI; 2001-290654/30.
 XX N-PSDB; AAF30807.
 XX
 PT Polypeptide for the treatment of pain and the reduction of tissue damage
 PT comprises an inhibitor of human matrix metalloproteinase.
 XX
 XX PS Claim 1; Fig 2; 61pp; English.
 XX
 CC The present sequence is that of human matrix metalloproteinase-2 (MMP-2),
 CC previously known as 72 kDa gelatinase and gelatinase A. MMP-2 is capable
 CC of degrading the extracellular matrix components of the basement
 CC membrane. The invention relates to methods for treating pain in a patient
 CC by administering a dual inhibitor of MMP-2 and MMP-9 (see AAB20491). The
 CC administration of an inhibitor of MMP-2 is useful for treating nerve
 CC tissue damage (claimed), where the patient is suffering from a disease or
 CC disorder selected from stroke, haemorrhage, reperfusion injury, cerebral
 CC ischaemia and cerebral infarction (claimed). The method is useful for
 CC treating a disease, disorder or nerve tissue damage selected from
 CC enhanced or exaggerated sensitivity to acute pain, burn pain, atypical
 CC facial pain, neuropathic pain, back pain, complex regional pain syndrome
 CC I and II, arthritic pain, sports injury pain, pain related to virus
 CC infection, post-herpetic neuralgia, phantom limb pain, labour pain,
 CC cancer pain, post-chemotherapy pain, post-operative pain, post-stroke
 CC pain, physiological pain, inflammatory pain, acute inflammatory
 CC conditions/visceral pain, neuralgia, painful diabetic retinopathy,
 CC traumatic nerve injury, and tolerance to narcotics or withdrawal from
 CC narcotics (claimed). MMP-2 polypeptides can also be used to screen for
 CC agonist or antagonist (inhibitor) compounds
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 29; DB 4; Length 644;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 515 KAVFFA 520
 |||||
 RESULT 65
 AAR06420
 ID AAR06420 standard; protein; 660 AA.
 XX
 AC AAR06420;
 XX
 XX 25-MAR-2003 (revised)
 DT 13-DEC-1990 (first entry)
 DT
 XX Type IV collagenase cDNA product.
 XX
 XX hypertrophic scars; keloids; intervertebral disc disease; ds.
 XX Homo sapiens.
 XX US4923818-A.
 XX 08-MAY-1990.
 PD

XX PF 15-MAY-1989; 89US-00352069.
 XX XX
 XX PR 15-MAY-1989; 89US-00352069.
 XX PA (UNIW) UNIV WASHINGTON.
 XX XX
 XX PI Goldberg GL, Eisen AZ;
 XX XX
 XX DR N-PSDB; AAQ05620.
 XX DR WPI; 1990-245482/32.
 XX XX
 XX PT Recombinant human type IV collagenase - used in treatment of hypertrophic
 PT scars, keloids and intervertebral disc disease.
 XX PS Claim 3; Fig 9; 23pp; English.
 XX CC cDNA clone enables production of type IV collagenase, useful in
 CC catalysing cleavage of extracellular matrix macromolecules, and in
 CC treatment of hypertrophic scars, keloids and intervertebral disc disease.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX
 XX SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 |||||
 Db 531 KAVFFFA 536
 RESULT 66
 AAB84607
 ID AAB84607 standard; protein; 660 AA.
 XX AC AAB84607;
 XX XX
 XX DT 05-SEP-2001 (first entry)
 XX XX
 XX DE Amino acid sequence of matrix metalloproteinase gelatinase A.
 XX KW Growth factor; protein inhibitor; protease; damaged tissue;
 KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
 KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
 KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
 KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
 KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
 KW vascular endothelial growth factor; urokinase plasminogen activator;
 KW dermal ulcer; wound.
 XX OS Homo sapiens.
 XX XX
 XX PN WO200149309-A2.
 XX XX
 XX PD 12-JUL-2001.
 XX XX
 XX PF 21-DEC-2000; 2000WO-IB001935.
 XX XX
 XX PR 29-DEC-1999; 99GB-00030768.
 XX XX
 XX PA (PFIZ) PFIZER LTD.
 XX PA (PFIZ) PFIZER INC.
 XX XX
 XX PI Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
 XX XX
 XX DR WPI; 2001-418351/44.
 XX DR N-PSDB; AAH28222.
 XX XX
 XX PT Composition for the treatment of damaged tissue i.e. chronic wounds and
 PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
 PT factor.

XX PS Disclosure; Page 552; 572pp; English.
 XX XX
 XX CC The specification describes a pharmaceutical composition, comprising a
 CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
 CC inhibits the action of at least one specific adverse protein, i.e. a
 CC protease, that is upregulated in a damaged tissue such as a wound
 CC environment. Growth factors which are included in the composition of the
 CC invention are platelet-derived growth factor (PDGF), fibroblast growth
 CC factor (FGF), connective tissue derived growth factor (CTGF),
 CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
 CC (TGF-beta), granulocyte macrophage colony stimulating growth factor (GM-CSF),
 CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
 CC and chrysalin. Inhibitors which are included in the composition of the
 CC invention include inhibitors of urokinase-type plasminogen activator
 CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
 CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
 CC The present sequence represents a human MMP-2, and is used to produce the
 CC composition of the invention
 XX SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 4; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 |||||
 Db 531 KAVFFFA 536
 RESULT 67
 AAE10431
 ID AAE10431 standard; protein; 660 AA.
 XX AC AAE10431;
 XX XX
 XX DT 10-DEC-2001 (first entry)
 XX XX
 XX DE Human matrix metalloproteinase-2 (MMP-2) protein.
 XX KW Human; matrix metalloproteinase; MMP-2; hair growth; antisense therapy;
 KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..27 /label= Signal_peptide
 FT Protein 28..660 /label= Mature_MMP_2_protein
 FT Domain 100..106 /label= Cysteine_switch_domain
 FT Domain 171..195 /note= "Zinc and calcium binding domain"
 XX PN WO200166766-A2.
 XX XX
 XX PD 13-SEP-2001.
 XX XX
 XX PF 06-MAR-2001; 2001WO-US007167.
 XX XX
 XX PR 06-MAR-2000; 2000US-0187196P.
 XX XX
 XX PA (DARW-) DARWIN MOLECULAR CORP.
 XX PA (SCHA/) SCHATZMAN R.
 XX XX
 XX PI Fajardo M, Wang K, Smith R, Moss P;
 XX XX
 XX DR WPI; 2001-582276/65.
 XX XX
 XX PT Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
 PT proteins encoded by them whose inhibition is useful for modulation of

PT hair growth in mammals.
 XX
 XX Example 2; Fig 3; 119pp; English.
 XX
 CC The present sequence is human matrix metalloproteinase (MMP)-2 protein
 CC used in the exemplification of the inventions. MMP-25 DNA is located on
 CC chromosome 11q22. Matrix metalloproteinases are a family of zinc
 CC dependent endopeptidases that function extracellularly to degrade
 CC proteins typically found in the extracellular matrix. MMP-25 is expressed
 CC in skin cells of mammals, particularly in breast cells and hair
 CC follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
 CC encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
 CC sample and identifying a sequence that hybridises in the nucleic acid
 CC sample. The identification step involves performing polymerase chain
 CC reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
 CC useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
 CC to modulate hair growth and breast cancer in a mammal
 XX
 SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 4; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 531 KAVFFA 536
 |||||
 |||||
 RESULT 68
 ABB79413
 ID ABB79413 standard; protein; 660 AA.
 XX
 AC ABB79413;
 XX
 DT 08-JUL-2002 (first entry)
 XX
 DE Human matrix metalloproteinase 2 protein.
 XX
 KW Human; matrix metalloproteinase-2; MMP-2; enzyme; thrombolytic;
 KW anticoagulant; cardiant; antiarteriosclerotic; cytostatic; osteopathic;
 KW antiinflammatory; antibacterial; virucide; fungicide; antipsoriatic;
 KW vulnerary; cerebroprotective; antianginal; ophthalmological;
 KW antirheumatic; antiarthritic; antitumor; vasotropic; nephrotropic;
 KW alpha-v-beta-3 integrin receptor; thrombosis; tumour; osteoporosis;
 KW infection; veterinary medicine; rheumatoid arthritis; Crohn's disease;
 KW antimicrobial; antiseptic.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Domain 466..660
 FT /label= PEX
 FT Binding-site 489..497
 FT /label= alpha-v-beta-3_integrin_receptor_binding_site
 FT Binding-site 570..585
 FT /label= alpha-v-beta-3_integrin_receptor_binding_site
 FT Binding-site 588..597
 FT /label= alpha-v-beta-3_integrin_receptor_binding_site
 XX
 PN WO200220566-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 28-AUG-2001; 2001WO-EP009899.
 XX
 PR 07-SEP-2000; 2000DE-01044325.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Jonczyk A, Diefenbach B, Groth U, Zischinsky G;
 XX
 DR WPI; 2002-329868/36.

XX New matrix metalloprotease-2 derivative peptides, are alpha-v-beta-3
 PT integrin receptor inhibitors useful e.g. for treating thrombosis, cardiac
 PT infarction, tumors, osteoporosis, inflammation or infections.
 XX
 XX Disclosure; Page 11; 35pp; German.
 PS
 XX The invention relates to peptides (ABB79414-ABB79426) derived from the C-
 CC terminal fragment PXX of matrix metalloprotease-2 (MMP-2). Matrix MMP-2
 CC derivatives of formula X-Y-Z (I) and their salts and solvates are
 CC described. X = H, 1-10C alkanoyl or peptide fragment consisting of 1-20
 CC naturally occurring amino acid residues; Y = peptide fragment consisting of 1-20
 CC from the sequence region 466-660 of human Pro-MMP-2; and Z = OH, NH 2, NH
 CC -1-10C alkyl N(1-10C alkyl) 2 or peptide fragment consisting of 1-20
 CC naturally occurring amino acid residues. Primary amino groups are
 CC optionally protected conventionally. The peptides and MMP-2 derivatives
 CC are used for combating diseases involving interaction of ligands
 CC (specifically MMP-2) with the alpha-v-beta-3 integrin receptor,
 CC especially pathological processes supported or propagated by
 CC angiogenesis, thrombosis, cardiac infarction, coronary heart disease,
 CC arteriosclerosis, tumours, osteoporosis, fibrosis, inflammation,
 CC infections, psoriasis or wound healing deficiency. More generally the
 CC peptides and MMP-2 derivatives are useful in human and veterinary
 CC medicine for the treatment and/or prophylaxis of thrombosis, myocardial
 CC infarction, apoplexy, angina pectoris, tumour diseases, osteolytic
 CC diseases (e.g. osteoporosis or hypercalcaemia), pathological angiogenic
 CC diseases (e.g. inflammation), ophthalmological diseases (e.g. diabetic
 CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or
 CC rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
 CC colitis, Crohn's disease, atherosclerosis, psoriasis, restenosis after
 CC angioplasty, viral, bacterial or fungal infections, acute renal failure
 CC or wound healing deficiency; as antimicrobial/antiseptic agents in
 CC operations involving biomaterials, implants, catheters or cardiac
 CC pacemakers; or as diagnostic agents or reagents. The present sequence is
 CC that of the human MMP-2 protein
 XX
 SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 5; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 531 KAVFFA 536
 |||||
 |||||
 RESULT 69
 ABB90738
 ID ABB90738 standard; protein; 660 AA.
 XX
 AC ABB90738;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 208.
 XX
 KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.
 XX
 OS Homo sapiens.
 XX
 XX WO200210217-A2.
 PN
 XX 07-FEB-2002.
 PD
 XX 01-AUG-2001; 2001WO-US024031.
 PF
 XX 02-AUG-2000; 2000US-0222599P.
 PR
 PR 11-AUG-2000; 2000US-0224360P.

PR 11-APR-2001; 2001US-0282850P.
XX (UYJO) UNIV JOHNS HOPKINS.
PA St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
XX N-PSDB; ABL92092.
XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Claim 54; Page 166-168; 331pp; English.
XX The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neovascularization in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 660 AA;
Query Match 100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFPA 6
Db 531 KAVFFPA 536
RESULT 70
AAU84348
ID AAU84348 standard; protein; 660 AA.
XX
AC AAU84348;
XX
DT 08-MAY-2002 (first entry)
XX Protein MMP2 differentially expressed in breast cancer tissue.
XX Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
XX MAI; mitotic activity index; cytostatic.
XX
XX Homo sapiens.
XX WO200210436-A2.
XX
XX 07-FEB-2002.
XX
XX 27-JUL-2001; 2001WO-US023642.
XX
XX 28-JUL-2000; 2000US-0222093P.
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX (BAAK/) BAAK J.
XX Baak J, Mutter GL;
XX WPI; 2002-180084/23.
XX N-PSDB; ABK35568.
XX
XX Diagnosing breast cancer comprises determining expression of nucleic acid
PT molecules or expression products that are differentially expressed in

PT normal and malignant tissue.
XX Claim 37; Page 185-187; 219pp; English.
XX The present invention relates to a method for diagnosing breast cancer in
CC a subject suspected of having endometrial cancer. The method comprises
CC determining the expression of a set of human genes or expression products
CC in an endometrial sample suspected of being cancerous. The human genes of
CC the invention are differentially expressed in breast tumours
CC characterised as high or low MAI (mitotic activity index). These sets of
CC genes can be used to discriminate between high and low MAI breast
CC tumours. The invention also provides DNA and protein microarrays for
CC analysing the expression of the human genes and their protein products.
CC The methods and arrays are useful for the diagnosis and prognosis of
CC endometrial cancer, selecting and monitoring treatment regimes, and
CC identification of compounds useful for the treatment of endometrial
CC cancer. AAU84311-AAU84361 represent the human proteins of the invention
CC that are differentially expressed in breast cancer tissue
XX
SQ Sequence 660 AA;
Query Match 100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFPA 6
Db 531 KAVFFPA 536
RESULT 71
ABU54445
ID ABU54445 standard; protein; 660 AA.
XX
AC ABU54445;
XX
DT 12-MAR-2003 (first entry)
XX
XX Human tumour endothelial marker TEM 7.
XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
XX Tumour endothelial marker; normal endothelial marker; PEM;
XX pan-endothelial marker; polycystic kidney disease; psoriasis;
XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
XX neovascularization; immune response; cytostatic; antidiabetic;
XX ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
XX
XX Homo sapiens.
XX WO200283874-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US008253.
XX
XX 11-APR-2001; 2001US-0282850P.
XX 06-FEB-2002; 2002US-0354262P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2003-093016/08.
XX N-PSDB; ABX72017.
XX
XX New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors, or
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX
XX Disclosure; Page 173-174; 374pp; English.
XX The present invention relates to a novel method for the isolation of
CC

Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.

Example 1; Page 43-44; 103pp; English.

The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnervary, cardiant, cerebroprotective, antidiabetic, ophthalmological and dermatological activities. (I) can be used for inhibiting expression of VEGF, and so can be used for inhibiting growth of tumours and diminishing tumours size. The tumour can be

The invention comprises a crystalline form of a polypeptide corresponding to the catalytic domain of matrix metalloproteinase 9 (MMP9) protein - a gelatinase. The crystalline polypeptide of the invention is useful for treating a metalloproteinase mediated disease or condition in a warm-blooded animal. The crystalline polypeptide is also useful for determining the three-dimensional structure of the MMP9 catalytic domain to high resolution. The three-dimensional structure of the MMP9 catalytic domain is useful for rational drug design, and the atomic coordinates of the catalytic domain of MMP9 are useful for selecting or designing chemical modulators (preferably inhibitors) of MMP9. The crystalline polypeptide of the invention is useful in the treatment of a metalloproteinase mediated disease or condition, such as: tumour growth; metastasis in cancer; arthritis; osteoarthritis; atherosclerosis;

CC restenosis; periodontitis; multiple sclerosis; glomerulonephritis; graft-versus-host disease; and non-insulin dependent diabetes. The present amino acid sequence represents a human matrix metalloproteinase 2 (MMP2)

XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 74
ABG76322
ID ABG76322 standard; protein; 660 AA.

XX AC ABG76322;

XX 10-MAY-2003 (first entry)

XX Human matrix metalloproteinase-2 (MMP-2).

XX Human; peptide inhibitor; matrix metalloproteinase-2; MMP-2; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

XX WO2003016520-A1.

XX 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix metalloproteinases, e.g. matrix metalloproteinase-2, useful for stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Example 1; Page 41-42; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPs. The peptide inhibitors are useful for stimulating cellular proliferation of fibroblasts or keratinocytes, promoting healthy skin tone, development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for stimulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. The present sequence represents human MMP-2

XX Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 75
ADD18578
ID ADD18578 standard; protein; 660 AA.

XX AC ADD18578;

XX 15-JAN-2004 (first entry)

XX Human disease related protein SeqID9.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological; antiarteriosclerotic; vulnerary; gene therapy; angiogenesis; apoptosis; hypoxia-regulated condition; tumorigenesis; glycolysis; gluconeogenesis; inflammation; erythropoiesis; catecholamine synthesis; iron transport; glucose transport; cancer; ischaemic condition; reperfusion injury; nitric oxide synthesis; cancer; pre-eclampsia; atherosclerosis; retinopathy; neonatal stress; wound healing.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX N-PSDB; ADD18579.

XX New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.

XX Claim 25; SEQ ID NO 9; 424pp; English.

XX This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, the ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.

XX Sequence 660 AA;

Query Match 100.0%; Score 29; DB 7; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

Search completed: December 29, 2005, 17:33:40
Job time : 82.7742 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-12
Perfect score: 31
Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	47	2 Q8Q9Y9_FUGRU	Q8Q9Y9_fugu rubrip
2	31	100.0	229	2 Q6RS99_TRTTU	Q6RS99_triticum tu
3	31	100.0	241	2 Q7XYC3_WHEAT	Q7XYC3_triticum ae
4	31	100.0	331	2 Q6K5X9_ORYSA	Q6K5X9_oryza sativ
5	31	100.0	331	2 Q84N87_ORYSA	Q84N87_oryza sativ
6	31	100.0	335	2 Q6I5W9_ORYSA	Q6I5W9_oryza sativ
7	31	100.0	353	2 Q4HQ66_CAMUP	Q4HQ66_campylobact
8	31	100.0	519	2 Q5ATG9_EMENI	Q5ATG9_aspergillus
9	31	100.0	935	2 Q7XM01_ORYSA	Q7XM01_oryza sativ
10	31	100.0	3044	2 Q7QYR7_GIALA	Q7QYR7_giardia lam
11	30	96.8	224	2 Q84NG7_HORVU	Q84NG7_hordeum vul
12	30	96.8	395	2 Q98GC2_RHILO	Q98GC2_triticum l
13	30	96.8	397	2 Q2Y1Y6_RHIME	Q2Y1Y6_rhizobium m
14	30	96.8	2643	2 Q5A3W3_CANAL	Q5A3W3_candida alb
15	30	96.8	2643	2 Q5A3Q1_CANAL	Q5A3Q1_candida alb
16	28	90.3	23	2 Q4XK85_PLACH	Q4XK85_plasmodium
17	28	90.3	43	2 Q73M63_TREDE	Q73M63_treponema d
18	28	90.3	49	2 Q8KAX7_BACHD	Q8KAX7_bacillus ha
19	28	90.3	150	2 Q7R979_PLAYO	Q7R979_plasmodium
20	28	90.3	152	2 Q4J122_AZOVI	Q4J122_azotobacter
21	28	90.3	177	2 Q20070_CAEEL	Q20070_caenorhabdi
22	28	90.3	199	2 Q6LSA9_PHOPR	Q6LSA9_photobacter
23	28	90.3	225	2 Q6UJY8_TFITU	Q6UJY8_triticum tu
24	28	90.3	226	2 Q8LKV8_AEGTA	Q8LKV8_eglilops ta
25	28	90.3	241	2 Q7R8V4_PLAYO	Q7R8V4_plasmodium
26	28	90.3	242	2 Q7RA05_PLAYO	Q7RA05_plasmodium
27	28	90.3	250	2 Q7RNP5_PLAYO	Q7RNP5_plasmodium
28	28	90.3	251	2 Q7PDC0_PLAYO	Q7PDC0_plasmodium
29	28	90.3	251	2 Q7RPS1_PLAYO	Q7RPS1_plasmodium
30	28	90.3	252	2 Q7RAS7_PLAYO	Q7RAS7_plasmodium
31	28	90.3	252	2 Q7RF37_PLAYO	Q7RF37_plasmodium

32	28	90.3	255	2	Q7RLK2_PLAYO	Q7RLK2_plasmodium
33	28	90.3	262	2	Q7RCL4_PLAYO	Q7RCL4_plasmodium
34	28	90.3	265	2	Q7RC37_PLAYO	Q7RC37_plasmodium
35	28	90.3	268	2	Q7RB86_PLAYO	Q7RB86_plasmodium
36	28	90.3	285	2	Q529U4_MAGGR	Q529U4_magnaporthe
37	28	90.3	293	2	Q94284_CAEEL	Q94284_caenorhabdi
38	28	90.3	294	2	Q7RBUI_PLAYO	Q7RBUI_plasmodium
39	28	90.3	300	2	Q5UWP7_HALMA	Q5UWP7_haloarcula
40	28	90.3	321	2	Q7RBJ3_PLAYO	Q7RBJ3_plasmodium
41	28	90.3	326	2	F74429_SYN3C	F74429_synchocyst
42	28	90.3	380	2	Q6KI05_MYCMA	Q6KI05_mycoplasma
43	28	90.3	388	2	Q4MSJ5_BACCE	Q4MSJ5_bacillus ce
44	28	90.3	388	2	Q6HLH8_BACHK	Q6HLH8_bacillus th
45	28	90.3	388	2	Q73BD3_BACCI	Q73BD3_bacillus ce
46	28	90.3	388	2	Q63E03_BACCC	Q63E03_bacillus ce
47	28	90.3	388	2	Q8IT98_BACAN	Q8IT98_bacillus an
48	28	90.3	391	2	Q8IG40_BACCR	Q8IG40_bacillus ce
49	28	90.3	398	2	Q5NEA9_FRATT	Q5NEA9_francisella
50	28	90.3	409	2	Q73V08_MYCPA	Q73V08_mycobacteri
51	28	90.3	421	2	Q722C3_CAEEL	Q722C3_caenorhabdi
52	28	90.3	422	2	Q9PGG2_UREPA	Q9PGG2_ureaplasma
53	28	90.3	430	2	Q8FW04_BRUSU	Q8FW04_brucella su
54	28	90.3	432	2	Q6Q8W8_9GAMM	Q6Q8W8_uncultured
55	28	90.3	436	2	Q8M9J3_9AQUA	Q8M9J3_ilex pubesc
56	28	90.3	452	2	Q44595_CAEEL	Q44595_caenorhabdi
57	28	90.3	456	2	Q6GVJ4_9BURK	Q6GVJ4_burkholderi
58	28	90.3	465	1	RBL_NEPAL	R28434_nepenthes a
59	28	90.3	472	2	Q9NSQ8_CAEEL	Q9NSQ8_caenorhabdi
60	28	90.3	480	2	Q625W2_CAEER	Q625W2_caenorhabdi
61	28	90.3	482	2	Q5JJ16_PYRKO	Q5JJ16_pyrococcus
62	28	90.3	488	2	Q966D7_CAEEL	Q966D7_caenorhabdi
63	28	90.3	492	2	Q621X3_CAEER	Q621X3_caenorhabdi
64	28	90.3	506	2	Q38860_ARATH	Q38860_arabidopsis
65	28	90.3	508	1	MURE_BORBU	O51219_borrelia bu
66	28	90.3	509	2	P93058_BRAJU	P93058_brassica ju
67	28	90.3	509	2	Q8LSC7_BACRM	Q8LSC7_brassica ca
68	28	90.3	509	2	Q8S384_BRAJU	Q8S384_brassica ju
69	28	90.3	517	2	Q80729_ARATH	Q80729_arabidopsis
70	28	90.3	529	2	Q6NI23_CORDI	Q6NI23_corynebacte
71	28	90.3	538	2	Q7PQZ0_ANOGA	Q7PQZ0_anopheles g
72	28	90.3	558	2	Q5TTR3_ANOGA	Q5TTR3_anopheles g
73	28	90.3	571	2	Q97KUB_CLOAB	Q97KUB_clostridium
74	28	90.3	584	2	Q4UGB4_THEAN	Q4UGB4_theileria a
75	28	90.3	615	2	Q7PS12_ANOGA	Q7PS12_anopheles g
76	28	90.3	664	2	Q966D8_CAEEL	Q966D8_caenorhabdi
77	28	90.3	746	2	Q9NSQ9_CAEEL	Q9NSQ9_caenorhabdi
78	28	90.3	802	2	Q7R8Y2_PLAYO	Q7R8Y2_plasmodium
79	28	90.3	853	2	Q7QTQ4_GIALA	Q7QTQ4_giardia lam
80	28	90.3	922	1	GYRA_AURSA	P48369_aeromonas s
81	28	90.3	1072	2	Q94537_SCHPO	Q94537_schistosacch
82	28	90.3	1165	2	Q962L9_PLAVI	Q962L9_plasmodium
83	28	90.3	1285	2	Q9WXU3_THENA	Q9WXU3_thermotoga
84	28	90.3	1558	2	Q5RH87_BRARE	Q5RH87_brachydanio
85	27	87.1	31	2	Q4YNS6_PLABE	Q4YNS6_plasmodium
86	27	87.1	36	2	Q4XB83_PLACH	Q4XB83_plasmodium
87	27	87.1	38	2	Q32187_EUGGR	Q32187_euglena gra
88	27	87.1	46	2	Q867A4_TRAJA	Q867A4_trapelus ja
89	27	87.1	60	2	Q4YK86_PLABE	Q4YK86_plasmodium
90	27	87.1	77	2	Q52R02_CHICK	Q52R02_gallus gall
91	27	87.1	90	2	Q4XC01_PLACH	Q4XC01_plasmodium
92	27	87.1	92	2	Q8MPY0_CAEEL	Q8MPY0_caenorhabdi
93	27	87.1	96	2	Q611Z3_CAEER	Q611Z3_caenorhabdi
94	27	87.1	99	2	Q4T7Q1_TETNG	Q4T7Q1_tetradon n
95	27	87.1	114	2	Q6ZB28_ORYSA	Q6ZB28_oryza sativ
96	27	87.1	117	2	Q74KX8_LACJO	Q74KX8_lactobacill
97	27	87.1	121	2	Q6R983_MAIZE	Q6R983_zea mays (m
98	27	87.1	128	2	Q4MQN4_BACCE	Q4MQN4_bacillus ce
99	27	87.1	128	2	Q6HNK6_BACHK	Q6HNK6_bacillus th
100	27	87.1	128	2	Q81116_BACCR	Q81116_bacillus ce
101	27	87.1	128	2	Q73DN7_BACCC	Q73DN7_bacillus ce
102	27	87.1	128	2	Q63G38_BACCC	Q63G38_bacillus ce
103	27	87.1	128	2	Q81V92_BACAN	Q81V92_bacillus an
104	27	87.1	134	2	Q7R7Y0_PLAYO	Q7R7Y0_plasmodium

105	27	87.1	134	2	Q4XU22_PLACH	Q4xu22 plasmodium	178	27	87.1	345	2	Q4Z9Y8_9VIRU	Q4z9y8 bacterioph
106	27	87.1	135	2	Q8MYN0_CABEL	Q8myno caenorhabdi	179	27	87.1	345	2	Q8KZ48_9PROT	Q8kz48 uncultured
107	27	87.1	138	2	O51365_BORBU	O51365 borrelia bu	180	27	87.1	346	1	ACSF_GLOVI	Q7nfal gloebacter
108	27	87.1	140	2	Q9G4E5_FASGI	Q9g4e5 fasciola gi	181	27	87.1	349	1	ACSF_GRATL	Q6b8ul gracillaria
109	27	87.1	140	2	O814D1_CABEL	O814d1 caenorhabdi	182	27	87.1	349	1	ACSF_PORPU	P51277 porphyra pu
110	27	87.1	144	2	O81WA3_HUMAN	O81wa3 homo sapien	183	27	87.1	350	2	Q9Y370_HUMAN	Q9y370 homo sapien
111	27	87.1	144	2	Q6WGM2_BDEBA	Q6wgm2 bdellovibri	184	27	87.1	351	2	Q8TCX1_HUMAN	Q8tcx1 homo sapien
112	27	87.1	146	2	Q6MUK5_MYCMS	Q6muk5 mycoplasma	185	27	87.1	352	2	Q96J00_HUMAN	Q96j00 homo sapien
113	27	87.1	148	2	Q6ZUC5_HUMAN	Q6zuc5 homo sapien	186	27	87.1	352	2	O17576_CABEL	O17576 caenorhabdi
114	27	87.1	148	2	O97657_CANFA	O97657 canis famil	187	27	87.1	354	1	ACSF_SYACA	Q7u6v8 cyaneichoc c
115	27	87.1	148	2	Q6QLX0_CANFA	Q6qlx0 canis famil	188	27	87.1	356	1	ACSF_SYNXP	Q7u6v8 synechococc
116	27	87.1	151	2	Q4WKU9_ASPFU	Q4wku9 aspergillus	189	27	87.1	356	2	Q5NPT3_ZYMMO	Q5npt3 zymonomas m
117	27	87.1	164	2	Q6KAU3_MOUSE	Q6kau3 mus musculus	190	27	87.1	358	1	ACSF3_SYNY3	Q72584 synechocyst
118	27	87.1	171	1	RT25_MOUSE	Q9dl25 mus musculus	191	27	87.1	358	1	ACSF3_ANASP	Q7y222 anabaena sp
119	27	87.1	171	2	Q4QR80_RAT	Q4qr80 rattus norv	192	27	87.1	362	2	Q75AT8_ASHGO	Q75at8 ashba goss
120	27	87.1	172	2	Q4RJV4_TETNG	Q4rjv4 tetraodon n	193	27	87.1	362	2	Q7RGM5_PLAYO	Q7rgm5 plasmodium
121	27	87.1	173	1	RT25_HUMAN	P82663 homo sapien	194	27	87.1	365	1	ACSF_RHOPA	Q6n9j7 rhodopseudo
122	27	87.1	176	2	Q63507_9TREM	Q63507 echinostoma	195	27	87.1	369	2	Q6ZMI8_BRARE	Q6zmi8 brachydanio
123	27	87.1	176	2	Q63508_9TREM	Q63508 echinostoma	196	27	87.1	370	2	Q40093_IPONI	Q40093 ipomoea nil
124	27	87.1	176	2	Q63509_9TREM	Q63509 echinostoma	197	27	87.1	370	2	Q8A715_BACTN	Q8a715 bacteroides
125	27	87.1	179	2	Q420C8_PLABE	Q420c8 plasmodium	198	27	87.1	370	2	Q98QH7_MYCPU	Q98qh7 mycoplasma
126	27	87.1	185	1	LEP1_BACAM	P41026 bacillus am	199	27	87.1	371	2	Q84RD7_TOBAC	Q84rd7 nicotiana t
127	27	87.1	185	2	O51736_BORBU	O51736 borrelia bu	200	27	87.1	375	2	Q6FVI2_CANGA	Q6fvi2 candida gla
128	27	87.1	193	1	LEP2_BACAM	P41025 bacillus am	201	27	87.1	376	2	Q95NI2_CAEEL	Q95ni2 caenorhabdi
129	27	87.1	193	1	LEPT_BACSU	F71013 bacillus su	202	27	87.1	393	2	Q8LEF4_ARATH	Q8lee4 arabidopsis
130	27	87.1	194	2	Q5OXJ3_ENTHI	Q5oxj3 entamoeba h	203	27	87.1	405	1	CRD1_EUPES	Q945b7 euphorbia e
131	27	87.1	194	2	Q5NT24_ENTHI	Q5nt24 entamoeba h	204	27	87.1	405	1	CTH1_CHLRE	Q6sjv8 gossypium h
132	27	87.1	201	2	Q96B03_HUMAN	Q96b03 homo sapien	205	27	87.1	407	1	Q45653_CAEEL	Q45653 caenorhabdi
133	27	87.1	201	2	Q6PDB2_HUMAN	Q6pdb2 homo sapien	206	27	87.1	408	2	Q45653_CAEEL	Q45653 caenorhabdi
134	27	87.1	208	2	Q83455_ADEP3	Q83455 porcine ade	207	27	87.1	408	2	Q9SDJ2_ORYSA	Q9sdj2 oryza sativ
135	27	87.1	211	2	Q7RNJ3_PLAYO	Q7rnj3 plasmodium	208	27	87.1	409	1	CRD1_ARATH	Q9ms91 a magnesium
136	27	87.1	227	2	Q6PWQ4_XENLA	Q6pwq4 xenopus lae	209	27	87.1	415	2	Q5LH15_BACFN	Q5lhi5 bacteroides
137	27	87.1	228	2	Q9LHM5_ARATH	Q9lhm5 arabidopsis	210	27	87.1	415	2	Q64YF9_BACFR	Q64yf9 bacteroides
138	27	87.1	232	2	Q8ZDV0_YERPE	Q8zdv0 yersinia pe	211	27	87.1	417	1	CRD1_HORVU	Q5efu4 hordeum vul
139	27	87.1	238	1	Y014_BEL2	P42549 bacterioph	212	27	87.1	423	2	Q6NKY4_ARATH	Q6nky4 arabidopsis
140	27	87.1	239	2	Q5HRC1_STABQ	Q5hrc1 staphylococ	213	27	87.1	428	2	Q601R3_MYCHY	Q601r3 mycoplasma
141	27	87.1	239	2	Q8CTN5_STAEP	Q8ctn5 staphylococ	214	27	87.1	431	2	Q98TF3_ORYLA	Q98tf3 oryza lat
142	27	87.1	244	2	Q5B4B1_EMENI	Q5b4b1 aspergillus	215	27	87.1	432	2	Q681Y3_ARATH	Q681y3 arabidopsis
143	27	87.1	246	2	Q4N8X3_THEPA	Q4n8x3 theileria p	216	27	87.1	435	2	Q6XRC0_9BACT	Q6xrc0 uncultured
144	27	87.1	246	2	Q8FB21_ECOL6	Q8fb21 escherichia	217	27	87.1	436	2	Q9C954_ARATH	Q9c954 arabidopsis
145	27	87.1	247	2	O81B21_PLAF7	O81b21 plasmodium	218	27	87.1	437	2	Q51EE2_ENTHI	Q51ee2 entamoeba h
146	27	87.1	256	2	O51209_GEOKA	O51209 geobacillus	219	27	87.1	438	1	ENGA_CLOPE	Q8xjk1 clostridium
147	27	87.1	258	2	Q9C1L0_NEUCR	Q9c1l0 neurospora	220	27	87.1	459	2	Q9WZ33_THEMA	Q9wz33 thermotoga
148	27	87.1	262	2	Q9BGL3_SHEEP	Q9bgl3 ovis aries	221	27	87.1	467	2	Q8VUM4_STAHO	Q8vum4 staphylococ
149	27	87.1	262	2	Q6PWQ5_XENLA	Q6pwq5 xenopus lae	222	27	87.1	469	2	Q51FM2_ENTHI	Q51fm2 entamoeba h
150	27	87.1	274	2	Q9WZS5_THEMA	Q9wzs5 thermotoga	223	27	87.1	472	2	Q4UDY3_THEAN	Q4udy3 theileria a
151	27	87.1	278	2	O9U336_CABEL	O9u336 caenorhabdi	224	27	87.1	478	2	Q6UR08_ANOGA	Q6ur08 anopheles g
152	27	87.1	287	2	Q72P77_LEPIC	Q72p77 leptospira	225	27	87.1	479	2	Q7QCC7_ANOGA	Q7qcc7 anopheles g
153	27	87.1	287	2	Q8F779_LEPIN	Q8f779 leptospira	226	27	87.1	488	2	Q18760_CABEL	Q18760 caenorhabdi
154	27	87.1	300	2	Q34521_FASHE	Q34521 fasciola he	227	27	87.1	499	2	P87212_9APHY	P87212 polyporacea
155	27	87.1	300	2	Q9B8Y4_FASHE	Q9b8y4 fasciola he	228	27	87.1	504	2	Q8NKF3_9AGAR	Q8nkf3 termitomyce
156	27	87.1	300	2	Q88XR9_LACPL	Q88xr9 lactobacill	229	27	87.1	522	2	Q6QNE9_CABEL	Q6qne9 caenorhabdi
157	27	87.1	301	2	Q7XJ11_TRIRP	Q7xj11 trifolium r	230	27	87.1	522	2	Q91PY0_ARATH	Q91py0 arabidopsis
158	27	87.1	301	2	Q7XJ16_WHEAT	Q7xj16 triticum ae	231	27	87.1	524	2	Q75819_ASHGO	Q75819 ashba goss
159	27	87.1	308	2	Q7XJ12_BRANA	Q7xj12 brassica na	232	27	87.1	527	1	IPT1_YEAST	P38954 saccharomyc
160	27	87.1	308	2	Q66917_YERPS	Q66917 yersinia ps	233	27	87.1	543	2	Q7QXS6_GIALA	Q7qxs6 giardia lam
161	27	87.1	309	2	Q5L1S8_SILPO	Q5l1s8 silicibacte	234	27	87.1	546	2	Q98TF2_ORYLA	Q98tf2 oryza lat
162	27	87.1	310	1	Y160_BUCAP	Q8k9x4 buchnera ap	235	27	87.1	553	2	Q4SKD2_TETNG	Q4skd2 tetraodon n
163	27	87.1	321	1	YCF39_CYAPA	P48279 cyanophora	236	27	87.1	560	2	Q4SOT5_TETNG	Q4sot5 tetraodon n
164	27	87.1	324	2	Q6HKI3_BACHK	Q6hki3 bacillus th	237	27	87.1	574	2	Q7T2J2_BRARE	Q7t2j2 brachydanio
165	27	87.1	325	2	Q81SA4_BACAN	Q81sa4 bacillus an	238	27	87.1	575	2	Q5USC3_XENLA	Q5usc3 xenopus lae
166	27	87.1	332	2	Q84RD6_CUGSA	Q84rd6 cucumis sat	239	27	87.1	576	2	Q6DCW8_XENLA	Q6dcw8 xenopus lae
167	27	87.1	333	2	Q7XJ13_9ROSA	Q7xj13 rosa davuri	240	27	87.1	578	2	Q5BL52_XENTR	Q5bl52 xenopus tro
168	27	87.1	333	2	Q7XJ14_9ROSI	Q7xj14 salix babyi	241	27	87.1	580	1	MMPL14_FIG	Q9xt90 sus scrofa
169	27	87.1	335	1	ACSF_CYAME	Q85fx6 cyanidiosch	242	27	87.1	581	2	O68921_NEIGO	O68921 neisseria g
170	27	87.1	335	2	Q5LE41_BACFN	Q5le41 bacteroides	243	27	87.1	581	2	Q5F8K1_NEIGI	Q5f8k1 neisseria g
171	27	87.1	335	2	Q9F749_BACFR	Q9f749 bacteroides	244	27	87.1	581	2	Q9J293_NEIMB	Q9j293 neisseria m
172	27	87.1	336	2	Q688Q2_ORYSA	Q688q2 oryza sativ	245	27	87.1	581	2	Q9JUB8_NEIMA	Q9jub8 neisseria m
173	27	87.1	339	2	Q9XDJ2_BACFR	Q9xdj2 bacteroides	246	27	87.1	582	1	MMPL14_HUMAN	P50281 homo sapien
174	27	87.1	339	2	Q5LGH6_BACFN	Q5lgh6 bacteroides	247	27	87.1	582	1	MMPL14_MOUSE	P53690 mus musculu
175	27	87.1	340	2	O5L1R4_BACFN	O5l1r4 bacteroides	248	27	87.1	582	1	MMPL14_RABIT	Q95220 oryctolagus
176	27	87.1	340	2	Q64ZV1_BACFR	Q64zv1 bacteroides	249	27	87.1	582	1	MMPL14_RAT	Q10739 rattus norv
177	27	87.1	345	2	Q6Y7P5_9VIRU	Q6y7p5 staphylococ	250	27	87.1	582	2	Q6GSF3_HUMAN	Q6gsf3 homo sapien

251 27 87.1 582 2 Q9GLE4 BOVIN
252 27 87.1 582 2 Q9RES1_PONPY
253 27 87.1 582 2 Q9XSP0_CAPHI
254 27 87.1 582 2 Q99PG1_CRIGR
255 27 87.1 582 2 Q8BTX2_MOUSE
256 27 87.1 582 2 Q6DFU5_MOUSE
257 27 87.1 582 2 Q6IN06_RAT
258 27 87.1 585 2 Q7RDB0_PLAYO
259 27 87.1 585 2 Q4N9F3_THEPA
260 27 87.1 592 2 Q4RWY3_TETNG
261 27 87.1 599 2 Q752M5_ASHGO
262 27 87.1 607 2 Q76LU7_ORYLA
263 27 87.1 610 2 Q4W889_ORYLA
264 27 87.1 621 2 Q7R2J1_BRARE
265 27 87.1 626 2 Q98HT9_RHILO
266 27 87.1 689 1 SOIB2_MOUSE
267 27 87.1 695 2 Q419L8_GIBZE
268 27 87.1 698 2 Q5BD98_EMENI
269 27 87.1 721 2 Q16363_CAEEL
270 27 87.1 732 2 Q4SKX7_TETNG
271 27 87.1 763 2 Q4Y7S4_PLACH
272 27 87.1 773 1 YOD3_CAEEL
273 27 87.1 780 2 Q6A1B3_ECHMU
274 27 87.1 789 2 Q5AGA4_CANAL
275 27 87.1 794 2 Q7R8G4_PLAYO
276 27 87.1 796 2 Q9LSC5_9ALPH
277 27 87.1 833 1 HMDH_AGRIP
278 27 87.1 846 2 Q4SL98_TETNG
279 27 87.1 856 1 HMDH_BLAG
280 27 87.1 923 2 Q73177_TREDE
281 27 87.1 1024 1 CAR12_HUMAN
282 27 87.1 1049 2 Q528F0_MAGGR
283 27 87.1 1068 2 Q55DX7_DICDI
284 27 87.1 1099 2 Q8IE72_PLAF7
285 27 87.1 1126 2 Q73ME8_TREDE
286 27 87.1 1144 2 Q86J82_DICDI
287 27 87.1 1145 2 Q5SA20_DICDI
288 27 87.1 1269 2 Q4YNH1_PLABE
289 27 87.1 1279 2 Q761L3_BRARE
290 27 87.1 1469 2 Q4YZQ1_PLABE
291 27 87.1 1508 2 Q7RHF5_PLAYO
292 27 87.1 1563 2 Q61CM5_CAEER
293 27 87.1 1897 2 Q81BK2_PLAF7
294 27 87.1 1917 2 Q4X570_PLACH
295 27 87.1 2118 2 Q7RR57_PLAYO
296 27 87.1 2921 2 Q5WNK5_CAEER
297 27 87.1 3978 2 Q97236_PLAF7
298 27 87.1 6739 2 Q7QYB8_GIALA
299 26 83.9 24 2 Q4X467_PLACH
300 26 83.9 27 2 Q4Z5I9_PLABE

ALIGNMENTS

RESULT 1
Q8QGY9_FUGRU
ID Q8QGY9_FUGRU PRELIMINARY; PRT; 47 AA.
AC Q8QGY9;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Guanine nucleotide binding protein (Fragment).
GN Name=Gnat2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97129408; PubMed=8973916;

RA Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;
RT "G protein alpha subunit multigene family in the Japanese puffer fish
RL Fugu rubripes: PCR from a compact vertebrate genome.";
DR EMBL; L79897; AAL77630.1; -; Genomic_DNA.
DR HS9P; P04695; 1TND.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
FT NON_TER 1 1
FT NON_TER 47 47
SQ SEQUENCE 47 AA; 5255 MW; 9770A35D36B1FABC CRC64;

Query Match 100.0%; Score 31; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFPPA 6
DB 15 KVFPPA 20
|||||

RESULT 2

Q6RS99_TRITU PRELIMINARY; PRT; 229 AA.
ID Q6RS99_TRITU PRELIMINARY; PRT; 229 AA.
AC Q6RS99;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Globulin.
OS Triticum turgidum (Poulard wheat) (Rivet wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15122014; DOI=10.1104/pp.103.038083;
RA Gu Y.Q., Coleman-Derr D., Kong X., Anderson O.D.;
RT "Rapid Genome Evolution Revealed by Comparative Sequence Analysis of
Orthologous Regions from Four Triticeae Genomes.";
RL Plant Physiol. 135:459-470(2004).
DR EMBL; AY494981; AAR95703.1; -; Genomic DNA.
DR GO; GO:0045733; P:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Ttyp alpha amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 229 AA; 25000 MW; 18E769DAB08E41E3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFPPA 6
DB 3 KVFPPA 8
|||||

RESULT 3

Q7XYC3_WHEAT PRELIMINARY; PRT; 241 AA.
ID Q7XYC3_WHEAT PRELIMINARY; PRT; 241 AA.
AC Q7XYC3;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE 19 kDa globulin (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.

```

OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seed;
RA Li J.R., Wang F., Li Q.Z., Zhang X.S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF475121; AAP80642.1; -; mRNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha.amyl. 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
FT NON TER
SQ SEQUENCE 241 AA; 26139 MW; AAD8F2BB859DA016 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 15 KFVFFA 20

RESULT 4
Q6KX9 ORYSA
ID Q6KX9 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q6KX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Transmembrane protein-like.
GN Name=O2055.H10.27-1; Synonyms=P0407A09.6-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005300; BAD19727.1; -; Genomic DNA.
DR EMBL; AP004747; BAD19452.1; -; Genomic DNA.
DR Gramene; Q6KX9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
DR Transmembrane.
SQ SEQUENCE 331 AA; 36397 MW; EACAC4769463B9EA CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 80 KFVFFA 85

RESULT 5
Q84NE7 ORYSA
ID Q84NE7 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q84NE7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transmembrane protein.

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Lee R.H., Chen S.C.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY030360; AAK50365.1; -; mRNA.
DR Gramene; Q84NE7; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
DR Transmembrane.
SQ SEQUENCE 331 AA; 36384 MW; 289C89F3D3F8229A CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 80 KFVFFA 85

RESULT 6
Q615W9 ORYSA
ID Q615W9 ORYSA PRELIMINARY; PRT; 335 AA.
AC Q615W9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transmembrane protein.
GN Name=OJ1076.H08.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC108498; AAT47018.1; -; Genomic DNA.
DR Gramene; Q615W9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
DR Transmembrane.
SQ SEQUENCE 335 AA; 36826 MW; 5A0EF43F8578E46F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 80 KFVFFA 85

RESULT 7
Q4HQ66 CAMUP
ID Q4HQ66 CAMUP PRELIMINARY; PRT; 353 AA.
AC Q4HQ66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE GDP-fucose synthetase.
 GN Names-fcl; ORFNames=CUP1255;
 OS Campylobacter upsaliensis RM3195.
 CC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=306264;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RM3195;
 RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
 RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
 RA Nelson K.E.;
 RT "Major structural and novel potential virulence mechanisms from the
 RL genomes of multiple Campylobacter species.";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC SEQUENCE 353 AA; 39798 MW; 59CCBA43D31EFAE CRC64;
 DR EMBL; AAFJ01000007; EAL52977.1; -; Genomic DNA.
 SQ SEQUENCE 353 AA; 39798 MW; 59CCBA43D31EFAE CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 KFVFFA 6
 |||||
 DB 58 KFVFFA 63
 |||||
 RESULT 8
 QSATG9 EMENI
 ID QSATG9 EMENI PRELIMINARY; PRT; 519 AA.
 AC QSATG9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN8411.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Chepel Y., Collamore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage B., Galagan J.,
 RA Gadyana S., Ghera S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhuan P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer B., Schupbach R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Hydroxylation of N-alkanes at the terminal
 CC position.
 CC -1- CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-
 CC methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + 3
 CC NADP(+) + 3 H(2)O.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC EMBL; AACD01000153; EAA67033.1; -; Genomic DNA.
 DR GO; GO:0046872; F-metal ion binding; IEA.
 DR GO; GO:0004497; F-monooxygenase activity; IEA.
 DR GO; GO:0006118; P-electron transport; IEA.
 DR GO; GO:0008152; P-metabolism; IEA.
 DR GO; GO:0016126; P-sterol biosynthesis; IEA.
 DR InterPro; IPR001128; Cytochrome P450.
 DR InterPro; IPR002974; EP450 II_CYP52.
 DR InterPro; IPR002403; EP450IV.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR01239; EP450IICYP52.
 DR PRINTS; PR00465; EP450IV.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
 DR Heme; Hypothetical protein; Iron; Lipid synthesis; Membrane;
 KW Metal-binding; Monooxygenase; Oxidoreductase; Steroid biosynthesis;
 KW Sterol biosynthesis.
 SQ SEQUENCE 519 AA; 60440 MW; B367EB6EB6FPA287 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 519;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 KFVFFA 6
 |||||
 DB 26 KFVFFA 31
 |||||
 RESULT 9
 Q7XM01 ORYSA
 ID Q7XM01 ORYSA PRELIMINARY; PRT; 935 AA.
 AC Q7XM01;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE OSJNBa0086006.8 protein.
 GN Names=OSJNBa0086006.8;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 RL EMBL; AL662981; CA804860.2; -; Genomic DNA.
 DR Gramene; Q7XM01;
 DR GO; GO:0006512; P-ubiquitin cycle; IEA.
 DR InterPro; IPR001810; P-box.
 DR Pfam; PF00646; P-box; 2.
 DR SMART; SM00256; FBOX; 2.
 DR PROSITE; PS00181; FBOX; 1.
 SQ SEQUENCE 935 AA; 103910 MW; 735DD287C6E1BC69 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 935;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KVFVFA 6
|||||
Db 74 KVFVFA 79

RESULT 10

ID Q7QVR7 GIALA PRELIMINARY; PRT; 3044 AA.
AC Q7QVR7
DT 01-WAR-2004 (TRENBLrel. 26, Created)
DT 01-WAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE GLP 70 49040 39906.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gallin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000048; EAA40229.1; -; Genomic_DNA.
DR InterPro; IPR012351; Cytochrome_4_hlx.
KW Cytochrome.
SQ SEQUENCE 3044 AA; 347085 MW; 24F737600F128C6D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 3044;
Best Local Similarity 100.0%; Pred. No. 9.6e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 KVFVFA 6
|||||
Db 382 KVFVFA 387

RESULT 11

ID Q84NG7 HORVU PRELIMINARY; PRT; 224 AA.
AC Q84NG7
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Globulin.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=14663527; DOI=10.1139/g03-071;
RA Gu Y.Q., Anderson O.D., Londeore C.F., Kong X., Chibbar R.N.,
RA Lazo G.R.;
RT "Structural organization of the barley D-hordein locus in comparison
RT with its orthologous regions of wheat genomes."
RL Genome 46:1084-1097(2003).
DR EMBL; AY268139; AAP31050.1; -; Genomic_DNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amyl1.1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 224 AA; 24561 MW; 91A5BFF15C86394D CRC64;

Query Match 96.8%; Score 30; DB 2; Length 224;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||
Db 3 KFIFFA 8

RESULT 12

ID Q98GC2 RHIL0 PRELIMINARY; PRT; 395 AA.
AC Q98GC2
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative peptidase.
CN OrderedLocusNames=ml13393;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; BA000012; BAB50294.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000994; Peptidase M24.
DR InterPro; IPR001714; Pept M24 MAP.
DR Pfam; PF00557; Peptidase M24_1.
DR PRINTS; PR00599; MAPEPTIDASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 395 AA; 43302 MW; E9ADDF4AADB1D472 CRC64;

Query Match 96.8%; Score 30; DB 2; Length 395;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||
Db 48 KFIFFA 53

RESULT 13

ID Q92YY6 RHIME PRELIMINARY; PRT; 397 AA.
AC Q92YY6
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative proline dipeptidase.
CN OrderedLocusNames=RA0726; ORFNames=Sma1329;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,


```

RA Barloy-Hubler P., Bowser L., Capela D., Galibert P., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR EMBL; AE007260; AAK65384.1; -; Genomic_DNA.
DR FJ9352; F95352.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008235; F:metalloexopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000994; Peptidase M24.
DR Pfam; PF00557; Peptidase M24; I.
DR Complete proteome; HydroLase; Plasmid.
SQ SEQUENCE 397 AA; 43264 MW; 670896A4950C718D CRC64;

Query Match 96.8%; Score 30; DB 2; Length 397;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 25 KFIFFA 30
||:||||

RESULT 14
QSA3W3 CANAL PRELIMINARY; PRT; 2643 AA.
ID QSA3W3;
AC QSA3W3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein IRA2.
GN Name=IRA2; ORFNames=CaO19.12686;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000071; EAK97292.1; -; Genomic_DNA.
DR InterPro; IPR002114; HPr SerP_S.
DR Pfam; PF00616; RasGAP; 1.
DR SMART; SM00323; RasGAP; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
DR PROSITE; PS00509; RAS_GTPASE_ACTIV_1; 1.
DR PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 2643 AA; 304839 MW; 3C1EAAAC60BD583AF CRC64;

Query Match 96.8%; Score 30; DB 2; Length 2643;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 253 KFIFFA 258
||:||||

RESULT 16
Q4XXR5 PLACH PRELIMINARY; PRT; 23 AA.
ID Q4XXR5;
AC Q4XXR5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC104709.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;

```

```

Db 253 KFIFFA 258

RESULT 15
QSA3Q1 CANAL PRELIMINARY; PRT; 2643 AA.
ID QSA3Q1;
AC QSA3Q1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein IRA2.
GN Name=IRA2; ORFNames=CaO19.5219;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000071; EAK97292.1; -; Genomic_DNA.
DR InterPro; IPR002114; HPr SerP_S.
DR Pfam; PF00616; RasGAP; 1.
DR SMART; SM00323; RasGAP; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
DR PROSITE; PS00509; RAS_GTPASE_ACTIV_1; 1.
DR PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 2643 AA; 304839 MW; 3C1EAAAC60BD583AF CRC64;

Query Match 96.8%; Score 30; DB 2; Length 2643;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 253 KFIFFA 258
||:||||

RESULT 16
Q4XXR5 PLACH PRELIMINARY; PRT; 23 AA.
ID Q4XXR5;
AC Q4XXR5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC104709.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;

```

RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses.";
 CC Science 307:82-86(2005).

CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CAJ01002391; CAH78296.1; -; Genomic_DNA.

FT NON TER 1

SQ SEQUENCE 23 AA; 3051 MW; ECFB64E8BCC09AA0 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 23;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 Db 16 KVFVFA 21
 |||||
 |:||||

RESULT 17

Q73M63 TREDE

ID Q73M63 TREDE PRELIMINARY; PRT; 43 AA.

AC Q73M63;

DT 05-JUL-2004 (TReMBLrel. 27, Created)

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)

DE Hypothetical protein.

GN OrderedLocusNames=TFDE1646;

OS Treponema denticola.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI_TaxID=158;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35405 / DSM 14222;

RX PubMed=15064399; DOI=10.1073/pnas.0307639101;

RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,

RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,

RA Durkin S.A., Daugherty S.C., Shetye J., Shvartsbeyn A.,

RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,

RA Shastman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,

RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,

RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;

RT "Comparison of the genome of the oral pathogen Treponema denticola

RT with other spirochete genomes.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

DR EMBL; AE017251; AAS12163.1; -; Genomic_DNA.

DR TIGR; TDE1646; -.

KW Complete proteome.

SQ SEQUENCE 43 AA; 5202 MW; E1189103B62C9173 CRC64;

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 43;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

Db 20 KVFVFA 25

|||||

|||:|

RESULT 18

Q9KAX7 BACHD

ID Q9KAX7 BACHD PRELIMINARY; PRT; 49 AA.

AC Q9KAX7;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE BH2159 protein.

GN OrderedLocusNames=BH2159;

OS Bacillus halodurans.

OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.

OX NCBI_TaxID=86665;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C-125 / JCM 9153;

RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

RA Horikoshi K.;

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus

RT halodurans and genomic sequence comparison with Bacillus subtilis.";

RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; BA000004; BAB05878.1; -; Genomic_DNA.

DR FIR; G83919; G83919.

KW Complete proteome.

SQ SEQUENCE 49 AA; 5463 MW; D669731B66DCD0B1 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 49;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

Db 34 KVFVFA 39

|||||

|||||

RESULT 19

Q7R979 PLAYO

ID Q7R979 PLAYO PRELIMINARY; PRT; 150 AA.

AC Q7R979;

DT 01-MAR-2004 (TReMBLrel. 26, Created)

DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN Name=PY06986;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=73239;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=17XNL;

RX MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,

RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,

RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,

RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,

RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,

RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite Plasmodium yoelii yoelii.";

RL Nature 419:512-519(2002).

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AABL01002464; EAA19320.1; -; Genomic_DNA.

DR InterPro; IPR006484; PYST_B.

DR TIGRFAMs; TIGR01597; PYST-B; 1.

KW Hypothetical protein.

SQ SEQUENCE 150 AA; 17794 MW; DA68536D398B37AC CRC64;

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 150;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

Db 7 KVFVFA 12

|||||

|||||

RESULT 20

QAJ122_AZOVI

ID Q4J122_AZOVI PRELIMINARY; PRT; 152 AA.
AC Q4J122;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Glyoxalase/Bleomycin resistance protein/dioxygenase domain.
GN ORFNames=AvindRAFT 6949;
OS Azotobacter vinelandii AVOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RN Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer P., Land W.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RN Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RL [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute;
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RN Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RN Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAU03000001; EAM08399.1; -; Genomic_DNA.
KW Dioxygenase.
SQ SEQUENCE 152 AA; 16984 MW; 05A60BD5E879ED93 CRC64;
Query Match 90.3%; Score 28; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFFA 6
Db 111 RFVFFA 116
RESULT 21'
ID Q20070_CAEEL PRELIMINARY; PRT; 177 AA.
AC Q20070;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypothetical protein F35H10.6.
GN ORFNames=F35H10.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;

RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; U40934; AAA81680.1; -; Genomic_DNA.
DR PIR; T16280; T16280.
DR Ensembl; F35H10.6; Caenorhabditis elegans.
DR GO; GO:0016272; C:prefoldin complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006457; F:protein folding; IEA.
DR InterPro; IPR004127; PFD_alpha_like.
DR Pfam; PF02996; Prefoldin; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 177 AA; 21142 MW; E8B71144250DB915 CRC64;
Query Match 90.3%; Score 28; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFFA 6
Db 10 KVFVFS 15
RESULT 22
ID Q6LSA9_PROPR PRELIMINARY; PRT; 199 AA.
AC Q6LSA9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PBPA1406;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Castaro A., Malacrida G., Simonati B., Cannata N.,
RA Romualdi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461 (2005).
DR EMBL; CR378667; CAG19817.1; -; Genomic DNA.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; 1.
KW Complete proteome.
SQ SEQUENCE 199 AA; 22203 MW; AF44E115663FD3F6 CRC64;
Query Match 90.3%; Score 28; DB 2; Length 199;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFFA 6
Db 47 KLFVFA 52
RESULT 23
ID Q6UJY8_TRITU PRELIMINARY; PRT; 225 AA.
AC Q6UJY8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Globulin.
OS Triticum turgidum (Poulard wheat) (Rivet wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

```

OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15159634; DOI=10.1023/B:PLAN.0000028768.21587.dc;
RA Kong X.-Y., Gu Y.-Q., You F.M., Dubcovsky J., Anderson O.D.;
RT "Dynamics of the evolution of orthologous and paralogous portions of a
RT complex locus region in two genomes of allopolyploid wheat.";
RL Plant Mol. Biol. 54:55-69(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kong X.-Y., Gu Y.-Q., Anderson O.D.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY368673; AAQ93632.1; -; Genomic DNA.
DR GO; GO:0045735; F.nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 225 AA; 24502 MW; 45F4D19403BCDCC2 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 225;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db :|||||
3 RFVFFA 8

RESULT 24
OBLKV8_AEGTA
ID OBLKV8_AEGTA PRELIMINARY; PRT; 226 AA.
AC OBLKV8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Seed globulin.
GN Name=Glo-2;
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22478028; PubMed=12590343;
RA Anderson O.D., Rausch C., Mouillet O., Lagudah E.S.;
RT "The wheat D-genome HMW-glutenin locus: BAC sequencing, gene
RT distribution, and retrotransposon clusters.";
RL Funct. Integr. Genomics 3:56-68(2003).
DR EMBL; AF497474; AAM77580.1; -; Genomic DNA.
DR GO; GO:0045735; F.nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 226 AA; 24515 MW; 95397B83C63D50AD CRC64;

Query Match 90.3%; Score 28; DB 2; Length 226;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db :|||||
3 RFVFFA 8

RESULT 25
Q7R8Y4_PLAYO
ID Q7R8Y4_PLAYO PRELIMINARY; PRT; 241 AA.

```

```

AC Q7R8Y4;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY07086;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002524; EAA19443.1; -; Genomic DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 241 AA; 28789 MW; BE9AD8A3E5924873 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 241;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db :|||||
7 KVFVFS 12

RESULT 26
Q7RA05_PLAYO
ID Q7RA05_PLAYO PRELIMINARY; PRT; 242 AA.
AC Q7RA05;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06703;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).

```

CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AABL01002310; EAA18966.1; -; Genomic_DNA.
 DR InterPro; IPR006484; PYST-B.
 DR TIGRFAMs; TIGR01597; PYST-B; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 242 AA; 28514 MW; FF31C7DBB82957EF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 242;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 Db 7 KVFVFS 12
 |||||
 7 KVFVFS 12

RESULT 27
 Q7RNP5 PLAYO PRELIMINARY; PRT; 250 AA.
 ID Q7RNP5;
 AC Q7RNP5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Hypothetical protein.
 GN Name=PY01770;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AABL01000477; EAA21136.1; -; Genomic_DNA.
 DR InterPro; IPR006484; PYST-B.
 DR TIGRFAMs; TIGR01597; PYST-B; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 250 AA; 29944 MW; EBF3D5B5C001C9C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 250;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 Db 7 KVFVFS 12
 |||||
 7 KVFVFS 12

RESULT 28
 Q7PDC0 PLAYO PRELIMINARY; PRT; 251 AA.
 ID Q7PDC0;
 AC Q7PDC0;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Hypothetical protein.

GN Name=PY00554; Synonyms=PY01592;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AABL01000150; EAA16801.1; -; Genomic_DNA.
 DR InterPro; IPR006484; PYST-B.
 DR TIGRFAMs; TIGR01597; PYST-B; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 251 AA; 30043 MW; 3D608A4EC7F432D5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 251;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 Db 7 KVFVFS 12
 |||||
 7 KVFVFS 12

RESULT 29
 Q7RPS1 PLAYO PRELIMINARY; PRT; 251 AA.
 ID Q7RPS1;
 AC Q7RPS1;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Hypothetical protein.
 GN Name=PY01385;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AABL01000363; EAA20702.1; -; Genomic_DNA.
 DR InterPro; IPR006484; PYST-B.

```

DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 251 AA; 30054 MW; 3D6A80EE6DFE9275 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 251;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db      |||||:
       7 KPVFFS 12

RESULT 30
QTRA57 PLAYO
ID Q7RA57 PLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RA57;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY06647;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01001507; EAA16812.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29757 MW; 64EB5B4C1F49786D CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 252;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db      |||||:
       7 KPVFFS 12

RESULT 31
Q7RF37 PLAYO
ID Q7RF37 PLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RF37;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY04873;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01002275; EAA18895.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29750 MW; 86406549DB86516D CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 252;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db      |||||:
       7 KPVFFS 12

RESULT 32
Q7RLK2 PLAYO
ID Q7RLK2 PLAYO PRELIMINARY; PRT; 255 AA.
AC Q7RLK2;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY02539;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01000695; EAA21989.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 255 AA; 30283 MW; 51F1FD33FED980B3 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 255;

```

Best Local Similarity 83.3%; Pred. No. 5.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
Db 7 KVFVFFS 12

RESULT 33

Q7RC37 PLAYO
ID O7RC37 PLAYO PRELIMINARY; PRT; 262 AA.
AC O7RC37;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY05947;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AABL01001873; EAA17841.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 7A520F097ABF0573 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 262;
Best Local Similarity 83.3%; Pred. No. 5.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
Db 7 KVFVFFS 12

RESULT 34

Q7RC37 PLAYO
ID O7RC37 PLAYO PRELIMINARY; PRT; 265 AA.
AC O7RC37;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY05947;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AABL01001955; EAA18074.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 7CD7DBBCC3A26FF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 265;
Best Local Similarity 83.3%; Pred. No. 5.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
Db 7 KVFVFFS 12

RESULT 35

Q7RB86 PLAYO
ID Q7RB86 PLAYO PRELIMINARY; PRT; 268 AA.
AC Q7RB86;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY06262;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AABL01002095; EAA18444.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
FT NON_TER 268 268
SQ SEQUENCE 268 AA; 32060 MW; D273B20E61AA181C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 5.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6

```
Db          |||||:
            7 KVFVFS 12

RESULT 36
Q529U4 MAGGR
ID Q529U4_MAGGR PRELIMINARY; PRT; 285 AA.
AC Q529U4;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=M02290.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachatsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Consideine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseelis M., Karlsson E.,
RA Kellis C., Kieu A., Kienner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Okosawo O., O'Leary S., Omotosho B.,
RA Norbu N., O'donnell P., Oksawo O., Nielsen C., Nizzari M., Norbu C.,
RA O'Neill K., Osmann S., Parker S., Perrin D., Phunkhang P., Pigani B.,
RA Purcell S., Rachupka T., Ramasamy U., Raneau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutnan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsanla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wanchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; AACU01000444; EAA54305.1; -; Genomic_DNA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR007568; RTA1.
DR Pfam; PF04479; RTA1; 1.
KW Hypothetical protein.
SQ SEQUENCE 285 AA; 31531 MW; DCE48A5EB9E4D1BD CRC64;

Query Match 90.3%; Score 28; DB 2; Length 285;
Best Local Similarity 83.3%; Pred. NO. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 6 KVFVFA 11
|||||:

RESULT 37
Q94284 CAEEL
ID Q94284_CAEL PRELIMINARY; PRT; 293 AA.
AC Q94284;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein M02B7.4.
GN ORFNames=M02B7.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; U70851; AAB09129.1; -; Genomic_DNA.
DR PIR; T29899; T29899.
DR Ensembl; M02B7.4; Caenorhabditis elegans.
DR WormBase; WBGene0019725; M02B7.4.
DR WormPep; M02B7.4; CEL2326.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 293 AA; 33247 MW; 90CE020650E5065 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. NO. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 258 KVFVFS 263
|||||:

RESULT 38
Q7RBUI PLAYO
ID Q7RBUI_PLAYO PRELIMINARY; PRT; 294 AA.
AC Q7RBUI;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06045;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Emdolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
```



```

RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002005; EAA18193.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 34611 MW; 281A85D322236659 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 294;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 7 KVFVFS 12

RESULT 39
Q5UWP7 HALMA
ID Q5UWP7 HALMA PRELIMINARY; PRT; 300 AA.
AC Q5UWP7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Sugar ABC transport system permease protein.
GN Name=malFG-9; OrderedLocustNames=rrnB0104;
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RA "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea."
RL Genome Res. 14:2221-2234(2004).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AY596238; ANV48306.1; -; Genomic_DNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005215; F: transporter activity; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD_transp_1; 1.
DR PROSITE; PS00928; ABC_TM1; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 32975 MW; 9C230B44EF19CE5A CRC64;

Query Match 90.3%; Score 28; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

```

```

DB 86 KVFVFA 91
[1]
O7REJ3 PLAYO PRELIMINARY; PRT; 321 AA.
RESULT 40
O7REJ3 PLAYO
ID O7REJ3 PLAYO PRELIMINARY; PRT; 321 AA.
AC O7REJ3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06150;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=17XNL;
RC MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;
RX Carlton J.M., Anguioi S.V., Sun B.B., Koolf T.W., Perlea M.,
RX Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.D.,
RX Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RX Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RX Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RX Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RX Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RX van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RX Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RX Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002053; EAA18307.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 38948 MW; E1127BA81EB58FDB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 51 KVFVFS 56
[1]

RESULT 41
P74429 SYNY3
ID P74429 SYNY3 PRELIMINARY; PRT; 326 AA.
AC P74429;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ynf39 gene product.
GN Name=ynf39; OrderedLocustNames=slr0399;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=97061201; PubMed=8905231;
RX Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RX Miyajima N., Hiroseawa M., Sugita M., Sasaki K., Kimura T.,
RX Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RX Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M.,
RX Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

```

```

RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; BA000022; BAA18529.1; -; Genomic_DNA.
DR PIR; S76400; S76400.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0051287; F:NAD binding; IEA.
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 326 AA; 36519 MW; 99F522C1E980B943 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 326;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 104 KVFVFS 109

RESULT 42
Q6KI05 MYCMO
ID Q6KI05 MYCMO PRELIMINARY; PRT; 380 AA.
AC Q6KI05.
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Restriction-modification enzyme mpuUVIII s subunit (EC 3.1.21.3).
GN Name=hds; OrderedLocusNames=MMOB2850;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=163K / ATCC 43663;
RX PubMed=15289470; DOI=10.1101/gr.2674004;
RA Jaffe J.D., Stange-Thomann N., Smith C., DeCaprio D., Fisher S.,
RA Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
RA Kodira C.D., Major J., Wang J., Wilkinson J., Nicol R., Nusbaum C.,
RA Birren B., Berg H.C., Church G.M.;
RT "The complete genome and proteome of Mycoplasma mobile.";
RL Genome Res. 14:1447-1461(2004).
DR EMBL; AE017336; AAT27771.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0009035; F:Type I site-specific deoxyribonuclease acti. .; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR InterPro; IPR000055; Rest_mod_DNA.
DR Pfam; PF01420; Methylase_S; 2.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 380 AA; 44463 MW; D42428E38774F9CE CRC64;

Query Match          90.3%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 294 KVFVFA 299

RESULT 43
Q4MSJ5 BACCE
ID Q4MSJ5 BACCE PRELIMINARY; PRT; 388 AA.
AC Q4MSJ5.
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Basic membrane protein dtlB.
GN Name=dtlB; ORFNames=BCE_G9241_1384;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

```

```

OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Rillstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA00100009; EAL15142.1; -; Genomic_DNA.
SQ SEQUENCE 388 AA; 45590 MW; E21AEA22BA0511CF CRC64;

Query Match          90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 286 RRVFPA 291

RESULT 44
Q6HLH8 BACHK
ID Q6HLH8 BACHK PRELIMINARY; PRT; 388 AA.
AC Q6HLH8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE D-alanyl transfer protein.
GN Name=dlb; OrderedLocusNames=BT9727_1258;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DDJ databases.
DR EMBL; AE017355; AAT61956.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45999 MW; DFB6794B3247A66B CRC64;

Query Match          90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 286 RRVFPA 291

RESULT 45
Q73BD3 BACCI
ID Q73BD3 BACCI PRELIMINARY; PRT; 388 AA.
AC Q73BD3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE DltB protein.

```

```

GN Name=dltB; OrderedLocusNames=BCE1486;
OS Bacillus cereus (strain ATCC 10987);
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01."
RL Nucleic Acids Res 32:977-988(2004).
DR EMBL; AB017269; AA540415.1; -; Genomic_DNA.
DR TIGR; BCE1486; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 74CBF3D745AE3EC6 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
DB 286 RFVFFA 291

RESULT 46
Q63E03_BACCZ
ID Q63E03_BACCZ PRELIMINARY; PRT; 388 AA.
AC Q63E03;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE D-alanyl transfer protein.
GN Name=dltB;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18989.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D466DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
DB 286 RFVFFA 291

RESULT 47
Q81T98_BACAN
ID Q81T98_BACAN PRELIMINARY; PRT; 388 AA.
AC Q81T98; G61H5; Q6KVC6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE DltB protein..

```

```

GN Name=dltB; OrderedLocusNames=BA1388, BAS1286, GBAA1388;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Bailly L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman W.C.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.B., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.P., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017028; AAP25332.1; -; Genomic_DNA.
DR EMBL; AB017334; AAT30485.1; -; Genomic_DNA.
DR EMBL; AB017225; AAT53606.1; -; Genomic_DNA.
DR TIGR; BA1388; -.
DR TIGR; GBAA1388; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D466DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
DB 286 RFVFFA 291

RESULT 48
Q81G40_BACCR
ID Q81G40_BACCR PRELIMINARY; PRT; 391 AA.
AC Q81G40;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein dltB.
GN OrderedLocusNames=BC1371;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapatal V., Bhattacharyya A., Renik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AE017002; AAP08353.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 391 AA; 46119 MW; E875D0033C91C54 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 289 RVVFA 294

RESULT 49
Q5NEA9 FRATT PRELIMINARY; PRT; 398 AA.
AC Q5NEA9;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Aromatic amino acid transporter of the HAAAP family.
GN OrderedLocusNames=FTW1732c;
OS Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCHU S4 / Schu 4;
RX PubMed=15640799; DOI=10.1038/ng1499;
RA Larsson P., Oyston P.C.E., Chain P., Chu M.C., Duffield M.,
RA Fuxelius H.-H., Garcia E., Haeiltoirp G., Johansson D., Isherwood K.E.,
RA Karp P.D., Larsson E., Liu Y., Michell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vergez L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Forsman M.,
RA Titball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
RT agent of tularemia."
RL Nat. Genet. 37:153-159(2005).
DR EMBL; AJ749949; CAG46365.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0008665; P:amino acid transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR002091; AAA_permease.
DR Pfam; PF03222; Tnp_Tyr_perm; 1.
DR PRINTS; PR00166; AROAPRMEASE.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 398 AA; 44437 MW; 1A93FFD1DBAA4A38 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 398;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 152 KFLVFA 157

RESULT 50

```

```

Q73V08 MYCPA
ID Q73V08 MYCPA PRELIMINARY; PRT; 409 AA.
AC Q73V08;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Nuoh.
GN Name=nuoh; OrderedLocusNames=MAP3208;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017238; AAS05756.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44971 MW; 693518B9DDF94B11 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 409;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 67 KVFVFA 72

RESULT 51
Q7Z2C3 CAEEL
ID Q7Z2C3 CAEEL PRELIMINARY; PRT; 421 AA.
AC Q7Z2C3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y19D10A.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68421.2; -; Genomic DNA.
DR Ensemble; Y19D10A.8; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS.
DR Pfam; PF07690; MFS; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 421 AA; 46361 MW; 75B7CF15ABE2C432 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 421;

```

```
Best Local Similarity 83.3%; Pred. No. 8.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 291 RVVFFA 296

RESULT 52
Q9PQ2_UREPA PRELIMINARY; PRT; 422 AA.
AC Q9PQ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unique hypothetical.
GN OrderedLocusNames=UU329;
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 700970;
RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum."
RL Nature 407:757-762(2000).
DR EMBL; AS002130; AAF30738.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 422 AA; 49219 MW; 8EA05B3F2F76C8E8 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 208 KYVFFA 213

RESULT 53
Q8FW04_BRUSU PRELIMINARY; PRT; 430 AA.
AC Q8FW04;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Uracil-xanthine permease, putative.
GN OrderedLocusNames=BR0661;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1330 / Blovax 1;
RX MEDLINE=2247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kral M., Shetty J., Malek J.A.,
Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014292; AAN33850.1; -; Genomic DNA.
DR TIGR; BR0661; -;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
```

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; campanulids; Aquifoliales; Aquifoliaceae; Ilex.
 OX NCBI_TaxID=185543;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RA Manen J.F.;
 RT "The complex history of the genus Ilex L. (Aquifoliaceae): evidence
 RT from the comparison of plastid and nuclear DNA sequences and from
 RT fossil data.";
 RL Plant Syst. Evol. 0:0-0(0).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Manen J.F.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Rubisco catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process (By
 CC similarity).
 CC -!- FUNCTION: Rubisco catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process. Both
 CC reactions occur simultaneously and in competition at the same
 CC active site (By similarity).
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 CC 2 3-phospho-D-glycerate.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
 CC phospho-D-glycerate + 2-phosphoglycolate.
 CC -!- SUBUNIT: 8 large chains + 8 small chains (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
 CC -!- SIMILARITY: Belongs to the RuBisCO large chain family.
 DR EMBL; AJ492722; CAD37439.1; -; Genomic_DNA.
 DR SMR; Q8W9J3; 9-436.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
 DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
 DR GO; GO:0009853; P:photorespiration; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 DR InterPro; IPR000685; RuBisCO_large.
 DR Pfam; PF00016; RuBisCO_large; 1.
 DR Pfam; PF02788; RuBisCO_large; 1.
 KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
 KW Oxidoreductase; Photorespiration; Photosynthesis.
 FT NON_TER 436 436
 SQ SEQUENCE 436 AA; 48367 MW; E1A65FFCF93985A1 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 436;
 Best Local Similarity 83.3%; Pred. No. 8.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFFA 6
 Db 217 RFVFFFA 222
 RESULT 56
 O44595 CAEBL
 ID O44595 CAEBL PRELIMINARY; PRT; 452 AA.
 AC O44595;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DE Hypothetical protein F56A4.10.
 GN ORFNames=F56A4.10;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae;
 OC Rhabditidae; Feloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=93069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; AC006645; AAF39848.1; -; Genomic_DNA.
 DR PIR; C88969; C88969.
 DR Ensembl; F56A4.10; Caenorhabditis elegans.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 452 AA; 49858 MW; F1BED2FBB60CAE59 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 452;
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFFA 6
 Db 291 RFVFFFA 296
 RESULT 57
 Q6GVJ4_9BURK
 ID Q6GVJ4_9BURK PRELIMINARY; PRT; 456 AA.
 AC Q6GVJ4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glycosyltransferase.
 GN Name=wbce;
 OS Burkholderia cenocepacia.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
 OX NCBI_TaxID=95486;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K56-2;
 RX PubMed=15887196; DOI=10.1128/JB.187.4.1324-1333.2005;
 RA Ortega X., Hunt T.A., Louet S., Vinion-Dubiel A.D., Datta A.,
 RA Choudhury B., Goldberg J.B., Carlson R., Valvano M.A.;
 RT "Reconstitution of O-Specific Lipopolysaccharide Expression in
 RT Burkholderia cenocepacia Strain J2315, Which Is Associated with
 RT Transmissible Infections in Patients with Cystic Fibrosis.";
 RL J. Bacteriol. 187:1324-1333(2005).
 DR EMBL; AY633623; AAT48329.1; -; Genomic_DNA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR001296; Glyco_transf_1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Transferase.
 SQ SEQUENCE 456 AA; 50801 MW; E5B3648E1BE54A54 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 456;
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFFA 6
 Db 6 KFLFFFA 11
 RESULT 58
 RBL_NEPAL
 ID RBL_NEPAL
 AC P28434; STANDARD; PRT; 465 AA.

DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ribulose biphosphate carboxylase large chain (EC 4.1.1.39) (RuBisCO
 DE large subunit) (Fragment).
 GN Namerbcd, alata (winged pitcher plant).
 OS Nepenthes alata (winged pitcher plant).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Caryophyllales; Nymphaeaceae; Nymphaeaceae; Nymphaeaceae.
 OX NCBI_TaxID=4376;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92397008; PubMed=1523408;
 RA Albert V.A., Williams S.E., Chase M.W.;
 RT "Carnivorous plants: phylogeny and structural evolution."; Science
 RL 257:1491-1495 (1992).
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process. Both
 CC reactions occur simultaneously and in competition at the same
 CC active site.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 CC 2 3-phospho-D-glycerate + 2 H(+).
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
 CC phospho-D-glycerate + 2-phosphoglycolate.
 CC -1- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
 CC -1- SUBUNIT: Heterohexameric of 8 large chains and 8 small chains;
 CC disulfide-linked. The disulfide link is formed within the large
 CC subunit homodimers (By similarity).
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- DOMAIN: The basic functional RuBisCO is composed of a large chain
 CC homodimer in a "head-to-tail" conformation. In form I RuBisCO this
 CC homodimer is arranged in a barrel-like tetramer with the small
 CC subunits forming a tetrameric "cap" on each end of the "barrel"
 CC (By similarity).
 CC -1- PTM: The disulfide bond which can form in the large chain dimeric
 CC partners within the hexadecamer appears to be associated with
 CC oxidative stress and protein turnover (By similarity).
 CC -1- SIMILARITY: Belongs to the RuBisCO large chain family. Type I
 CC subfamily.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR EMBL; L01936; AAA84502.2; -; Genomic DNA.
 DR HSPSP; P00875; LAUS.
 DR SWR; P28434; 1-465.
 DR HAMAP; MF_01338; -; 1.
 DR InterPro; IPR000685; RuBisCO_large.
 DR Pfam; PF00016; RuBisCO_large; 1.
 DR Pfam; PF02788; RuBisCO_large; 1.
 DR PROSITE; PS00157; RUBISCO_LARGE; 1.
 KW Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Magnesium;
 KW Metal-binding; Methylation; Monooxygenase; Oxidoreductase;
 KW Photorespiration; Photosynthesis.
 FT ACT SITE 165 165 Proton acceptor (By similarity).
 FT ACT SITE 284 284 Proton acceptor (By similarity).
 FT METAL 191 191 Magnesium (via carbamate group) (By
 FT similarity).
 FT METAL 193 193 Magnesium (By similarity).
 FT METAL 194 194 Magnesium (By similarity).
 FT BINDING 113 113 Substrate (in homodimeric partner) (By
 FT similarity).
 FT BINDING 163 163 Substrate; C1 phosphate group (By
 FT similarity).
 FT BINDING 167 167 Substrate (By similarity).
 FT BINDING 285 285 Substrate; C5 phosphate group (By

FT BINDING 317 317 similarity).
 FT Substrate; C5 phosphate group (By
 FT similarity).
 FT BINDING 369 369 Substrate; C5 phosphate group (By
 FT similarity).
 FT SITE 324 324 Transition state stabilizer (By
 FT similarity).
 FT MOD_RES 4 4 N6,N6,N6-trimethyllysine (By similarity).
 FT MOD_RES 191 191 N6-carboxyllysine (By similarity).
 FT DISULFID 237 237 Interchain (in linked form) (By
 FT similarity).
 FT NON_TER 1 1
 SQ SEQUENCE 465 AA; 51614 MW; 29B322894FE92451 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 465;
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVFVFA 6
 Db 207 RVVFFA 212
 RESULT 59
 Q9NSQ8 CAEBL PRELIMINARY; PRT; 472 AA.
 ID Q9NSQ8 CAEBL PRELIMINARY; PRT; 472 AA.
 AC Q9NSQ8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein F56A4.12.
 GN ORFNames=F56A4.12;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology"; Science 282:2012-2018 (1998).
 RL EMBL; AC006645; AAP39850.1; -; Genomic DNA.
 DR Ensembl; F56A4.12; Caenorhabditis elegans.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 472 AA; 52251 MW; C06DFDB6AAG7555AE CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 472;
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVFVFA 6
 Db 340 RVVFFA 345
 RESULT 60
 Q625W2 CAEBR PRELIMINARY; PRT; 480 AA.
 ID Q625W2 CAEBR PRELIMINARY; PRT; 480 AA.
 AC Q625W2;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG01115.

```
GN Name=CBG01115;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC01000007; CAES8039.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS0850; MFS; 1.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 53324 MW; BDC735BE20A6CC51 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 343 REVFFA 348

RESULT 61
Q5JU16_PYRKO
ID Q5JU16_PYRKO PRELIMINARY; PRT; 482 AA.
AC Q5JU16;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical membrane protein, conserved.
GN OrderedLocusNames=TKI1728;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=69014;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KOD1;
RA PubMed=15710748; DOI=10.1101/gr.3003105;
RX Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Inanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
RT Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
RT genomes.";
RL Genome Res. 15:352-363(2005).
DR EMBL; AP006878; BAD85917.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 482 AA; 54068 MW; 097052D348C3BB4D CRC64;

Query Match 90.3%; Score 28; DB 2; Length 482;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 336 REVFFA 341

RESULT 62
Q966D7_CAEEL
ID Q966D7_CAEEL PRELIMINARY; PRT; 488 AA.
AC Q966D7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y19D10A.11;
```

```
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68411.2; -; Genomic DNA.
DR Ensembl; Y19D10A.11; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS0850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 488 AA; 54121 MW; A145401A124DB716 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 488;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 356 REVFFA 361

RESULT 63
Q521X3_CAEER
ID Q521X3_CAEER PRELIMINARY; PRT; 492 AA.
AC Q521X3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG02310 (Fragment).
GN Name=CBG02310;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000012; CAE59030.1; -; Genomic DNA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc phosphatse.
DR Pfam; PF00328; Acid_phosphat_A; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 492
SQ SEQUENCE 492 AA; 57471 MW; 4F1D61BB64DC5CFB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 492;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 188 REVFFA 193

RESULT 64
```



```

Q38860 ARATH
ID Q38860 ARATH PRELIMINARY; PRT; 506 AA.
AC Q38860;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-PBB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase 1.
GN Names:fael; Synonyms=AF4934520, T4L20.100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=95252821; PubMed=7734965; DOI=10.1105/tpc.7.3.309;
RA James D.W. Jr., Lim E., Keller J., Plooy I., Ralston E., Dooner H.K.;
RT "Directed tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1)
RT gene with the maize transposon activator.";
RL Plant Cell 7:309-319(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Terry N., Ardiles W., Buyschaert C., Daseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielens J., Van Montagu M., Jesse T., Heijnen L., Vos P.,
RA Hohelsel J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Terry N., Ardiles W., Buyschaert C., Daseville R., De Clerck R.,
RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel R.,
RA Gielens J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29142; AAA70154.1; -; Genomic DNA.
DR EMBL; AL023094; CAA18831.1; -; Genomic DNA.
DR EMBL; AL161585; CAB80169.1; -; Genomic DNA.
DR PIR; T05272; T05272.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 506 AA; 56263 MW; 4516D0E8E453D18 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
DB 356 KFLFFA 361

RESULT 65
MURE BORBU
ID MURE BORBU STANDARD; PRT; 508 AA.
AC 051219;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNAC-tripeptide synthetase).
GN Name=mure; OrderedLocusName=BB0201;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;

Q38860 ARATH PRELIMINARY; PRT; 506 AA.
AC Q38860;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-PBB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase 1.
GN Names:fael; Synonyms=AF4934520, T4L20.100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=95252821; PubMed=7734965; DOI=10.1105/tpc.7.3.309;
RA James D.W. Jr., Lim E., Keller J., Plooy I., Ralston E., Dooner H.K.;
RT "Directed tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1)
RT gene with the maize transposon activator.";
RL Plant Cell 7:309-319(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Terry N., Ardiles W., Buyschaert C., Daseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielens J., Van Montagu M., Jesse T., Heijnen L., Vos P.,
RA Hohelsel J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Terry N., Ardiles W., Buyschaert C., Daseville R., De Clerck R.,
RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel R.,
RA Gielens J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29142; AAA70154.1; -; Genomic DNA.
DR EMBL; AL023094; CAA18831.1; -; Genomic DNA.
DR EMBL; AL161585; CAB80169.1; -; Genomic DNA.
DR PIR; T05272; T05272.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 506 AA; 56263 MW; 4516D0E8E453D18 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
DB 356 KFLFFA 361

RESULT 66
P33058 BRAJU
ID P33058 BRAJU PRELIMINARY; PRT; 509 AA.
AC P33058;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fatty acid elongation 1.
GN Name=fael;
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Brassica.

```

```

OX NCBI_TaxID=3707;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypocotyl;
RA Venkateswari J., Kanrar S., Kirti P.B., Malathi V.G., Chopra V.L.;
RT "Molecular cloning and characterization of fatty acid elongation 1
RT (fae 1) gene of Brassica juncea cv. Pusa Bold.";
RL J. Plant Biochem. Biotechnol. 8:53-55(1999).
DR EMBL; Y11007; CAA71898.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56663 MW; B204DA5AB5887C5C CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 359 KFLFFA 364

RESULT 67
QBLSCT7_BRACM
ID QBLSCT7_BRACM PRELIMINARY; PRT; 509 AA.
AC QBLSCT7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fatty acid elongase.
OS Brassica campestris (Field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491878; AM33539.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56661 MW; 59ED8F07457CB6F5 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 358 KFLFFA 363

RESULT 68
QBS384_BRAJU
ID QBS384_BRAJU PRELIMINARY; PRT; 509 AA.
AC QBS384;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase.
GN Name=Fael.2; Synonyms=fae 1.1;
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL; AF491877; AM311648.1; -; Genomic DNA.
DR EMBL; AF491876; AM34043.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56616 MW; F6C553739AD86C23 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 358 KFLFFA 363

RESULT 69
O80729_ARATH
ID O80729_ARATH PRELIMINARY; PRT; 517 AA.
AC O80729;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative cytochrome P450 (At2g46950).
GN Name=At2g46950;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AC004411; AAC34228.1; -; Genomic DNA.
DR EMBL; BT014808; AAT41791.1; -; mRNA.
DR EMBL; BT011625; AAS47631.1; -; mRNA.
DR PIR; T02192; T02192.
DR HSP; P14779; 1JFZ.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
KW Transmembrane.
SQ SEQUENCE 517 AA; 59021 MW; 3963BCCE988C19A2 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 123 KVFVFS 128

```

CC **-|- CAUTION:** The sequence shown here is derived from an
CC **EMBL/GenBank/DBSJ** whole genome shotgun (WGS) entry which is

```

DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTPHPTASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRODOM; PD000093; SH2; 1.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC_motif; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 558 558
SQ SEQUENCE 558 AA; 63773 MW; 2EC76E5D5BAFE310 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 558;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFFA 6
DB 519 KEVYFA 524

RESULT 73
Q97KU8 CLOAB PRELIMINARY; PRT; 571 AA.
AC Q97KU8_
DT 01-OCT-2001 (TremBLrel. 18, Created)
DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Diguanylate cyclase/phosphodiesterase domain (GGDEF) containing
DE protein.
GN OrderedLocusNames=CAC0818;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RX DOI=10.1126/JB.183.16.4823-4838.2001;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838 (2001).
DR EMBL; AE007597; RAK78794.1; -; Genomic_DNA.
DR PIR; G97000; G97000.
DR InterPro; IPR011623; 7TMR-DISM_7TM.
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF07695; 7TMR-DISM_7TM; 1.
DR Pfam; PF00990; GGDEF; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRfam; TIGR00254; GGDEF; 1.
DR PROSITE; PS50887; GGDEF; 1.
KW Complete proteome.
SQ SEQUENCE 571 AA; 66225 MW; 64B51A5D9F5BD23F CRC64;

Query Match 90.3%; Score 28; DB 2; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFFA 6
DB 314 KEVYFA 319

```

```

RESULT 74
Q4UGB4 THEAN PRELIMINARY; PRT; 584 AA.
AC Q4UGB4_
DT 13-SEP-2005 (TremBLrel. 31, Created)
DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
DE Seryl-trna synthetase, putative (EC 6.1.1.11).
GN ORFNames=TA19195;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 1 sequence of Theileria annulata."
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940347; CAI73875.1; -; Genomic_DNA.
KW Aminoacyl-tRNA synthetase; Ligase.
SQ SEQUENCE 584 AA; 66617 MW; 76FEB10EEF7C6691 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 584;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFFA 6
DB 13 RPFVFA 18

RESULT 75
Q7PS12 ANOGA PRELIMINARY; PRT; 615 AA.
AC Q7PS12_
DT 01-MAR-2004 (TremBLrel. 26, Created)
DT 01-MAR-2004 (TremBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE ENSANGP0000017331.
GN ORFNames=ENSANGG00000021622;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008846; EAA06305.3; -; Genomic_DNA.
DR SMR; Q7PS12; 1-355.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0036020; C:membrane; IEA.
DR GO; GO:0008092; F:Cytoskeletal protein binding; IEA.
DR InterPro; IPR000299; Band_4.1.
DR InterPro; IPR011174; ERM.
DR InterPro; IPR011259; ERM_C.
DR InterPro; IPR000798; Ez/Rad/moesin.
DR Pfam; PF00373; Band_41; 1.
DR Pfam; PF00769; ERM; 1.

```

DR PIRSF; PIRSF002305; ERM; 1.
 DR PRINTS; PRO0661; ERMFAMILY.
 DR SMART; SM00295; B41; 1.
 DR PROSITE; PS00661; FERM 2; 1.
 DR PROSITE; PS00661; FERM 3; 1.
 DR PROSITE; PS00661; FERM 3; 1.
 SQ SEQUENCE 615 AA; 72579 MW; 804168798B4C5DDC CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 615;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVFVFA 6
 Db 96 KVFVFS 101

Search completed: December 29, 2005, 17:47:28
 Job time : 79.1936 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KVFVFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

PIR 80:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	96.8	397	2 F95352	probable proline d
2	28	90.3	479	2 G83919	hypothetical prote
3	28	90.3	177	2 T16280	hypothetical prote
4	28	90.3	293	2 T29899	hypothetical prote
5	28	90.3	326	2 S76400	hypothetical prote
6	28	90.3	422	2 E82904	hypothetical prote
7	28	90.3	452	2 C88969	protein F15E11.8 [
8	28	90.3	506	2 T05272	fatty acid elongas
9	28	90.3	508	2 A70125	UDP-N-acetylmuram
10	28	90.3	517	2 T02152	probable cytochrom
11	28	90.3	571	2 G97000	diguanylate cyclas
12	28	90.3	1072	2 T37742	serine threonine-p
13	28	90.3	1285	2 B72420	hypothetical prote
14	27	87.1	38	4 S07937	hypothetical prote
15	27	87.1	138	2 C70150	hypothetical prote
16	27	87.1	185	2 I40051	signal peptidase I
17	27	87.1	185	2 C70159	hypothetical prote
18	27	87.1	193	2 S45032	signal peptidase I
19	27	87.1	193	2 G69707	signal peptidase I
20	27	87.1	232	2 A80299	probable membrane
21	27	87.1	274	2 E72329	hypothetical prote
22	27	87.1	298	2 T29189	hypothetical prote
23	27	87.1	321	2 T06845	hypothetical prote
24	27	87.1	349	2 S73198	hypothetical prote
25	27	87.1	358	2 S74431	hypothetical prote
26	27	87.1	358	2 A82218	hypothetical prote
27	27	87.1	370	2 H30559	hypothetical prote
28	27	87.1	408	2 T23285	hypothetical prote
29	27	87.1	409	2 T47754	leucine zipper-con

30	27	87.1	436	2 E95635	hypothetical prote
31	27	87.1	459	2 B72361	conserved hypothet
32	27	87.1	488	2 T20124	hypothetical prote
33	27	87.1	522	2 H66248	protein T23J18.22
34	27	87.1	527	2 S49827	probable membrane
35	27	87.1	581	2 B81107	exodeoxyribonuclea
36	27	87.1	581	2 B81909	exodeoxyribonuclea
37	27	87.1	582	2 I38028	matrix metalloprot
38	27	87.1	582	2 I84471	matrix metalloprot
39	27	87.1	689	2 JC7286	liver-specific org
40	27	87.1	856	2 S30338	hydroxymethylgluta
41	27	87.1	857	2 S44883	ZC262.3 protein -
42	27	87.1	870	2 T31795	hypothetical prote
43	26	83.9	107	2 S56900	probable membrane
44	26	83.9	127	2 G87731	protein W10C8.3 [i
45	26	83.9	171	2 C81280	probable periplasm
46	26	83.9	183	2 T47707	hypothetical prote
47	26	83.9	188	2 A86806	transcription regu
48	26	83.9	203	2 S73449	MG028 homolog B01
49	26	83.9	216	2 G70437	soluble hydrogenas
50	26	83.9	218	2 F86844	hypothetical prote
51	26	83.9	243	2 T22101	hypothetical prote
52	26	83.9	255	2 B81693	conserved hypothet
53	26	83.9	265	2 T44114	hypothetical prote
54	26	83.9	289	2 B81857	probable acetyltra
55	26	83.9	289	2 D81085	HtrB/MsbB family p
56	26	83.9	294	2 A27692	sarcotoxin IIA pre
57	26	83.9	294	2 B36351	sarcotoxin II-2 -
58	26	83.9	297	2 S75656	hypothetical prote
59	26	83.9	323	2 D86216	protein T23G18.8 [
60	26	83.9	324	2 T24424	hypothetical prote
61	26	83.9	337	2 S08459	hypothetical prote
62	26	83.9	344	2 E90564	potassium channel
63	26	83.9	381	2 T34333	hypothetical prote
64	26	83.9	389	2 S68155	ubiquinol-cytochro
65	26	83.9	390	2 T22810	hypothetical prote
66	26	83.9	395	2 T00516	hypothetical prote
67	26	83.9	395	2 D81040	cytochrome c-type
68	26	83.9	395	2 B81986	probable membrane
69	26	83.9	397	2 T46710	multidrug resistat
70	26	83.9	397	2 AE1613	multidrug-efflux t
71	26	83.9	397	2 A11250	hypothetical prote
72	26	83.9	398	2 T44331	conserved hypothet
73	26	83.9	401	2 H69833	probable sugar upt
74	26	83.9	404	2 C95990	ubiquinol-cytochro
75	26	83.9	405	1 CBQFR	conserved hypothet
76	26	83.9	406	2 T43120	hypothetical prote
77	26	83.9	416	2 T23977	probable transmem
78	26	83.9	431	2 B81254	ubiquinol-cytochro
79	26	83.9	432	2 AD3311	probable transmem
80	26	83.9	436	2 A81443	probable MFS trans
81	26	83.9	438	2 H82974	MFS permease/proli
82	26	83.9	443	2 AB2841	probable mfs trans
83	26	83.9	443	2 D97618	probable transport
84	26	83.9	462	2 AF0057	hypothetical prote
85	26	83.9	483	2 T20895	cytochrome oxidase
86	26	83.9	486	2 S50644	proline/betaine tr
87	26	83.9	503	2 AC3296	probable chromatin
88	26	83.9	544	2 T40058	NADH2 dehydrogenas
89	26	83.9	664	2 T14132	probable membrane
90	26	83.9	749	2 S62171	chloride channel p
91	26	83.9	780	2 T02939	beta-adaptin-like
92	26	83.9	841	2 T48508	hypothetical prote
93	26	83.9	884	2 T25205	hypothetical prote
94	26	83.9	903	2 G82516	major merozoite su
95	26	83.9	1772	2 A45532	major merozoite su
96	26	83.9	1785	2 A45546	ribulose biphosph
97	26	83.9	2149	2 C96695	hypothetical prote
98	26	83.9	2948	2 T22664	beta-amyloloid prote
99	25	80.6	33	2 S23094	hypothetical prote
100	25	80.6	42	2 PN0512	hypothetical prote
101	25	80.6	50	2 A69055	Alzheimer's disease
102	25	80.6	57	2 A60045	

103 25 80.6 57 2 F60045 Alzheimer's diseases
 104 25 80.6 57 2 D60045 Alzheimer's diseases
 105 25 80.6 57 2 E60045 Alzheimer's diseases
 106 25 80.6 57 2 G60045 Alzheimer's diseases
 107 25 80.6 57 2 B60045 Alzheimer's diseases
 108 25 80.6 78 2 E69969 hypothetical prote
 109 25 80.6 82 2 FQ0438 Alzheimer's diseases
 110 25 80.6 114 2 T33289 hypothetical prote
 111 25 80.6 152 2 T06645 hypothetical prote
 112 25 80.6 159 2 T30445 hypothetical prote
 113 25 80.6 169 2 T15611 hypothetical prote
 114 25 80.6 174 2 T15658 hypothetical prote
 115 25 80.6 177 2 T22603 hypothetical prote
 116 25 80.6 179 2 T17915 hypothetical prote
 117 25 80.6 191 2 A96765 hypothetical prote
 118 25 80.6 198 2 H84646 hypothetical prote
 119 25 80.6 210 2 F64609 conserved hypothet
 120 25 80.6 210 2 B71906 hypothetical prote
 121 25 80.6 220 2 T41562 hypothetical prote
 122 25 80.6 222 2 AE3114 hypothetical prote
 123 25 80.6 231 2 H85138 hypothetical prote
 124 25 80.6 237 2 AC1953 rubrerythrin [limp
 125 25 80.6 242 2 A82512 hypothetical prote
 126 25 80.6 267 2 A0269 cyclin C - fruit f
 127 25 80.6 270 2 H98172 amino acid ABC tra
 128 25 80.6 273 2 B85896 probable dimethyl
 129 25 80.6 273 2 F91051 probable dimethyl
 130 25 80.6 277 2 F75187 sugar abc transpor
 131 25 80.6 277 2 D71220 probable sugar tra
 132 25 80.6 286 2 H86664 outer membrane lip
 133 25 80.6 288 2 T37709 hypothetical prote
 134 25 80.6 300 2 T26245 hypothetical prote
 135 25 80.6 303 2 T25501 hypothetical prote
 136 25 80.6 327 2 A83766 hypothetical prote
 137 25 80.6 339 2 A30754 hypothetical prote
 138 25 80.6 342 2 A48454 cathepsin B-like c
 139 25 80.6 342 2 T09355 hypothetical prote
 140 25 80.6 346 2 A83686 hypothetical prote
 141 25 80.6 349 2 T26247 hypothetical prote
 142 25 80.6 352 2 T48903 wax synthase [limp
 143 25 80.6 356 2 G72386 conserved hypothet
 144 25 80.6 361 2 T34411 hypothetical prote
 145 25 80.6 389 2 T20811 hypothetical prote
 146 25 80.6 397 2 A96925 uncharacterized co
 147 25 80.6 404 2 F87753 protein C43E11.7
 148 25 80.6 406 2 C86904 transporter yxpb [m
 149 25 80.6 421 2 A9309 membrane transport
 150 25 80.6 428 2 T48008 hypothetical prote
 151 25 80.6 439 2 E70371 apolipoprotein N-a
 152 25 80.6 497 2 AD3514 D-serine/D-alanine
 153 25 80.6 501 2 C70420 NADH2 dehydrogenas
 154 25 80.6 508 2 T05156 probable glucose t
 155 25 80.6 516 2 S34525 hypothetical prote
 156 25 80.6 520 2 D90014 hypothetical prote
 157 25 80.6 534 2 E82269 conserved hypothet
 158 25 80.6 543 2 S62012 probable membrane
 159 25 80.6 568 2 D90525 hypothetical prote
 160 25 80.6 573 2 AB2401 hypothetical prote
 161 25 80.6 582 2 F71052 hypothetical prote
 162 25 80.6 584 2 F75090 archaeosine trna-r
 163 25 80.6 616 2 B90554 lipoprotein [impor
 164 25 80.6 632 2 A25784 hypothetical 70K p
 165 25 80.6 663 2 T26835 hypothetical prote
 166 25 80.6 692 2 C87644 fatty oxidation co
 167 25 80.6 695 1 A43795 Alzheimer's diseases
 168 25 80.6 695 2 A27485 Alzheimer's diseases
 169 25 80.6 695 2 S00550 Alzheimer's diseases
 170 25 80.6 703 2 H45456 NADH2 dehydrogenas
 171 25 80.6 707 1 LEEBBV hemolysin secretio
 172 25 80.6 707 1 LEECB hemolysin secretio
 173 25 80.6 707 2 A61378 leukotoxin express
 174 25 80.6 707 2 D43599 hemolysin I secret
 175 25 80.6 708 2 C30169 leukotoxin express

176 25 80.6 711 2 C49219 toxin apxIII secre
 177 25 80.6 747 2 JH0773 Alzheimer's diseases
 178 25 80.6 764 2 T48446 hypothetical prote
 179 25 80.6 770 1 QRHUA4 Alzheimer's diseases
 180 25 80.6 771 2 AD3126 ATP-dependent DNA
 181 25 80.6 771 2 E98161 probable ATP-depen
 182 25 80.6 841 2 A43254 protein-tyrosine-p
 183 25 80.6 902 2 D70116 transcription elon
 184 25 80.6 942 2 T20287 hypothetical prote
 185 25 80.6 962 2 G86479 F14D7_6 protein -
 186 25 80.6 975 2 T22788 hypothetical prote
 187 25 80.6 1016 2 S30236 genome polyprotein
 188 25 80.6 1046 2 F71432 hypothetical prote
 189 25 80.6 1436 2 S67655 probable membrane
 190 25 80.6 1549 2 T13940 ankrynin - fruit fl
 191 25 80.6 1683 2 S56811 probable membrane
 192 25 80.6 1717 2 T50247 probable helicase
 193 25 80.6 1848 2 S37771 ankrynin, erythrocy
 194 25 80.6 1856 2 B35049 ankrynin 1, erythro
 195 25 80.6 1862 2 I49502 ankrynin - mouse
 196 25 80.6 1880 2 A35049 ankrynin 1, erythro
 197 25 80.6 1881 1 SJHUK ankrynin 1, erythro
 198 25 80.6 39 2 S00318 photosystem I chai
 199 24 77.4 47 2 G70191 hypothetical prote
 200 24 77.4 51 2 T07326 hypothetical prote
 201 24 77.4 71 2 T26661 hypothetical prote
 202 24 77.4 71 2 T26663 hypothetical prote
 203 24 77.4 72 2 T26662 hypothetical prote
 204 24 77.4 84 2 S77771 probable ribonucle
 205 24 77.4 93 2 A89057 protein K09H11.5 [p
 206 24 77.4 94 2 F90448 hypothetical prote
 207 24 77.4 109 2 S57547 hypothetical prote
 208 24 77.4 113 2 PN0091 pullulanase [EC 3.
 209 24 77.4 126 2 C96930 glyoxalase I [glyo
 210 24 77.4 134 2 G69382 response regulator
 211 24 77.4 134 2 B83804 small multidrug ex
 212 24 77.4 138 2 T25620 hypothetical prote
 213 24 77.4 139 2 G69543 conserved hypothet
 214 24 77.4 140 2 H81959 patch repair prote
 215 24 77.4 143 2 S20937 photosystem I chai
 216 24 77.4 143 2 A88093 hypothetical prote
 217 24 77.4 143 2 F85938 hypothetical prote
 218 24 77.4 143 2 B65069 hypothetical prote
 219 24 77.4 149 2 A13586 xanthine/uracil pe
 220 24 77.4 156 2 T43957 hypothetical prote
 221 24 77.4 161 2 F72861 ACOrf_93 protein -
 222 24 77.4 161 2 T41833 ACOrf_93 protein -
 223 24 77.4 167 1 F1SP5 photosystem I chai
 224 24 77.4 171 2 C86367 protein F26F24.18
 225 24 77.4 171 2 D86475 unknown protein, 3
 226 24 77.4 176 2 G90120 hypothetical prote
 227 24 77.4 177 2 S34499 hypothetical prote
 228 24 77.4 177 2 AE1410 hypothetical prote
 229 24 77.4 184 2 S23381 signal peptidase I
 230 24 77.4 186 1 WMR219 19K globulin precu
 231 24 77.4 186 2 JC4784 alpha-globulin pre
 232 24 77.4 188 2 B85481 yaaH protein [simi
 233 24 77.4 188 2 B90630 yaaH protein [simi
 234 24 77.4 188 2 E56688 protein yaaH - Esc
 235 24 77.4 191 2 T09553 conserved hypothet
 236 24 77.4 197 2 S42129 light-harvesting c
 237 24 77.4 197 2 T33525 hypothetical prote
 238 24 77.4 211 2 T05276 hypothetical prote
 239 24 77.4 211 2 T12013 cuticular protein
 240 24 77.4 217 2 T31830 cuticular protein
 241 24 77.4 219 2 C85834 hypothetical prote
 242 24 77.4 219 2 A98989 hypothetical prote
 243 24 77.4 220 2 S62598 cuticular protein
 244 24 77.4 220 2 C62598 conserved hypothet
 245 24 77.4 231 2 T12012 cuticular protein
 246 24 77.4 236 2 A97233 uncharacterized co
 247 24 77.4 239 2 S27789 hypothetical prote
 248 24 77.4 250 2 F84977 deoxyribonuclease

249 24 77.4 255 2 B82813
 250 24 77.4 257 2 AC1290
 251 24 77.4 259 2 A11661
 252 24 77.4 259 2 E72218
 253 24 77.4 263 2 D72303
 254 24 77.4 267 2 S52347
 255 24 77.4 268 2 AB2498
 256 24 77.4 270 2 T44049
 257 24 77.4 277 2 T50722
 258 24 77.4 279 2 E97849
 259 24 77.4 284 2 H86183
 260 24 77.4 285 2 F71851
 261 24 77.4 286 2 AH2943
 262 24 77.4 294 2 G81118
 263 24 77.4 297 2 T25817
 264 24 77.4 298 2 H95195
 265 24 77.4 298 2 E98062
 266 24 77.4 301 2 S50737
 267 24 77.4 307 2 C90549
 268 24 77.4 312 2 G70114
 269 24 77.4 313 2 E98339
 270 24 77.4 314 2 G86835
 271 24 77.4 315 2 T07314
 272 24 77.4 317 2 B98208
 273 24 77.4 317 2 AG3078
 274 24 77.4 319 2 S73359
 275 24 77.4 320 2 T16311
 276 24 77.4 321 2 H71729
 277 24 77.4 327 2 AH2312
 278 24 77.4 328 2 AH2399
 279 24 77.4 334 2 T19127
 280 24 77.4 335 2 T04029
 281 24 77.4 340 1 MMBE5
 282 24 77.4 345 2 C45456
 283 24 77.4 347 2 T15672
 284 24 77.4 348 2 T20167
 285 24 77.4 358 2 A64424
 286 24 77.4 358 2 T50897
 287 24 77.4 361 2 A86841
 288 24 77.4 364 2 T16376
 289 24 77.4 368 2 D90596
 290 24 77.4 375 2 A39622
 291 24 77.4 385 2 T05049
 292 24 77.4 391 2 T20752
 293 24 77.4 394 2 T19028
 294 24 77.4 397 2 T19029
 295 24 77.4 398 2 F72335
 296 24 77.4 401 2 S49393
 297 24 77.4 404 2 T32998
 298 24 77.4 405 2 E97171
 299 24 77.4 406 2 T32922
 300 24 77.4 409 2 E97218

ALIGNMENTS

RESULT 1
 F95352
 C:Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A;Reference number: A95262; MUID:21396509; PMID:11481432
 A;Accession: F95352
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-397 <KUR>
 A;Cross-references: UNIPROT:Q92YY6; UNIPARC:UPI00000CB1AA; GB:AE006469; PIDN:AAK65384.1

A;Experimental source: strain 1021, megaplasmid pSymA
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
 L.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Pederspiel, N.A.; Fisher, R.F.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
 heault, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMal329
 A;Genome: plasmid

Query Match 96.8%; Score 30; DB 2; Length 397;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFPA 6
 |||||
 Db 25 KFIFFA 30

RESULT 2

G83919
 C:Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: G83919
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: G83919
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-49 <STO>
 A;Cross-references: UNIPROT:Q9KAX7; UNIPARC:UPI00000C3E07; GB:AP001514; GB:BA0000004; NI
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH2159

Query Match 90.3%; Score 28; DB 2; Length 49;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFPA 6
 |||||
 Db 34 KFVFPS 39

RESULT 3

T16280
 C:Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T16280
 R;Woessner, J.
 submitted to the EMBL Data Library, November 1995
 A;Description: The sequence of C. elegans cosmid F35H10.
 A;Reference number: Z18490
 A;Accession: T16280
 A;Status: preliminary; translated from GB/EMBL/DDBU
 A;Molecule type: DNA
 A;Residues: 1-177 <WOE>
 A;Cross-references: UNIPROT:Q20070; UNIPARC:UPI000007F0D0; EMBL:U40934; NID:gi072149;
 C;Genetics:
 A;Gene: CESP:F35H10.6
 A;Introns: 18/1; 39/2; 74/3; 97/2

Query Match 90.3%; Score 28; DB 2; Length 177;
 Best Local Similarity 83.3%; Pred. No. 43;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 KVFVFA 6
Db      10 KVFVFS 15

RESULT 4
T29899
hypothetical protein M02B7.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29899
R:Nelson, J.; Wohlmann, P.
submitted to the EMBL Data Library, September 1996
A:Description: The sequence of C. elegans cosmid M02B7.
A:Reference number: Z20706
A:Accession: T29899
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-293 <NEL>
A:Cross-references: UNIPROT:Q94284; UNIPARC:UPI0000078391; EMBL:U70851; PIDN:AAB09129.1;
A:Experimental source: strain Bristol N2; clone M02B7
C:Genetics:
A:Gene: CESP-M02B7.4
A:Map position: 4
A:Introns: 42/3; 150/2; 198/1; 230/3; 276/3

Query Match      90.3%; Score 28; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      258 KVFVFS 263

RESULT 5
S76400
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76400
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76400
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <KAN>
A:Cross-references: UNIPROT:P74429; UNIPARC:UPI00000C1025; EMBL:D90915; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      90.3%; Score 28; DB 2; Length 326;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      104 KVFVFS 109

RESULT 6
E82904
hypothetical protein U0329 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: E82904
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: E82904
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-422 <GLA>
A:Cross-references: UNIPARC:UPI00000C1C1F; GB:AE002130; GB:AF222894; NID:G6899302; PIDN:
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: U0329
A:Genetic code: SGC3

Query Match      90.3%; Score 28; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      208 KVFVFA 213

RESULT 7
C88969
protein F15B11.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C88969
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: C88969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <STO>
A:Cross-references: UNIPROT:O44595; UNIPARC:UPI0000075D10; GB:chr_V; PIDN:AAB94205.1; PI
C:Genetics:
A:Gene: F15B11.8
A:Map position: 5

Query Match      90.3%; Score 28; DB 2; Length 452;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      291 RFVFFA 296

RESULT 8
T05272
fatty acid elongase 1 - Arabidopsis thaliana
N:Alternate names: protein T4L20.100
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05272
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, September 1998
A:Reference number: Z15406
A:Accession: T05272
A:Molecule type: DNA
A:Residues: 1-506 <BEV>
A:Cross-references: UNIPROT:Q38860; UNIPARC:UPI0000047264; EMBL:AL023094
A:Experimental source: cultivar Columbia; BAC clone T4L20
C:Genetics:
A:Map position: 4
A:Note: T4L20.100
C:Superfamily: very-long-chain 3-ketoacyl-CoA synthase

Query Match      90.3%; Score 28; DB 2; Length 506;
```

Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
||:||||
Db 356 KFLFFA 361

RESULT 9
A70125
UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase (murE) homolog - Lyme
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Oct-2004
C;Accession: A70125
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: A70125
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-508 <KLE>
A;Cross-references: UNIPROT:O51219; UNIPARC:UPI00000573B3; GB:AE001130; GB:AE000783; NID
A;Experimental source: strain B31
C;Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 90.3%; Score 28; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
||:||||
Db 41 RFVFFA 46

RESULT 10
T02192
probable cytochrome P450 At2g46950 [imported] - Arabidopsis thaliana
N;Alternate names: cytochrome P450 homolog F14M4.22
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02192; C84909
R;Roundley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ro
submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
A;Reference number: Z14609
A;Accession: T02192
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-517 <ROU>
A;Cross-references: UNIPROT:O80729; UNIPARC:UPI00000A147A; EMBL:AC004411; NID:G3522932;
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-517 <STO>
A;Cross-references: UNIPARC:UPI00000A147A; GB:AE002093; NID:G3522946; PIDN:AAC34228.1; G
C;Genetics:
A;Gene: At2g46950; F14M4.22
A;Map position: 2
A;Introns: 95/1; 169/3; 252/2; 374/3
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;321-485/Domain: cytochrome P450 homology <P45>

F;463/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.3%; Score 28; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
||:||||
Db 123 KVFVFFS 128

RESULT 11
G97000
diguanylate cyclase/phosphodiesterase domain (GGDEF) containing protein [imported] - Clo
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97000
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-571 <KUR>
A;Cross-references: UNIPROT:Q97KU8; UNIPARC:UPI00000C9FBF; GB:AE001437; PIDN:AAK78794.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0818

Query Match 90.3%; Score 28; DB 2; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
||:||||
Db 314 KWFVFA 319

RESULT 12
T37742
serine threonine-protein kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: T37742
R;Rieger, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: Z21743
A;Accession: T37742
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1072 <RIE>
A;Cross-references: UNIPROT:O94537; UNIPARC:UPI0000069E8D; EMBL:AL035248; PIDN:CAA22846
A;Experimental source: strain 972h-; cosmid c167
C;Genetics:
A;Gene: spaci67.01; SPDB:SPAC167.01
A;Map position: 1
A;Introns: 1015/3

Query Match 90.3%; Score 28; DB 2; Length 1072;
Best Local Similarity 83.3%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
||:||||
Db 13 KVFVFFS 18

RESULT 13
B72420
hypothetical protein TM0088 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: B72420
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: B72420
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1285 <ARN>
 A:Cross-references: UNIPROT:Q9WUX3; UNIPARC:UPI00000D3A9B; GB:AE001695; GB:AE000512; NID
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TW0088

Query Match 90.3%; Score 28; DB 2; Length 1285;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 |||||
 Db 341 KVFVFA 346

RESULT 14
 S07937
 hypothetical protein atpH 5'-region - Euglena gracilis chloroplast (fragment)
 C:Species: chloroplast Euglena gracilis
 C>Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 09-Jul-2004
 C:Accession: S07937
 R:Passavant, C.W.; Hallick, R.B.
 Plant Mol. Biol. 4, 347-354, 1985
 A:Title: Location, nucleotide sequence and expression of the proton-translocating subuni
 A:Reference number: S07400
 A:Accession: S07937
 A:Molecule type: DNA
 A:Residues: 1-38 <PAS>
 A:Cross-references: UNIPROT:Q32187; UNIPARC:UPI00000965CE; EMBL:M16844; NID:g336867; PID
 C:Comment: This is the hypothetical translation of a sequence that was not reported as a
 C:Genetics:
 A:Genome: chloroplast
 C:Keywords: chloroplast

Query Match 87.1%; Score 27; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 |||||
 Db 18 KVFVFF 22

RESULT 15
 C70150
 hypothetical protein BB0404 - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C:Accession: C70150
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 i Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943; PMID:9403685
 A:Accession: C70150
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-138 <KLE>
 A:Cross-references: UNIPROT:O51365; UNIPARC:UPI000005747C; GB:AE001146; GB:AE000783; NID
 A:Experimental source: strain B31

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 |||||
 Db 7 KVFVFF 11

RESULT 18
 S45022

C:Superfamily: Borrelia burgdorferi hypothetical protein BB0404

Query Match 87.1%; Score 27; DB 2; Length 138;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 |||||
 Db 40 KVFVFA 45

RESULT 16
 I40051
 signal peptidase I (EC 3.4.21.89) - Bacillus amyloliquefaciens
 N:Alternate names: leader peptidase
 C:Species: Bacillus amyloliquefaciens
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I40051; S38885
 R:Tominson, I.M.; Cook, G.P.; Carter, N.P.; Elasarapu, R.; Smith, S.; Walter, G.; Bulu
 Hum. Mol. Genet. 3, 853-860, 1994
 A:Title: Human immunoglobulin VH and D segments on chromosomes 15q11.2 and 16p11.2.
 A:Reference number: 137619; MUID:95038735; PMID:7951227
 A:Accession: I40051
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-185 <RES>
 A:Cross-references: UNIPROT:P41026; UNIPARC:UPI000012E452; EMBL:Z27458; NID:g429069; PID
 C:Genetics:
 A:Gene: sipa
 A:Start codon: TTG
 C:Superfamily: signal peptidase I sips
 C:Keywords: hydrolase; serine proteinase

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 |||||
 Db 172 KVFVFF 176

RESULT 17
 C70199
 hypothetical protein BB0796 - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C:Accession: C70199
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 i Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943; PMID:9403685
 A:Accession: C70199
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-185 <KLE>
 A:Cross-references: UNIPROT:O51736; UNIPARC:UPI00000575FE; GB:AE001178; GB:AE000783; NID
 A:Experimental source: strain B31

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 |||||
 Db 7 KVFVFF 11

RESULT 18
 S45022

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C/Accession: AH0299
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N. Nature 413, 523-527, 2001

A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AH0299
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-232 <KUR>
A/Cross-references: UNIPROT:Q8ZDV0; UNIPARC:UPI00000DCD3E; GB:AL590842; PIDN:CAC91260.1
C/Genetics:
A/Gene: YPO2455

Query Match 87.1%; Score 27; DB 2; Length 232;
Best Local Similarity 100.0%; Pred.No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
|||
Db 19 KVFVF 23

RESULT 21
E72329
hypothetical protein TM0818 - *Thermotoga maritima* (strain MSB8)
C/Species: *Thermotoga maritima*
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: E72329
R/Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickie, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. C.M. Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: E72329
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-274 <ARN>
A/Cross-references: UNIPROT:Q9WZS5; UNIPARC:UPI00000D3985; GB:AE001749; GB:AE000512; NIN
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TM0818

Query Match 87.1%; Score 27; DB 2; Length 274;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
|||
Db 260 KVFVF 264

RESULT 22
T29189
hypothetical protein C55C3.2 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29189
R/Woessne, J.; Stellyes, L.
submitted to the EMBL Data Library, April 1996
A/Description: The sequence of *C. elegans* cosmid C55C3.
A/Reference number: Z20585
A/Accession: T29189
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-298 <WOB>
A/Cross-references: UNIPROT:Q18868; UNIPARC:UPI0000074B15; EMBL:U53335; PIDN:AAA96172.1
A/Experimental source: strain Bristol N2; clone C55C3
C/Genetics:
A/Gene: CESP:C55C3.2

A:Map position: 4
A:introns: 35/1; 64/3; 212/3; 260/1

Query Match 87.1%; Score 27; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
|||||
DB 85 KVVFF 89

RESULT 23
T06845
hypothetical protein ycf39 - Cyanophora paradoxa cyanelle
C:Species: cyanelle Cyanophora paradoxa
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06845
R:Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
submitted to the EMBL Data Library, July 1995
A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A:Reference number: Z15840
A:Accession: T06845
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-321 <STI>
A:Cross-references: UNIPROT:P48279; UNIPARC:UPI000013A4A8; EMBL:U30821; NID:g1016083; PI
A:Experimental source: cv. strain Pringsheim LB555
C:Genetics:
A:Gene: ycf39
A:Genome: cyanelle
C:Keywords: cyanelle

Query Match 87.1%; Score 27; DB 2; Length 321;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
DB 104 KTIFFS 109

RESULT 24
S73198
hypothetical protein 349 - red alga (Porphyra purpurea) chloroplast
C:Species: chloroplast Porphyra purpurea
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S73198
R:Keith, M.; Munholland, J.
Plant Mol. Biol. Rep. 13, 333-335, 1995
A:Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.
A:Reference number: S73108
A:Accession: S73198
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-349 <REI>
A:Cross-references: UNIPROT:P51277; UNIPARC:UPI000013A78F; EMBL:U38804; NID:g1276652; PI
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Genome: chloroplast
C:Superfamily: leucine zipper-containing protein AT103
C:Keywords: chloroplast

Query Match 87.1%; Score 27; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
DB 156 KTIFFA 161

RESULT 25

S74431
hypothetical protein sl1214 - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S74431
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, D.
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S74431
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74431
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <KAN>
A:Cross-references: UNIPROT:P72584; UNIPARC:UPI00000C0997; EMBL:D90899; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 358;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:
DB 165 KFIFFA 170

RESULT 26
AE2218
hypothetical protein alr3300 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2218
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2218
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <KUR>
A:Cross-references: UNIPROT:O8VEZ2; UNIPARC:UPI00000CE73B; GB:BA0000019; PIDN:BA874999.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3300
C:Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 358;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:
DB 165 KFIFFA 170

RESULT 27
H90559
hypothetical protein MYPV 3840 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90559
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: H90559
A>Status: preliminary
A:Molecule type: DNA

A;Residues: 1-370 <KUR>
A;Cross-references: UNIPROT:Q98QH7; UNIPARC:UPI00000C807C; GB:AL445566; PID:g14089798; P
A;Experimental source: strain UAB Crip
C;Genetics:
A;Gene: MYPU 3840
A;Genetic code: SGC3

Query Match 87.1%; Score 27; DB 2; Length 370;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
|::|||
Db 23 KYIFFA 28

RESULT 28
T23285
hypothetical protein K03D7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23285
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19721
A;Accession: T23285
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-408 <WIL>
A;Cross-references: UNIPROT:O45653; UNIPARC:UPI00000610BB; EMBL:Z81562; PIDN:CAB04555.1;
A;Experimental source: clone K03D7
C;Genetics:
A;Gene: CESP:K03D7.8
A;Map position: 5
A;Introns: 117/3; 304/1

Query Match 87.1%; Score 27; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|::|||
Db 243 KFVFF 247

RESULT 29
T47754
leucine zipper-containing protein AT103 - Arabidopsis thaliana
N;Alternate names: FNIL34 protein homolog; protein F24I3.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47754; S71218
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47754
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <NYA>
A;Cross-references: UNIPROT:Q9MK4; UNIPARC:UPI00000A741A; EMBL:AL138655
A;Experimental source: cultivar Columbia; BAC clone F24I3
R;Zheng, C.C.; O'Neill, S.D.
submitted to the EMBL Data Library, October 1995
A;Description: Molecular analysis of a novel phytochrome-regulated Phorbis cDNA and its
A;Reference number: S71218
A;Accession: S71218
A;Molecule type: mRNA
A;Residues: 37-156, 'S', 158-409 <ZHE>
A;Cross-references: UNIPARC:UPI00000A9BBC; EMBL:U38232; NID:g10333194; PID:g10333195
C;Genetics:
A;Gene: AT103
A;Map position: 3
A;Introns: 158/3; 180/2; 289/3; 322/3

A;Note: F24I3.20
C;Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
|::|||
Db 210 KFIFYA 215

RESULT 30
E96635
hypothetical protein T7P1.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-436 <STO>
A;Cross-references: UNIPROT:Q9C954; UNIPARC:UPI00000483C7; GB:AE005173; NID:g6751689; P
C;Genetics:
A;Gene: T7P1.13
A;Map position: 1

Query Match 87.1%; Score 27; DB 2; Length 436;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
|::|||
Db 185 KYIFFA 190

RESULT 31
B72361
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72361
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72361
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-459 <ARN>
A;Cross-references: UNIPROT:Q9WZ33; UNIPARC:UPI00000C13F0; GB:AE001731; GB:AE0000512; N
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0563

Query Match 87.1%; Score 27; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5

```

Db          210 KFVFF 214
|||||
RESULT 32
T20124
hypothetical protein C50H2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20124
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19226
A:Accession: T20124
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: S48758
A:Molecule type: DNA
A:Residues: 1-488 <WIL>
A:Cross-references: UNIPROT:Q18760; UNIPARC:UPI000007F0DB; EMBL:Z73971; PIDN:CAA98250.1;
A:Experimental source: clone C50H2
C:Genetics:
A:Gene: CESP:C50H2.2
A:Map position: 5
A:Introns: 67/2; 107/3; 138/3; 180/3; 337/2; 391/3; 445/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C50H2.2

Query Match      87.1%; Score 27; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
DB 203 KFVFF 207
|||||

RESULT 33
H86248
protein T23J18.22 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86248
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-522 <STO>
A:Cross-references: UNIPROT:Q9LPY0; UNIPARC:UPI00000A13DA; GB:AE005172; NID:G6554189; PI
C:Genetics:
A:Gene: T23J18.22
A:Map position: 1

Query Match      87.1%; Score 27; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
DB 257 KFVFF 261
|||||

RESULT 34
S49827
probable membrane protein YDR072c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D4405; hypothetical protein YD8554.05c

```

```

C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: S49827; S48758; S55820; S67889; S67888
R:Richards, C.; Harris, D.E.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49823
A:Accession: S49827
A:Molecule type: DNA
A:Residues: 1-527 <RIC>
A:Cross-references: UNIPROT:P38954; UNIPARC:UPI000012D81A; EMBL:Z46796; NID:G577794; PIL
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48758
A:Accession: S48758
A:Molecule type: DNA
A:Residues: 1-524 <COS>
A:Cross-references: UNIPARC:UPI0000168B70; EMBL:X82086; NID:G558241; PID:G558243
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
Yeast 11, 673-679, 1995
A:Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading fr
A:Reference number: S55819; MUID:96093910; PMID:7483840
A:Accession: S55820
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-525 <COW>
A:Cross-references: UNIPARC:UPI000017B30A; EMBL:X82086
R:Foury, F.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67889
A:Accession: S67889
A:Molecule type: DNA
A:Residues: 1-524 <FOU>
A:Cross-references: UNIPARC:UPI0000168B70; EMBL:Z74368; MIPS:YDR072C
A:Experimental source: strain S288C
R:Bloeker, H.; Brandt, F.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67587
A:Accession: S67888
A:Molecule type: DNA
A:Residues: 417-527 <BLO>
A:Cross-references: UNIPARC:UPI000017B30B; EMBL:Z74368; MIPS:YDR072C
C:Genetics:
A:Gene: SGD:SYR4
A:Cross-references: SGD:S0002479; MIPS:YDR072C
A:Map position: 4R
C:Keywords: transmembrane protein
F:24-40/Domain: transmembrane #status predicted <TM1>
F:101-117/Domain: transmembrane #status predicted <TM2>
F:153-169/Domain: transmembrane #status predicted <TM3>
F:194-210/Domain: transmembrane #status predicted <TM4>
F:294-310/Domain: transmembrane #status predicted <TM5>
F:462-478/Domain: transmembrane #status predicted <TM6>

Query Match      87.1%; Score 27; DB 2; Length 527;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFVFF 6
DB 62 KFVFF 67
|||||

RESULT 35
B81107
exodeoxyribonuclease V, alpha chain NMB1233 [imported] - Neisseria meningitidis (strain
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81107
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.B.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiagnani, V.; Pizza, M.
Science 287, 1809-1815, 2000

```


A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-581 <TET>
A;Cross-references: UNIPROT:Q9J293; UNIPARC:UPI000000C4671; GB:AE002098; NID
A;Experimental source: serogroup B, strain MC58
C;Genetics:
C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
|||||
546 KPVFF 550

Db

RESULT 36
B81909
exodeoxyribonuclease V alpha subunit NMA1401 [imported] - *Neisseria meningitidis* (strain
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81909
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moulle, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-581 <PAR>
A;Cross-references: UNIPROT:Q9JUB9; UNIPARC:UPI000000C48B0; GB:AL162755; NID
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: recD; NMA1401
C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
|||||
546 KPVFF 550

Db

RESULT 37
I38028
matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N;Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
C;Species: *Homo sapiens* (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: I38028; G03274; I38046; S78011; S45341; S71384
R;Will, H.; Hinzmann, B.
Eur. J. Biochem. 231, 602-608, 1995
A;Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote
A;Reference number: I38028; MUID:95377289; PMID:7649159
A;Accession: I38028
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-582 <WILL>
A;Cross-references: UNIPROT:P50281; UNIPARC:UPI00000048136; EMBL:Z48481; NID:G963053; PII
R;Luo, G.
submitted to the EMBL Data Library, November 1995
A;Reference number: H00963
A;Accession: G02274
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-582 <LUO>
A;Cross-references: UNIPARC:UPI00000048136; EMBL:U41078; NID:g1127836; PIDN:AAA83770.1;
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset,
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal c
A;Reference number: I38046; MUID:95224014; PMID:7708715
A;Accession: I38046
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-7,'S',9-582 <OKA>
A;Cross-references: UNIPARC:UPI000003096F; EMBL:X83535; NID:g804993; PIDN:CAA58519.1; P
R;Seiki, M.
submitted to the EMBL Data Library, January 1994
A;Reference number: S78011
A;Accession: S78011
A;Molecule type: mRNA
A;Residues: 1-7,'S',9-337,'K',339-582 <SEI>
A;Cross-references: UNIPARC:UPI000003DC76; EMBL:D26512; NID:g793762; PIDN:BAA05519.1; P
R;Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shingawa, A.; Yamamoto, E.; Seiki, M.
Nature 370, 61-65, 1994
A;Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A;Reference number: S45341; MUID:94286011; PMID:8015608
A;Accession: S45341
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-7,'S',9-188,'R',190,'A',192-267,'K',269-272,'HY',275,'P',277-285,'KQ',288
A;Cross-references: UNIPARC:UPI0000157586; EMBL:D26512
R;Sato, H.; Kinoschita, T.; Takino, T.; Nakayama, K.; Seiki, M.
FEBS Lett. 393, 101-104, 1996
A;Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A;Reference number: S71384; MUID:96397540; PMID:8804434
A;Accession: S71384
A;Molecule type: protein
A;Residues: 112-116 <SAW>
A;Cross-references: UNIPARC:UPI0000175D8E
C;Genetics:
A;Gene: GDB:MMP14; MT1-MMP
A;Cross-references: GDB:375731; OMIM:600754
A;Map position: 14q11-14q12
C;Superfamily: interstitial collagenase; matrix metalloproteinase; zinc; zymogen
C;Keywords: glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>
F;1-23/Domain: signal sequence #status predicted <PRO>
F;24-97/Domain: activation peptide #status predicted <PRO>
F;61-284/Domain: matrix metalloproteinase homology <MMP>
F;98-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>
F;285-313/Domain: hinge #status predicted <HNG>
F;314-508/Domain: hemopexin repeat homology <PXN>
F;539-562/Domain: transmembrane #status predicted <TMW>
F;93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;130/Binding site: carboxylate (Asn) (covalent) #status predicted
F;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F;240/Active site: Glu #status predicted
F;319-508/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
|||||
378 KPVFF 382

Db

RESULT 38
I84471
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
N;Alternate names: membrane-type metalloproteinase
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I84471; I61946
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset,
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995

A>Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cell
A:Reference number: 138046; MUID:95224014; PMID:7708715
A:Accession: I84471
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: UNIPROT:Q10739; UNIPARC:UPI0000030970; EMBL:X83537; NID:g805012; PID
A:Accession: I61946
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-67, 'M', '69-254', 'A', '256-582' <RE2>
A:Cross-references: UNIPARC:UPI00001679D1; EMBL:X91785; NID:g1001926; PIDN:CAA62897.1; P
C:Genetics:
A:Gene: mt-mmp
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>
F:61-284/Domain: matrix metalloproteinase homology <MPP>
F:313-508/Domain: hemopexin repeat homology <PXN>
F:93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted

Query Match 87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||||
Db 378 KFVFF 382

RESULT 39
JC7286
liver-specific organic anion transporter-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: JC7286
R:Ogura, K.; Choudhuri, S.; Klaassen, C.D.
Biochem. Biophys. Res. Commun. 272, 563-570, 2000
A>Title: Full-length cDNA cloning and genomic organization of the mouse liver-specific o
A:Reference number: JC7286
A:Accession: JC7286
A:Molecule type: mRNA
A:Residues: 1-689 <OGU>
A:Cross-references: UNIPROT:Q9JUL3; UNIPARC:UPI000023434; DDBJ:AB031959
C:Genetics:
A:Gene: lst-1
C:Keywords: glycolysis; transmembrane protein

Query Match 87.1%; Score 27; DB 2; Length 689;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||||
Db 404 KFVFF 408

RESULT 40
S30338
hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - German cockroach
C:Species: Blattella germanica (German cockroach)
C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 27-Oct-2003
C:Accession: S30338
R:Martinez-Gonzalez, J.; Buesa, C.; Piuilachs, M.D.; Belles, X.; Hegardt, F.G.
Eur. J. Biochem. 213, 233-241, 1993
A>Title: Molecular cloning, developmental pattern and tissue expression of 3-hydroxy-3-m
A:Reference number: S30338; MUID:93238692; PMID:8477698
A:Accession: S30338
A:Molecule type: mRNA
A:Residues: 1-856 <MAR>

A:Cross-references: UNIPARC:UPI0000174EF6
C:Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase
C:Keywords: coenzyme A; NADP; oxidoreductase

Query Match 87.1%; Score 27; DB 2; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||||
Db 360 KFVFF 364

RESULT 41
S44883
ZC262.3 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S44883
R:Anderson, K.
submitted to the EMBL Data Library, September 1993
A:Description: Sequence of the C. elegans cosmid ZC262.
A:Reference number: S44818
A:Accession: S44883
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-857 <AND>
A:Cross-references: UNIPROT:P34595; UNIPARC:UPI0000179325; EMBL:L23647; NID:g388612; PII
C:Genetics:
A:Introns: 72/2; 145/1; 191/1; 263/3; 297/1; 363/2; 403/2; 448/2; 523/2; 563/2; 613/2; 7
C:Superfamily: Caenorhabditis elegans ZC262.3 protein

Query Match 87.1%; Score 27; DB 2; Length 857;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||||
Db 87 KFVFF 91

RESULT 42
T31795
hypothetical protein R02F11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31795
R:Davidson, S.; Wohlmann, P.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid R02F11.
A:Reference number: Z21087
A:Accession: T31795
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-870 <DAV>
A:Cross-references: UNIPROT:O16363; UNIPARC:UPI000016423C; EMBL:AF016439; PIDN:AAB65898.
A:Experimental source: strain Bristol N2; clone R02F11
C:Genetics:
A:Gene: CESP:R02F11.2
A:Map position: 5
A:Introns: 44/2; 116/2; 164/3; 265/2; 335/2; 380/1; 419/3; 475/1; 582/2; 643/3; 6

Query Match 87.1%; Score 27; DB 2; Length 870;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
:|:|:|
Db 2 RFIFPA 7

RESULT 43
SS6900

probable membrane protein YJL119c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein J0738

C;Species: Saccharomyces cerevisiae

C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C;Accession: S56900

R;Cziepluch, C.; Kordes, E.; Fajol, A.; Jauniaux, J.C.

submitted to the Protein Sequence Database, September 1995

A;Reference number: S56891

A;Accession: S56900

A;Molecule type: DNA

A;Residues: 1-107 <CZI>

A;Cross-references: UNIPROT:P47021; UNIPARC:UPI000013B5B8; EMBL:Z49394; NID:g1008309; PI

C;Genetics:

A;Gene: MIPS:YJL119c

A;Cross-references: SGD:S0003655

A;Map position: 10L

C;Superfamily: Saccharomyces probable membrane protein YJL119c

C;Keywords: transmembrane protein

Query Match 83.9%; Score 26; DB 2; Length 107;

Best Local Similarity 83.3%; Pred. No. 76;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFVFFA 6

Db 102 KPFFFA 107

RESULT 44

G87731

protein W10C8.3 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C;Accession: G87731

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/c_ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: G87731

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-127 <STO>

A;Cross-references: UNIPARC:UPI0000164023; GB:chr_I; PIDN:AAB97593.1; PID:g2804486; GSPT

C;Genetics:

A;Gene: W10C8.3

A;Map position: 1

Query Match 83.9%; Score 26; DB 2; Length 127;

Best Local Similarity 80.0%; Pred. No. 89;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 83 KPIFF 87

RESULT 45

C81280

probable periplasmic cytochrome C Cj1358c [imported] - Campylobacter jejuni (strain NCTC

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C;Accession: C81280

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: C81280

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-171 <PAR>

A;Cross-references: UNIPROT:O9PMU1; UNIPARC:UPI00000C1EDC; GB:AL139078; GB:AL111168; NID

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj1358c

C;Superfamily: denitrification system component NapC/NirT(membrane-bound tetraheme cyto

Query Match 83.9%; Score 26; DB 2; Length 171;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6

Db 24 FVFFA 28

RESULT 46

T47707

hypothetical protein F116.90 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: T47707

R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.

submitted to the Protein Sequence Database, March 2000

A;Reference number: Z24473

A;Accession: T47707

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-183 <BEN>

A;Cross-references: UNIPROT:Q9M054; UNIPARC:UPI00000A2185; EMBL:AL161667

A;Experimental source: cultivar Columbia; BAC clone F116

C;Genetics:

A;Map position: 3

A;Introns: 70/3

A;Note: F116.90

Query Match 83.9%; Score 26; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6

Db 18 FVFFA 22

RESULT 47

A86806

transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C;Accession: A86806

R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrh

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: A86806

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-188 <STO>

A;Cross-references: UNIPROT:Q9CFL8; UNIPARC:UPI00000C6A3D; GB:AE005176; PID:g12724440;

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: yohC

Query Match 83.9%; Score 26; DB 2; Length 188;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 170 KPIFF 174

RESULT 48

S73449
 MG028 homolog B01_orf203 - Mycoplasma pneumoniae (strain ATCC 29342)
 C:Species: Mycoplasma pneumoniae
 A:Variety: ATCC 29342
 C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
 C:Accession: S73449
 R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkle, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
 A:Reference number: S73327; MUID:97105885; PMID:8948633
 A:Accession: S73449
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-203 <HIM>
 A:Cross-references: UNIPROT:P75083; UNIPARC:UPI000013912P; EMBL:AE000015; GB:U00089; NID
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C:Genetics:
 A:Genetic code: SGC3
 C:Superfamily: uncharacterized conserved protein

Query Match 83.9%; Score 26; DB 2; Length 203;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 89 FVFFA 93

RESULT 49
 G70437
 soluble hydrogenase small subunit - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
 C:Accession: G70437
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: G70437
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-216 <AQF>
 A:Cross-references: UNIPROT:Q67529; UNIPARC:UPI0000056670; GB:AE000746; NID:G2983925; PI
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: hys
 C:Superfamily: serine-pyruvate/aspartate aminotransferase

Query Match 83.9%; Score 26; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 61 FVFFA 65

RESULT 50
 F86844
 hypothetical protein ysbD [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: F86844
 R:Botolin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-755, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: F86844
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <STO>

A:Cross-references: UNIPROT:Q9CES6; UNIPARC:UPI0000006AFC; GB:AE005176; PID:g12724779; I
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: ysbD
 C:Superfamily: dedA protein

Query Match 83.9%; Score 26; DB 2; Length 218;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 DB 155 KFIFP 159

RESULT 51
 T22101
 hypothetical protein F42F12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22101
 R:Lloyd, C.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19514
 A:Accession: T22101
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-243 <WIL>
 A:Cross-references: UNIPROT:Q20344; UNIPARC:UPI000007AEF3; EMBL:Z68116; PIDN:CAA92173.1;
 A:Experimental source: Clone F42F12
 C:Genetics:
 A:Gene: CESP:F42F12.3
 A:Map position: X
 A:Introns: 85/2; 138/1; 222/2
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

Query Match 83.9%; Score 26; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 18 FVFFA 22

RESULT 52
 B81693
 conserved hypothetical protein TC0525 [imported] - Chlamydia muridarum (strain Nigg)
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: B81693
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 , C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: B81693
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-255 <TF>
 A:Cross-references: UNIPROT:Q9PKE0; UNIPARC:UPI0000057969; GB:AE002321; GB:AE002160; NII
 A:Experimental source: strain Nigg (MoPn)
 C:Genetics:
 A:Gene: TC0525
 C:Superfamily: Chlamydia trachomatis hypothetical protein CT254

Query Match 83.9%; Score 26; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 68 FVFFA 72

RESULT 55

```

Query Match      83.9%; Score 26; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
DB      4 FVFFFA 8

RESULT 58
S75656
hypothetical protein slr1980 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75656
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75656
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <KAN>
A:Cross-references: UNIPROT:P74131; UNIPARC:UPI00000C100A; EMBL:D90912; GB:AB001339; NID
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      83.9%; Score 26; DB 2; Length 297;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPEVFF 5
DB     104 KPEIFF 108

RESULT 59
D86216
protein T23G18.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86216
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86216
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <STO>
A:Cross-references: UNIPROT:Q9SGD8; UNIPARC:UPI000009EE07; GB:AE005172; NID:G6579209; PI
C:Genetics:
A:Gene: T23G18.8
A:Map position: 1

Query Match      83.9%; Score 26; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVEFFA 6
DB     99 FVFFFA 103

```

```

RESULT 60
T24424
hypothetical protein T04A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24424
R:Palmer, S.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19889
A:Accession: T24424
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <WIL>
A:Cross-references: UNIPROT:P46568; UNIPARC:UPI000006112C; EMBL:Z35663; PIDN:CAA84725.1;
A:Experimental source: clone T04A8
C:Genetics:
A:Gene: CESP:T04A8.1
A:Map position: 3
A:Introns: 77/3; 150/3; 198/3; 259/3

Query Match      83.9%; Score 26; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
DB     262 FVFFFA 266

RESULT 61
S08459
hypothetical protein 2 - spiroplasma virus 1
C:Species: spiroplasma virus 1, SpV1
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 02-Mar-2001
C:Accession: S08459; S08447
R:Renaudin, J.; Aulio, P.; Vignault, J.C.; Bove, J.M.
Nucleic Acids Res. 18, 1293, 1990
A:Title: Complete nucleotide sequence of the genome of Spiroplasma citri virus SpV1-R8A2
A:Reference number: S08447; MUID:90206799; PMID:2320423
A:Accession: S08459
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <REN>
A:Cross-references: UNIPARC:UPI0000138546; EMBL:X51344
A:Accession: S08447
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 262-337 <RE2>
A:Cross-references: UNIPARC:UPI0000161E8D; EMBL:X51344; NID:g61993; PIDN:CAA35725.1; PID
C:Genetics:
A:Genetic code: SGC3

Query Match      83.9%; Score 26; DB 2; Length 337;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFF 5
DB      3 KPIFF 7

RESULT 62
E90564
potassium channel protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90564
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21267165; PMID:1133084
A:Accession: E90564
A>Status: preliminary

```

A;Genome: mitochondrion
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; cytochrome b6 homology; plastoquinone C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrial protein; cytochrome b6 homology; cytochrome b6 homology <CBH>
F;10-340/Domain: cytochrome b6 homology <CBH>
F;10-210/Domain: cytochrome b6 homology <CB6>
F;35-51/Domain: transmembrane #status predicted <TM1>
F;80-98/Domain: transmembrane #status predicted <TM2>
F;118-134/Domain: transmembrane #status predicted <TM3>
F;179-201/Domain: transmembrane #status predicted <TM4>
F;222-340/Domain: plastocyanin-plastocyanin reductase 17K protein homology <17K>
F;230-246/Domain: transmembrane #status predicted <TM5>
F;289-305/Domain: transmembrane #status predicted <TM6>
F;324-344/Domain: transmembrane #status predicted <TM7>
F;354-370/Domain: transmembrane #status predicted <TM8>
F;82,183/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F;96,197/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 83.9%; Score 26; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||
Db 243 FVFFA 247

RESULT 65
T22810
hypothetical protein F56H9_4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22810
R;Burton, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19618
A;Accession: T22810
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-390 <WIL>
A;Cross-references: UNIPROT:Q20910; UNIPARC:UPI000007F97A; EMBL:Z74473; PIDN:CAA98953.1
A;Experimental source: clone F56H9
C;Genetics:
A;Gene: CSP:F56H9_4
A;Map position: 5
A;Introns: 51/1; 65/2; 112/3; 229/2; 247/3; 278/3; 330/1; 370/3
C;Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match 83.9%; Score 26; DB 2; Length 390;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
|||
Db 229 KVIFF 233

RESULT 66
T00516
hypothetical protein At2g23160 [imported] - Arabidopsis thaliana
C;Alternate names: hypothetical protein T20D16.21
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 31-Dec-2004
C;Accession: T00516; C84621
R;Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
A;Reference number: Z14164
A;Accession: T00516
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-395 <ROU>
A;Cross-references: UNIPROT:O22191; UNIPARC:UPI00000AAAFDA; EMBL:AC002391; NID:g2642427;
A;Experimental source: cultivar Columbia

R.;lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: AB4420; MUID:20083487; PMID:10617197

A;Accession: C84621

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <STO>

A;Cross-references: UNIPARC:UPI00000AAFDA; GB:AE002093; NID:g2642447; PIDN:AAB87115.1; C;Genetics:

A;Gene: At2g23160; T20D16.21

A;Map position: 2

A;Introns: 295/3

A;Note: T20D16.21

C;Superfamily: hypothetical protein containing F-box domain

Query Match 83.9%; Score 26; DB 2; Length 395;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFP 5
||:|
Db 245 KPIFF 249

RESULT 67

D81040

Cytochrome c-type biogenesis protein, probable NMB1803 [imported] - Neisseria meningitidis

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: D81040

R;Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.

A;Reference number: AB1000; MUID:20175755; PMID:10710307

A;Accession: D81040

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <TET>

A;Cross-references: UNIPROT:Q9JY05; UNIPARC:UPI00000C47CE; GB:AE002530; GB:AE002098; NID

A;Experimental source: serogroup B, strain MCS8

C;Genetics:

A;Gene: NMB1803

Query Match 83.9%; Score 26; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
Db 120 FVFFA 124

RESULT 68

B81986

probable membrane protein NMA0660 [imported] - Neisseria meningitidis (strain Z2491 sero

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: B81986

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel i; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: AB1775; MUID:20222556; PMID:10761919

A;Accession: B81986

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <PAR>

A;Cross-references: UNIPROT:Q9JVV9; UNIPARC:UPI00000C4A09; GB:AL162753; GB:AL157959; NID

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA0660

Query Match 83.9%; Score 26; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
Db 120 FVFFA 124

RESULT 69

T46710

multidrug resistance transporter [imported] - Listeria monocytogenes

C;Species: Listeria monocytogenes

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46710

R;Huillet, E.E.H.; Larpin, S.; Pardon, P.; Berche, P. FEMS Microbiol Lett. 174, 265-272, 1999

A;Title: Identification of a new locus in Listeria monocytogenes involved in cellobiose- A;Reference number: Z23136; MUID:99271176; PMID:10339818

A;Accession: T46710

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-397 <HUI>

A;Cross-references: UNIPROT:Q9X769; UNIPARC:UPI0000055470; EMBL:AJ009627; NID:g4914621;

C;Genetics:

A;Gene: lltB

Query Match 83.9%; Score 26; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
Db 245 FVFFA 249

RESULT 70

AE1613

multidrug-efflux transporter homolog lin1446 [imported] - Listeria innocua (strain Clip1

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AE1613

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wenland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AE1613

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-397 <GLA>

A;Cross-references: UNIPROT:Q92B08; UNIPARC:UPI00000CC57B; GB:AL592022; PIDN:CAC96677.1;

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin1446

Query Match 83.9%; Score 26; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
Db 245 FVFFA 249

RESULT 71
 A:Accession: A11250
 C:Species: Listeria monocytogenes (strain
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A:Authors: Kneft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
 A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: A11250
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-397 <GLA>
 A:Cross-references: UNIPROT:Q9X769; UNIPARC:UPI0000055470; GB:NC_003210; PIDN:CAC99487.1
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo1409

Query Match 83.9%; Score 26; DB 2; Length 397;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPPA 6
 |||||
 Db 245 FVFPPA 249

RESULT 72
 T44331
 C:Species: Vibrio cholerae
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T44331
 R:Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
 Gene 237, 321-332, 1999
 A:Title: The genes responsible for O-antigen synthesis of *Vibrio cholerae* O139 are close
 A:Reference number: 222749; MUID:99453293; PMID:10521656
 A:Accession: T44331
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-398 <YAM>
 A:Cross-references: UNIPROT:O87160; UNIPARC:UPI0000055419; EMBL:AB012957; NID:G4115688;
 A:Experimental source: strain O22
 C:Genetics:
 A:Note: wblD

Query Match 83.9%; Score 26; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPPA 6
 |||||
 Db 263 FVFPPA 267

RESULT 73
 H69833
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Broutillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galle
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maues
 Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Toato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A95580; MUID:98044033; PMID:9384377
 A:Accession: H69833
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-401 <KUN>
 A:Cross-references: UNIPROT:O07563; UNIPARC:UPI00000601AF; GB:Z99109; GB:AL009136; NID:
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yhj1

Query Match 83.9%; Score 26; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPPA 6
 |||||
 Db 215 FVFPPA 219

RESULT 74
 C95990
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: C95990
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing end
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: C95990
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <KUR>
 A:Cross-references: UNIPROT:Q92UB4; UNIPARC:UPI00000CB7A2; GB:AL591985; PIDN:CAC49587.1
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, J.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: gnuB; Smb20893
 A:Genome: plasmid
 C:Superfamily: l-arabinose transport system permease arah

Query Match 83.9%; Score 26; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPPA 6
 |||||
 Db 223 FVFPPA 227

RESULT 75
 CBQFR
 C:Species: Rhodospirillum rubrum
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: S12257; A38814
 R:Majewski, C.; Trebat, A.

Mol. Gen. Genet. 224, 373-382, 1990
A:Title: The pet Genes of Rhodospirillum rubrum: cloning and sequencing of the genes for
A:Reference number: S12255; MUID:91094774; PMID:2176269
A:Accession: S12257
A:Molecule type: DNA
A:Residues: 1-405 <MA1>
A:Cross-references: UNIPROT:P23134; UNIPARC:UPI0000128ACD; EMBL:X55387; NID:946382; PIDN
A>Note: the authors translated the codon AAT for residue 161 as Leu and CTG for residue
A:Accession: A38814
A:Molecule type: protein
A:Residues: 1-26, 'E' <MA2>
A:Cross-references: UNIPARC:UPI0000171D0F
C:Genetics:
A:Gene: petB
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; oxidoreductase
F:1-405/Product: cytochrome b #status experimental <MAT>
F:22-354/Domain: cytochrome b homology <CBH>
F:22-222/Domain: cytochrome b6 homology <CB6>
F:47-63/Domain: transmembrane #status predicted <TM1>
F:92-110/Domain: transmembrane #status predicted <TM2>
F:130-146/Domain: transmembrane #status predicted <TM3>
F:191-213/Domain: transmembrane #status predicted <TM4>
F:236-354/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F:244-260/Domain: transmembrane #status predicted <TM5>
F:303-319/Domain: transmembrane #status predicted <TM6>
F:338-356/Domain: transmembrane #status predicted <TM7>
F:368-384/Domain: transmembrane #status predicted <TM8>
F:94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:108,209/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 83.9%; Score 26; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 257 FVFFA 261

Search completed: December 29, 2005, 17:49:18
Job time : 13.9677 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KVFPPA 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA_New.*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pap.*
5: /cgn2_6/ptodata/2/pubppaa/US03_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	87.1	582	7	US-11-050-439-58
2	27	87.1	592	6	US-10-467-657-4888
3	27	87.1	738	7	US-11-147-047-48
4	27	87.1	1070	7	US-11-147-047-49
5	26	83.9	19	6	US-10-467-657-8712
6	26	83.9	220	6	US-10-467-657-3154
7	26	83.9	299	6	US-10-467-657-2190
8	26	83.9	395	6	US-10-467-657-1950
9	26	83.9	418	6	US-10-467-657-5788
10	25	80.6	19	6	US-10-923-605-5
11	25	80.6	19	6	US-10-934-818-5
12	25	80.6	40	7	US-11-016-706-36
13	25	80.6	40	7	US-11-098-674-12
14	25	80.6	42	6	US-10-923-605-1
15	25	80.6	42	6	US-10-934-818-1
16	25	80.6	42	7	US-11-016-706-37
17	25	80.6	43	6	US-10-934-818-6
18	25	80.6	43	6	US-10-250-581-1
19	25	80.6	43	6	US-10-250-581-1
20	25	80.6	184	6	US-10-467-657-7560
21	25	80.6	525	7	US-11-082-389-350
22	25	80.6	770	6	US-10-982-545-15
23	25	80.6	770	6	US-10-789-273-38
24	24	77.4	194	6	US-10-467-657-3978
25	24	77.4	229	6	US-10-793-626-62

26	24	77.4	443	6	US-10-793-626-1860	Sequence 1860, Ap
27	24	77.4	533	6	US-10-467-657-4566	Sequence 4566, Ap
28	24	77.4	657	7	US-11-080-991-48	Sequence 48, Appl
29	24	77.4	916	6	US-10-467-657-4242	Sequence 4242, Ap
30	24	77.4	4384	6	US-10-821-234-1120	Sequence 1120, Ap
31	23	74.2	49	6	US-10-467-657-1370	Sequence 1370, Ap
32	23	74.2	49	6	US-10-467-657-2308	Sequence 2308, Ap
33	23	74.2	49	6	US-10-467-657-5610	Sequence 5610, Ap
34	23	74.2	49	6	US-10-467-657-7516	Sequence 7516, Ap
35	23	74.2	49	6	US-10-467-657-8322	Sequence 8322, Ap
36	23	74.2	54	6	US-10-467-657-4324	Sequence 4324, Ap
37	23	74.2	56	6	US-10-467-657-8286	Sequence 8286, Ap
38	23	74.2	126	6	US-10-793-626-2766	Sequence 2766, Ap
39	23	74.2	209	6	US-10-793-626-304	Sequence 304, App
40	23	74.2	234	6	US-10-793-626-1034	Sequence 1034, Ap
41	23	74.2	288	6	US-10-467-657-4456	Sequence 4456, Ap
42	23	74.2	391	6	US-10-613-744-13	Sequence 13, Appl
43	23	74.2	410	6	US-10-467-657-4858	Sequence 4858, Ap
44	23	74.2	432	7	US-11-055-822-1096	Sequence 1096, Ap
45	23	74.2	432	7	US-11-113-424-186	Sequence 186, App
46	23	74.2	449	6	US-10-467-657-678	Sequence 678, App
47	23	74.2	534	7	US-11-082-389-348	Sequence 348, App
48	23	74.2	633	6	US-10-467-657-3440	Sequence 3440, Ap
49	23	74.2	633	6	US-10-467-657-4632	Sequence 4632, Ap
50	23	74.2	660	7	US-11-186-284-125	Sequence 125, App
51	23	74.2	708	6	US-10-821-234-917	Sequence 917, App
52	23	74.2	766	6	US-10-793-626-420	Sequence 420, App
53	23	74.2	1012	6	US-10-995-561-908	Sequence 908, App
54	23	74.2	2323	6	US-10-793-626-760	Sequence 760, App
55	23	71.0	30	6	US-10-467-657-8998	Sequence 8998, Ap
56	22	71.0	72	7	US-11-000-463-378	Sequence 378, App
57	22	71.0	72	7	US-11-000-463-850	Sequence 850, App
58	22	71.0	77	6	US-10-467-657-360	Sequence 360, App
59	22	71.0	79	6	US-10-467-657-2026	Sequence 2026, Ap
60	22	71.0	101	6	US-10-485-517-286	Sequence 286, App
61	22	71.0	139	6	US-10-467-657-6824	Sequence 6824, Ap
62	22	71.0	139	6	US-11-125-837-24	Sequence 24, Appl
63	22	71.0	149	6	US-10-467-657-6110	Sequence 6110, Ap
64	22	71.0	149	6	US-10-467-657-7550	Sequence 7550, Ap
65	22	71.0	154	6	US-10-467-657-6130	Sequence 6130, Ap
66	22	71.0	180	6	US-10-485-517-346	Sequence 346, App
67	22	71.0	187	6	US-10-980-388-65	Sequence 65, Appl
68	22	71.0	210	6	US-10-467-657-4386	Sequence 4386, Ap
69	22	71.0	222	6	US-10-467-657-3000	Sequence 3000, Ap
70	22	71.0	238	6	US-10-467-657-6248	Sequence 6248, Ap
71	22	71.0	240	7	US-11-054-515-1391	Sequence 1391, Ap
72	22	71.0	241	7	US-11-074-176-66	Sequence 66, Appl
73	22	71.0	250	6	US-10-793-626-1124	Sequence 1124, Ap
74	22	71.0	254	6	US-10-467-657-6144	Sequence 6144, Ap
75	22	71.0	288	6	US-10-467-657-1178	Sequence 1178, Ap
76	22	71.0	268	6	US-10-467-657-5704	Sequence 5704, Ap
77	22	71.0	277	6	US-10-667-295-85	Sequence 85, Appl
78	22	71.0	326	6	US-10-873-528-33	Sequence 33, Appl
79	22	71.0	328	6	US-10-848-375-1	Sequence 1, Appli
80	22	71.0	331	6	US-10-873-528-147	Sequence 147, App
81	22	71.0	341	6	US-10-858-730-124	Sequence 124, App
82	22	71.0	346	6	US-10-793-626-504	Sequence 504, App
83	22	71.0	347	6	US-10-821-234-1379	Sequence 1379, Ap
84	22	71.0	353	7	US-11-067-884-6	Sequence 6, Appli
85	22	71.0	353	6	US-10-467-657-2872	Sequence 2872, Ap
86	22	71.0	362	6	US-10-875-716-9	Sequence 9, Appli
87	22	71.0	366	7	US-11-055-822-400	Sequence 400, App
88	22	71.0	366	7	US-11-055-822-492	Sequence 492, App
89	22	71.0	376	6	US-10-793-626-490	Sequence 490, App
90	22	71.0	376	6	US-10-793-626-2260	Sequence 2260, Ap
91	22	71.0	383	6	US-10-793-626-2026	Sequence 2026, Ap
92	22	71.0	436	6	US-10-467-657-7578	Sequence 7578, Ap
93	22	71.0	445	6	US-10-821-234-1606	Sequence 1606, Ap
94	22	71.0	465	6	US-10-793-626-1676	Sequence 1676, Ap
95	22	71.0	481	6	US-10-995-561-959	Sequence 959, App
96	22	71.0	494	6	US-10-467-657-592	Sequence 592, App
97	22	71.0	505	6	US-10-873-528-120	Sequence 120, App
98	22	71.0	522	6	US-10-793-626-604	Sequence 604, App

99	22	71.0	528	6	US-10-864-758-7	Sequence 7, Appli	172	21	67.7	652	6	US-10-873-528-26	Sequence 26, Appl
100	22	71.0	541	7	US-11-000-463-238	Sequence 238, App	173	21	67.7	658	6	US-10-873-528-17	Sequence 17, Appl
101	22	71.0	566	6	US-10-467-657-8046	Sequence 8046, Ap	174	21	67.7	676	6	US-10-510-947-1	Sequence 1, Appli
102	22	71.0	578	6	US-11-083-800-2	Sequence 2, Appli	175	21	67.7	677	6	US-10-873-528-155	Sequence 155, App
103	22	71.0	607	7	US-11-080-991-88	Sequence 88, Appl	176	21	67.7	697	6	US-10-485-517-202	Sequence 202, App
104	22	71.0	709	6	US-10-131-826A-202	Sequence 202, App	177	21	67.7	756	6	US-10-467-657-8694	Sequence 8694, Ap
105	22	71.0	786	6	US-10-467-962B-103	Sequence 103, App	178	21	67.7	801	6	US-10-793-626-2020	Sequence 2020, Ap
106	22	71.0	940	6	US-10-131-826A-204	Sequence 204, App	179	21	67.7	837	7	US-11-094-519A-43	Sequence 43, Appl
107	22	71.0	943	6	US-10-821-234-1012	Sequence 1012, Ap	180	21	67.7	845	7	US-11-094-519A-42	Sequence 42, Appl
108	22	71.0	1062	6	US-10-821-234-1079	Sequence 1079, Ap	181	21	67.7	1052	6	US-10-467-657-3992	Sequence 3992, Ap
109	22	71.0	1070	7	US-11-000-463-721	Sequence 721, App	182	21	67.7	1076	6	US-10-467-657-5708	Sequence 5708, Ap
110	22	71.0	1194	7	US-11-000-463-249	Sequence 249, App	183	21	67.7	1170	7	US-11-080-026-2	Sequence 2, Appli
111	21	67.7	5	7	US-11-098-674-1	Sequence 1, Appli	184	21	67.7	1751	7	US-11-107-028-4	Sequence 4, Appli
112	21	67.7	39	6	US-10-467-657-4630	Sequence 4630, Ap	185	21	67.7	1751	7	US-11-103-957-45	Sequence 45, Appl
113	21	67.7	40	6	US-10-467-657-4616	Sequence 4616, Ap	186	20	64.5	16	7	US-11-089-764-65	Sequence 65, Appl
114	21	67.7	43	6	US-10-467-657-8642	Sequence 8642, Ap	187	20	64.5	16	7	US-11-089-764-66	Sequence 66, Appl
115	21	67.7	47	6	US-10-467-657-5436	Sequence 5436, Ap	188	20	64.5	23	7	US-11-085-812-16	Sequence 16, Appl
116	21	67.7	55	6	US-10-485-517-387	Sequence 387, App	189	20	64.5	23	7	US-11-085-812-16	Sequence 16, Appl
117	21	67.7	57	7	US-11-000-463-770	Sequence 770, App	190	20	64.5	28	6	US-10-250-581-14	Sequence 14, Appl
118	21	67.7	63	7	US-11-000-463-353	Sequence 353, App	191	20	64.5	28	6	US-10-250-581-14	Sequence 14, Appl
119	21	67.7	63	7	US-11-000-463-825	Sequence 825, App	192	20	64.5	28	6	US-10-250-581-17	Sequence 17, Appl
120	21	67.7	72	6	US-10-467-657-5578	Sequence 5578, Ap	193	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
121	21	67.7	72	6	US-11-000-463-298	Sequence 298, App	194	20	64.5	40	6	US-10-250-581-18	Sequence 18, Appl
122	21	67.7	75	6	US-10-467-657-8472	Sequence 8472, Ap	195	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
123	21	67.7	79	7	US-11-123-896-134	Sequence 134, App	196	20	64.5	40	6	US-10-250-581-18	Sequence 18, Appl
124	21	67.7	90	6	US-10-467-657-4374	Sequence 4374, Ap	197	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
125	21	67.7	91	6	US-10-821-234-1238	Sequence 1238, Ap	198	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
126	21	67.7	94	6	US-10-467-657-4730	Sequence 4730, Ap	199	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
127	21	67.7	102	6	US-10-467-657-5604	Sequence 5604, Ap	200	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
128	21	67.7	113	6	US-10-793-626-1848	Sequence 1848, Ap	201	20	64.5	44	6	US-10-467-657-1118	Sequence 1118, Ap
129	21	67.7	120	6	US-10-793-626-2376	Sequence 2376, Ap	202	20	64.5	45	6	US-10-467-657-8968	Sequence 8968, Ap
130	21	67.7	140	6	US-10-982-145-66	Sequence 66, Appl	203	20	64.5	50	6	US-10-467-657-7892	Sequence 7892, Ap
131	21	67.7	141	6	US-10-982-145-67	Sequence 67, Appl	204	20	64.5	54	6	US-10-467-657-2264	Sequence 2264, Ap
132	21	67.7	164	6	US-10-467-657-1450	Sequence 1450, Ap	205	20	64.5	54	6	US-10-467-657-4978	Sequence 4978, Ap
133	21	67.7	168	6	US-10-927-641-69	Sequence 69, Appl	206	20	64.5	56	6	US-10-467-657-1050	Sequence 1050, Ap
134	21	67.7	168	6	US-10-793-626-724	Sequence 724, App	207	20	64.5	66	6	US-10-467-657-766	Sequence 766, App
135	21	67.7	182	6	US-10-467-657-8302	Sequence 8302, Ap	208	20	64.5	79	7	US-11-080-991-10	Sequence 10, Appl
136	21	67.7	183	7	US-11-069-642-125	Sequence 125, App	209	20	64.5	92	6	US-10-467-657-5952	Sequence 5952, Ap
137	21	67.7	198	6	US-10-467-657-5440	Sequence 5440, Ap	210	20	64.5	105	6	US-10-467-657-9209	Sequence 9209, Ap
138	21	67.7	220	6	US-10-793-626-1822	Sequence 1822, Ap	211	20	64.5	115	6	US-10-793-626-1554	Sequence 1554, Ap
139	21	67.7	227	6	US-10-793-626-2396	Sequence 2396, Ap	212	20	64.5	120	6	US-10-467-657-6982	Sequence 6982, Ap
140	21	67.7	233	6	US-10-793-626-2842	Sequence 2642, Ap	213	20	64.5	120	6	US-10-467-657-7938	Sequence 7938, Ap
141	21	67.7	236	7	US-10-467-657-8268	Sequence 8268, Ap	214	20	64.5	123	6	US-10-821-234-988	Sequence 988, App
142	21	67.7	245	7	US-11-188-473-2	Sequence 2, Appli	215	20	64.5	123	6	US-10-467-657-6978	Sequence 6978, Ap
143	21	67.7	246	7	US-11-092-140-111	Sequence 111, Appl	216	20	64.5	127	7	US-11-106-796-10	Sequence 10, Appl
144	21	67.7	247	7	US-11-103-957-69	Sequence 69, Appl	217	20	64.5	129	6	US-10-501-039-8	Sequence 8, Appli
145	21	67.7	248	7	US-11-076-164-9	Sequence 9, Appli	218	20	64.5	135	6	US-10-793-626-2284	Sequence 2284, Ap
146	21	67.7	269	6	US-10-467-657-330	Sequence 330, App	219	20	64.5	138	6	US-10-793-626-1254	Sequence 1254, Ap
147	21	67.7	286	6	US-10-793-626-2192	Sequence 2192, Ap	220	20	64.5	150	6	US-10-793-626-2324	Sequence 2324, Ap
148	21	67.7	294	7	US-11-055-822-480	Sequence 480, App	221	20	64.5	154	7	US-11-082-389-424	Sequence 424, App
149	21	67.7	294	7	US-11-055-822-880	Sequence 880, App	222	20	64.5	155	6	US-10-467-657-2420	Sequence 2420, Ap
150	21	67.7	298	6	US-10-454-437-384	Sequence 384, App	223	20	64.5	160	7	US-11-009-939-44	Sequence 44, Appl
151	21	67.7	298	7	US-11-055-822-478	Sequence 478, App	224	20	64.5	166	6	US-10-821-234-1293	Sequence 1293, Ap
152	21	67.7	298	7	US-11-055-822-878	Sequence 878, App	225	20	64.5	166	6	US-10-878-556A-20	Sequence 20, Appl
153	21	67.7	301	6	US-10-793-626-206	Sequence 206, App	226	20	64.5	174	6	US-10-793-626-1520	Sequence 1520, Ap
154	21	67.7	355	6	US-10-467-657-7996	Sequence 7996, Ap	227	20	64.5	183	7	US-10-467-657-6906	Sequence 6906, Ap
155	21	67.7	400	6	US-10-793-626-1056	Sequence 1056, Ap	228	20	64.5	188	7	US-11-100-183-27	Sequence 27, Appl
156	21	67.7	403	7	US-11-109-156-29	Sequence 29, Appl	229	20	64.5	190	6	US-10-467-657-3436	Sequence 3436, Ap
157	21	67.7	407	6	US-10-821-234-1389	Sequence 1389, Ap	230	20	64.5	193	6	US-10-793-626-1240	Sequence 1240, Ap
158	21	67.7	419	7	US-11-084-624-18	Sequence 18, Appl	231	20	64.5	196	6	US-10-131-826A-168	Sequence 168, App
159	21	67.7	452	6	US-10-793-626-3092	Sequence 3092, Ap	232	20	64.5	196	6	US-10-793-626-2584	Sequence 2584, Ap
160	21	67.7	464	6	US-10-689-742-164	Sequence 164, App	233	20	64.5	201	5	US-09-940-308-5	Sequence 5, Appli
161	21	67.7	490	7	US-11-074-176-316	Sequence 316, Appl	234	20	64.5	211	6	US-10-821-234-1372	Sequence 1372, Ap
162	21	67.7	495	7	US-11-074-176-60	Sequence 60, Appl	235	20	64.5	211	6	US-10-467-657-6932	Sequence 4, Appli
163	21	67.7	502	6	US-10-821-234-1554	Sequence 1554, Ap	236	20	64.5	215	6	US-10-131-826A-4	Sequence 4, Appli
164	21	67.7	514	6	US-10-467-657-2664	Sequence 2664, Ap	237	20	64.5	215	6	US-10-131-826A-488	Sequence 488, App
165	21	67.7	514	7	US-11-103-037-3	Sequence 3, Appli	238	20	64.5	215	7	US-11-080-991-112	Sequence 112, App
166	21	67.7	515	6	US-10-630-203-6	Sequence 6, Appli	239	20	64.5	221	6	US-10-793-626-1992	Sequence 1992, Ap
167	21	67.7	521	6	US-10-793-626-532	Sequence 532, App	240	20	64.5	221	6	US-10-793-626-2420	Sequence 2420, Ap
168	21	67.7	526	6	US-10-606-302-5	Sequence 5, Appli	241	20	64.5	228	6	US-10-793-626-360	Sequence 360, App
169	21	67.7	526	6	US-10-606-302-7	Sequence 7, Appli	242	20	64.5	228	6	US-10-793-626-488	Sequence 488, App
170	21	67.7	528	6	US-10-793-626-1930	Sequence 1930, Ap	243	20	64.5	228	6	US-10-467-657-568	Sequence 568, App
171	21	67.7	537	6	US-10-467-657-6958	Sequence 6958, Ap	244	20	64.5	228	6	US-10-467-657-4838	Sequence 4838, Ap

245 20 64.5 233 6 US-10-821-234-1322
 246 20 64.5 234 6 US-10-793-626-192
 247 20 64.5 245 6 US-10-467-657-7884
 248 20 64.5 263 6 US-10-510-386-234
 249 20 64.5 275 7 US-11-110-977-4
 250 20 64.5 276 7 US-11-112-882-86
 251 20 64.5 277 6 US-10-454-437-8
 252 20 64.5 277 6 US-11-055-822-608
 253 20 64.5 281 6 US-10-821-234-1080
 254 20 64.5 288 6 US-10-467-657-1272
 255 20 64.5 291 7 US-11-102-883-22
 256 20 64.5 292 7 US-11-102-883-24
 257 20 64.5 294 6 US-10-467-657-7686
 258 20 64.5 294 7 US-11-112-882-85
 259 20 64.5 295 7 US-11-091-100-2
 260 20 64.5 298 7 US-11-085-812-4
 261 20 64.5 304 6 US-11-112-882-3
 262 20 64.5 306 6 US-10-467-657-7222
 263 20 64.5 311 6 US-10-793-626-2450
 264 20 64.5 319 6 US-10-131-826A-134
 265 20 64.5 321 6 US-10-467-657-2504
 266 20 64.5 323 6 US-10-467-657-556
 267 20 64.5 324 6 US-10-793-626-1262
 268 20 64.5 324 6 US-10-467-657-7692
 269 20 64.5 324 6 US-10-467-657-8440
 270 20 64.5 325 5 US-09-940-308-8
 271 20 64.5 325 6 US-10-454-437-142
 272 20 64.5 330 7 US-11-085-812-2
 273 20 64.5 335 6 US-10-467-657-3818
 274 20 64.5 337 6 US-10-875-716-2
 275 20 64.5 338 6 US-10-467-657-136
 276 20 64.5 338 6 US-10-467-657-6798
 277 20 64.5 338 6 US-10-878-556A-19
 278 20 64.5 344 6 US-10-131-826A-376
 279 20 64.5 347 6 US-10-467-657-2014
 280 20 64.5 350 6 US-10-485-517-288
 281 20 64.5 350 7 US-11-095-624-2
 282 20 64.5 350 7 US-11-095-624-3
 283 20 64.5 350 7 US-11-095-624-4
 284 20 64.5 351 7 US-11-095-624-5
 285 20 64.5 353 7 US-11-060-023-2
 286 20 64.5 353 7 US-11-060-023-4
 287 20 64.5 353 7 US-11-060-023-6
 288 20 64.5 353 7 US-11-060-023-8
 289 20 64.5 353 7 US-11-060-023-12
 290 20 64.5 353 7 US-11-060-023-14
 291 20 64.5 353 7 US-11-060-023-15
 292 20 64.5 353 7 US-11-060-023-16
 293 20 64.5 355 6 US-10-454-437-102
 294 20 64.5 356 7 US-11-055-822-972
 295 20 64.5 356 7 US-11-055-822-1052
 296 20 64.5 359 7 US-11-060-023-11
 297 20 64.5 359 7 US-11-060-023-13
 298 20 64.5 360 7 US-11-060-023-17
 299 20 64.5 378 7 US-11-080-091-3
 300 20 64.5 378 7 US-11-080-091-11

ALIGNMENTS

RESULT 1
 US-11-050-439-58
 ; Sequence 58, Application US/11090439
 ; Publication No. US20050268442A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Squillace, Rachel
 ; APPLICANT: Weiner, Michael P.
 ; TITLE OF INVENTION: Immortalized Human Tuberculous Sclerosis Null
 ; TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
 ; FILE REFERENCE: 24318-502
 ; CURRENT APPLICATION NUMBER: US/11/090,439
 ; CURRENT FILING DATE: 2005-03-25

Sequence 1322, Ap
 Sequence 192, App
 Sequence 7884, Ap
 Sequence 234, App
 Sequence 4, Appl
 Sequence 86, Appl
 Sequence 8, Appl
 Sequence 608, App
 Sequence 1080, App
 Sequence 1272, Ap
 Sequence 22, Appl
 Sequence 24, Appl
 Sequence 7686, Ap
 Sequence 85, Appl
 Sequence 2, Appl
 Sequence 4, Appl
 Sequence 3, Appl
 Sequence 7222, Ap
 Sequence 2450, Ap
 Sequence 134, App
 Sequence 2504, App
 Sequence 556, App
 Sequence 1262, Ap
 Sequence 7692, Ap
 Sequence 8440, Ap
 Sequence 8, Appl
 Sequence 142, App
 Sequence 2, Appl
 Sequence 3818, Ap
 Sequence 2, Appl
 Sequence 136, App
 Sequence 6798, Ap
 Sequence 19, Appl
 Sequence 376, App
 Sequence 2014, Ap
 Sequence 288, App
 Sequence 2, Appl
 Sequence 3, Appl
 Sequence 4, Appl
 Sequence 5, Appl
 Sequence 2, Appl
 Sequence 4, Appl
 Sequence 6, Appl
 Sequence 8, Appl
 Sequence 12, Appl
 Sequence 14, Appl
 Sequence 1052, Ap
 Sequence 11, Appl
 Sequence 13, Appl
 Sequence 17, Appl
 Sequence 11, Appl

Query Match 87.1%; Score 27; DB 7; Length 582;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 DB 378 KVFVF 382

RESULT 2
 US-10-467-657-4888
 ; Sequence 4888, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: Seqwin99, version 1.04
 ; SEQ ID NO 4888
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-4888

Query Match 87.1%; Score 27; DB 6; Length 592;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 DB 557 KVFVF 561

RESULT 3
 US-11-147-047-48
 ; Sequence 48, Application US/11147047
 ; Publication No. US20050260668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agarwal, Pankaj
 ; APPLICANT: Murdock, Paul R.
 ; APPLICANT: Rizvi, Safia K.
 ; APPLICANT: Smith, Randall F.
 ; APPLICANT: Xiang, Zhaoying
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP50016
 ; CURRENT APPLICATION NUMBER: US/11/147,047
 ; CURRENT FILING DATE: 2005-06-07
 ; PRIOR APPLICATION NUMBER: US/10/221,097
 ; PRIOR FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/07143
 ; PRIOR FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: 60/187,107
 ; PRIOR FILING DATE: 2000-03-06
 ; CURRENT APPLICATION NUMBER: 60/236,874

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-48

Query Match 87.1%; Score 27; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
Db 184 KVVFF 188

RESULT 4
US-11-147-047-49
; Sequence 49, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-49

Query Match 87.1%; Score 27; DB 7; Length 1070;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
Db 244 KVVFF 248

RESULT 5
US-10-467-657-8712
; Sequence 8712, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8712
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8712

Query Match 83.9%; Score 26; DB 6; Length 19;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
Db 15 KVVFF 19

RESULT 6
US-10-467-657-3154
; Sequence 3154, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3154
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3154

Query Match 83.9%; Score 26; DB 6; Length 220;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 204 FVFFA 208

RESULT 7
US-10-467-657-2190
; Sequence 2190, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2190
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2190

Query Match 83.9%; Score 26; DB 6; Length 299;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPP 5
|:|
Db 12 KTFPP 16

RESULT 8
US-10-467-657-1950
; Sequence 1950, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1950
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1950

Query Match 83.9%; Score 26; DB 6; Length 395;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPP 6
|:|
Db 120 FVFPP 124

RESULT 9
US-10-467-657-5788
; Sequence 5788, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5788
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5788

Query Match 83.9%; Score 26; DB 6; Length 418;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPP 6
|:|
Db 337 FVFPP 341

RESULT 10
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 80.6%; Score 25; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFPP 6
|:|
Db 4 KLVPP 9

RESULT 11
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue

```
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match      80.6%; Score 25; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      4 KLVFFA 9

RESULT 12
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match      80.6%; Score 25; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      16 KLVFFA 21

RESULT 13
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elmova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match      80.6%; Score 25; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      16 KLVFFA 21

RESULT 14
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match      80.6%; Score 25; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      16 KLVFFA 21

RESULT 15
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match      80.6%; Score 25; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


QY 1 KLVFFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 16

US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 80.6%; Score 25; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KLVFFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 17

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KLVFFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 18

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KLVFFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 19

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KLVFFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 20

US-10-467-657-7560
; Sequence 7560, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7560
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7560

Query Match 80.6%; Score 25; DB 6; Length 184;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KEVFFFA 6
|||||
Db 91 KEVFLA 96

RESULT 21

; Sequence 350, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16

; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 350
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-350

Query Match 80.6%; Score 25; DB 7; Length 525;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFFFA 6
|:|:|
Db 230 KVFYA 235

RESULT 22

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hvild
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.

; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982.545
; CURRENT FILING DATE: 2004-11-06

; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15

; LENGTH: 770
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:

; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein

; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)

; OTHER INFORMATION: signal peptide
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)

; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)

; OTHER INFORMATION: soluble APP-alpha
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)

; OTHER INFORMATION: soluble APP-beta
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)

; OTHER INFORMATION: C99
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)

; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)

; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)

; OTHER INFORMATION: C83

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(713)
OTHER INFORMATION: P3(42)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(711)
OTHER INFORMATION: P3(40)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (712)..(770)
OTHER INFORMATION: gamma-CTF(59)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (714)..(770)
OTHER INFORMATION: gamma-CTF(57)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (721)..(770)
OTHER INFORMATION: gamma-CTF(50)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (740)..(770)
OTHER INFORMATION: C31
US-10-982-545-15

Query Match 80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 687 KLVFFA 692

RESULT 23

US-10-789-273-38
Sequence 38, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Gurliq
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
FILE REFERENCE: BETA-AMYLLOID PEPTIDE
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
US-10-789-273-38

Query Match 80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 687 KLVFFA 692

RESULT 24

US-10-467-657-3978

Sequence 3978, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3978
LENGTH: 194
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3978

Query Match 77.4%; Score 24; DB 6; Length 194;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 13 RFAFFA 18

RESULT 25

US-10-793-626-62
Sequence 62, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 229
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-62

Query Match 77.4%; Score 24; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 59 KVVYFF 63

RESULT 26

US-10-793-626-1860
Sequence 1860, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04

```
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1860
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1860

Query Match          77.4%; Score 24; DB 6; Length 443;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
Db      168 KVFVF 172
      |:|

RESULT 27
US-10-467-657-4566
; Sequence 4566, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4566
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4566

Query Match          77.4%; Score 24; DB 6; Length 533;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      165 KDFVFA 170
      |||

RESULT 28
US-11-080-991-48
; Sequence 48, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petteer Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 657
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-48

Query Match          77.4%; Score 24; DB 7; Length 657;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
Db      90 KVFVF 94
      |:|

RESULT 29
US-10-467-657-4242
; Sequence 4242, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4242
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4242

Query Match          77.4%; Score 24; DB 6; Length 916;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      655 QVFVFA 660
      ::|||

RESULT 30
US-10-821-234-1120
; Sequence 1120, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1120
; LENGTH: 4384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1120

Query Match          77.4%; Score 24; DB 6; Length 4384;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

Qy      1 KFVFFA 6
Db      1320 KFVFFA 1325

RESULT 31
US-10-467-657-1370
; Sequence 1370, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1370
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1370

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 32
US-10-467-657-2308
; Sequence 2308, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2308
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2308

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 33
US-10-467-657-5610
; Sequence 5610, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5610
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5610

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 34
US-10-467-657-7516
; Sequence 7516, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7516
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7516

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 35
US-10-467-657-8322
; Sequence 8322, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8322
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8322

Query Match 74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 23 FVFFS 27

RESULT 36
US-10-467-657-4324
; Sequence 4324, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4324
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4324

Query Match 74.2%; Score 23; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 44 FVFFS 48

RESULT 37
US-10-467-657-8286
; Sequence 8286, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8286
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8286

Query Match 74.2%; Score 23; DB 6; Length 56;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 30 FVFFS 34

RESULT 38
US-10-793-626-2766
; Sequence 2766, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2766
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2766

Query Match 74.2%; Score 23; DB 6; Length 126;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 10 YVFFA 14

RESULT 39
US-10-793-626-304
; Sequence 304, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 304
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-304

Query Match 74.2%; Score 23; DB 6; Length 209;

Best Local Similarity 60.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
:|:|
Db 145 RPIFF 149

RESULT 40

US-10-793-626-1034
; Sequence 1034, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; PRIOR APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1034
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1034

Query Match 74.2%; Score 23; DB 6; Length 234;

Best Local Similarity 80.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPA 6
|:|:|
Db 124 FMPFA 128

RESULT 41

US-10-467-657-4456
; Sequence 4456, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4456
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4456

Query Match 74.2%; Score 23; DB 6; Length 288;

Best Local Similarity 80.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
|:|:|
Db 61 KPAPF 65

RESULT 42

US-10-613-744-13
; Sequence 13, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-613-744-13

Query Match 74.2%; Score 23; DB 6; Length 391;

Best Local Similarity 60.0%; Pred. No. 3.3e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
:|:|
Db 61 RPIFF 65

RESULT 43

US-10-467-657-4858
; Sequence 4858, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4858
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4858

Query Match 74.2%; Score 23; DB 6; Length 410;

Best Local Similarity 80.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPA 6
|:|:|
Db 207 FLFPA 211

RESULT 44

US-11-055-822-1096

; Sequence 1096, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habehauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1096
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1096

Query Match 74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 329 FVIFA 333

RESULT 45
US-11-113-424-186
; Sequence 186, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358

; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-11-113-424-186

Query Match 74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 399 FLFFA 403

RESULT 46
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 678
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-678

Query Match 74.2%; Score 23; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 395 FVIFA 399

RESULT 47
US-11-082-389-348
; Sequence 348, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habehauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389


```

; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 348
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-348

```

```

Query Match          74.2%; Score 23; DB 7; Length 534;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVFVF 5
    |||
Db 239 KFIY 243

```

```

RESULT 48
US-10-467-657-3440
; Sequence 3440, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3440
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3440

```

```

Query Match          74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 KVFVF 5
    |||
Db 367 KPAPF 371

```

```

RESULT 49
US-10-467-657-4632

```

```

; Sequence 4632, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4632
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4632

```

```

Query Match          74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 KVFVF 5
    |||
Db 367 KPAPF 371

```

```

RESULT 50
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

```

```

Query Match          74.2%; Score 23; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 KVFVPA 6
    |||
Db 531 KAVEFA 536

```

```
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 908
/ LENGTH: 1012
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-908

Query Match      74.2%; Score 23; DB 6; Length 1012;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|||
Db      988 FLFFA 992

RESULT 54
US-10-793-626-760
/ Sequence 760, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 760
/ LENGTH: 2323
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-760

Query Match      74.2%; Score 23; DB 6; Length 2323;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|||
Db      1210 FMFFA 1214

RESULT 55
US-10-467-657-8998
/ Sequence 8998, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 8998
```

```
US-10-821-234-917
/ Sequence 917, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 917
/ LENGTH: 708
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-917

Query Match      74.2%; Score 23; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KEVFFA 6
      |:|||
Db      579 KAVFFA 594

RESULT 52
US-10-793-626-420
/ Sequence 420, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 420
/ LENGTH: 766
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-420

Query Match      74.2%; Score 23; DB 6; Length 766;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|||
Db      357 FMFFA 361

RESULT 53
US-10-995-561-908
/ Sequence 908, Application US/10995561
/ Publication No. US2005027054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
```

```
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8998

Query Match          71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 7 FVFF 10

RESULT 56
US-11-000-463-378
; Sequence 378, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 378
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-378

Query Match          71.0%; Score 22; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 8 FVFF 11

RESULT 57
US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
```

```
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 850
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-850

Query Match          71.0%; Score 22; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 8 FVFF 11

RESULT 58
US-10-467-657-360
; Sequence 360, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 360
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-360

Query Match          71.0%; Score 22; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 8 FVFF 11
```

```
Db          32 FVFF 35

RESULT 59
US-10-467-657-2026
; Sequence 2026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2026
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2026

Query Match          71.0%; Score 22; DB 6; Length 79;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          1 KVVFF 5
           :|||
Db          10 QVFF 14

RESULT 60
US-10-485-517-286
; Sequence 286, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-286

Query Match          71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 FVFF 5
           :|||
Db          83 FVFF 86

RESULT 61
US-10-467-657-6824
; Sequence 6824, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6824
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6824

Query Match          71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 FVFF 5
           :|||
Db          62 FVFF 65

RESULT 62
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Query Match          71.0%; Score 22; DB 7; Length 139;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KVVFF 5
           :|||
Db          6 KVVFF 10

RESULT 63
US-10-467-657-6110
; Sequence 6110, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6110
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6110

Query Match 71.0%; Score 22; DB 6; Length 149;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
: ||||
Db 88 EFFFFA 93

RESULT 64
US-10-467-657-7550
; Sequence 7550, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7550
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7550

Query Match 71.0%; Score 22; DB 6; Length 149;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
: ||||
Db 88 EFFFFA 93

RESULT 65
US-10-467-657-6130
; Sequence 6130, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 6130
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6130

Query Match 71.0%; Score 22; DB 6; Length 154;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
: ||||
Db 93 EFFFFA 98

RESULT 66
US-10-485-517-346
; Sequence 346, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynex Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-346

Query Match 71.0%; Score 22; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5
: ||||
Db 134 FVFF 137

RESULT 67
US-10-980-388-65
; Sequence 65, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogell, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303

```

; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-65

Query Match          71.0%; Score 22; DB 6; Length 187;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 179 RVYFA 184

RESULT 68
US-10-467-657-4386
; Sequence 4386, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4386
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4386

Query Match          71.0%; Score 22; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 72 FVFF 75

RESULT 69
US-10-467-657-3000
; Sequence 3000, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```

```

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3000
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3000

Query Match          71.0%; Score 22; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 143 FVFF 146

RESULT 70
US-10-467-657-6248
; Sequence 6248, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6248
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6248

Query Match          71.0%; Score 22; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 218 FVFF 221

RESULT 71
US-11-054-515-1391
; Sequence 1391, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23F3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14

```

```
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1391
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1391

Query Match          71.0%; Score 22; DB 7; Length 240;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 56 RFVYVA 61

RESULT 72
US-11-074-176-66
; Sequence 66, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
; US-11-074-176-66

Query Match          71.0%; Score 22; DB 7; Length 241;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 229 KFDVFA 234

RESULT 73
US-10-793-626-1124
; Sequence 1124, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
```

```
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1124
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-1124

Query Match          71.0%; Score 22; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
DB 65 FVFF 68

RESULT 74
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-6144

Query Match          71.0%; Score 22; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
DB 197 FVFF 200

RESULT 75
US-10-467-657-1178
; Sequence 1178, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1178
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1178
```

```
Query Match      71.0%; Score 22; DB 6; Length 268;
Best Local Similarity 80.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 FVFFA 6
      | |||
Db      25 FAFFA 29
```

```
Search completed: December 29, 2005, 18:50:19
Job time : 3.29032 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep:
2: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep:
3: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep:
4: /cgn2_6/ptodata/1/pubpa/US10A_PUBCOMB.pep:
5: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep:
6: /cgn2_6/ptodata/1/pubpa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	3	US-09-867-847-13
2	31	100.0	6	3	US-09-867-847-21
3	31	100.0	6	3	US-09-915-092-3
4	31	100.0	6	3	US-09-915-092-11
5	31	100.0	6	3	US-09-747-408-4
6	31	100.0	6	3	US-09-747-408-12
7	31	100.0	6	5	US-10-728-028-3
8	31	100.0	6	5	US-10-728-028-11
9	31	100.0	6	5	US-10-825-958-11
10	31	100.0	6	5	US-10-825-958-19
11	31	100.0	59	4	US-10-424-599-174685
12	31	100.0	64	4	US-10-424-599-164908
13	31	100.0	102	4	US-10-424-599-203722
14	31	100.0	175	4	US-10-437-963-118848
15	31	100.0	372	4	US-10-437-963-118846
16	31	100.0	373	4	US-10-437-963-138916
17	30	96.8	420	4	US-10-437-963-118773
18	30	90.3	54	4	US-10-424-599-266901
19	28	90.3	115	4	US-10-425-115-327241
20	28	90.3	126	4	US-10-425-115-290464
21	28	90.3	159	4	US-10-425-115-193086
22	28	90.3	240	4	US-10-767-701-37567
23	28	90.3	452	4	US-10-369-493-6279
24	28	90.3	490	5	US-10-994-726-438
25	28	90.3	506	3	US-09-877-476-2
26	28	90.3	506	3	US-09-877-476-28
27	28	90.3	506	3	US-09-877-476-30

28	90.3	3	US-09-877-476-36	Sequence 36, Appl
28	90.3	4	US-10-276-977-7	Sequence 7, Appl
28	90.3	506	US-10-758-524-2	Sequence 2, Appl
28	90.3	506	US-10-758-524-28	Sequence 28, Appl
28	90.3	506	US-10-758-524-30	Sequence 30, Appl
28	90.3	506	US-10-758-524-36	Sequence 36, Appl
28	90.3	506	US-10-282-122A-47052	Sequence 47052, A
28	90.3	508	US-10-994-726-437	Sequence 437, App
28	90.3	508	US-10-994-726-437	Sequence 18725, A
28	90.3	509	US-10-732-923-18725	Sequence 18725, A
28	90.3	509	US-10-732-923-18726	Sequence 18726, A
28	90.3	509	US-10-732-923-18737	Sequence 18737, A
28	90.3	509	US-10-732-923-18737	Sequence 51929, A
28	90.3	571	US-10-369-493-2154	Sequence 2154, Ap
28	90.3	1089	US-10-425-115-236339	Sequence 236339, A
27	87.1	34	US-10-425-115-20545	Sequence 200545, A
27	87.1	46	US-10-424-599-232761	Sequence 232761, A
27	87.1	47	US-10-424-599-232761	Sequence 232761, A
27	87.1	48	US-10-425-115-206883	Sequence 206883, A
27	87.1	56	US-10-437-963-176215	Sequence 176215, A
27	87.1	57	US-10-425-114-38807	Sequence 38807, A
27	87.1	62	US-09-764-877-1136	Sequence 1136, Ap
27	87.1	62	US-10-242-515-1136	Sequence 1136, Ap
27	87.1	63	US-10-424-599-146372	Sequence 146372, A
27	87.1	72	US-10-425-115-248149	Sequence 248149, A
27	87.1	73	US-10-425-115-229605	Sequence 229605, A
27	87.1	80	US-10-425-115-259222	Sequence 259222, A
27	87.1	81	US-10-425-115-215979	Sequence 215979, A
27	87.1	82	US-10-424-599-195261	Sequence 195261, A
27	87.1	82	US-10-450-763-44156	Sequence 44156, A
27	87.1	83	US-10-425-115-275005	Sequence 275005, A
27	87.1	88	US-10-424-599-259257	Sequence 259257, A
27	87.1	92	US-10-424-599-246138	Sequence 246138, A
27	87.1	96	US-10-424-599-207674	Sequence 207674, A
27	87.1	99	US-10-425-115-221194	Sequence 221194, A
27	87.1	103	US-10-424-599-182454	Sequence 182454, A
27	87.1	103	US-10-437-963-201763	Sequence 201763, A
27	87.1	104	US-09-823-153-4	Sequence 4, Appl
27	87.1	104	US-10-713-981-4	Sequence 4, Appl
27	87.1	106	US-10-425-115-215097	Sequence 215097, A
27	87.1	107	US-10-424-599-207673	Sequence 207673, A
27	87.1	107	US-10-437-963-146282	Sequence 146282, A
27	87.1	109	US-10-424-599-278159	Sequence 278159, A
27	87.1	109	US-10-425-115-208261	Sequence 208261, A
27	87.1	110	US-10-425-115-286779	Sequence 286779, A
27	87.1	115	US-09-864-408A-4214	Sequence 4214, Ap
27	87.1	115	US-10-425-115-256025	Sequence 256025, A
27	87.1	125	US-10-425-115-289631	Sequence 289631, A
27	87.1	131	US-10-424-599-208184	Sequence 208184, A
27	87.1	131	US-10-424-599-221174	Sequence 221174, A
27	87.1	146	US-10-450-763-56921	Sequence 56921, A
27	87.1	146	US-10-424-599-214877	Sequence 214877, A
27	87.1	153	US-10-424-599-243854	Sequence 243854, A
27	87.1	158	US-10-424-599-169140	Sequence 169140, A
27	87.1	173	US-10-408-765A-1782	Sequence 1782, Ap
27	87.1	173	US-10-220-335-207	Sequence 207, App
27	87.1	189	US-10-432-198-4	Sequence 4, Appl
27	87.1	189	US-10-432-198-5	Sequence 5, Appl
27	87.1	189	US-10-432-198-6	Sequence 6, Appl
27	87.1	189	US-10-432-198-7	Sequence 7, Appl
27	87.1	189	US-10-432-198-7	Sequence 489, App
27	87.1	206	US-10-238-075-489	Sequence 359320, A
27	87.1	211	US-10-425-115-359320	Sequence 359320, A
27	87.1	212	US-10-425-115-359323	Sequence 359323, A
27	87.1	212	US-10-424-599-211252	Sequence 211252, A
27	87.1	218	US-10-276-722A-7	Sequence 7, Appl
27	87.1	221	US-10-450-763-53353	Sequence 53353, A
27	87.1	221	US-10-450-763-53342	Sequence 53342, A
27	87.1	240	US-10-724-972A-7100	Sequence 7100, Ap
27	87.1	249	US-10-437-963-183912	Sequence 183912, A
27	87.1	285	US-10-425-115-246512	Sequence 246512, A
27	87.1	297	US-09-864-921-180	Sequence 180, App
27	87.1	297	US-10-766-682-180	Sequence 247557, A
27	87.1	332	US-10-424-599-247557	Sequence 180, App
27	87.1	335	US-10-425-115-359332	Sequence 359332, A
27	87.1	335	US-10-739-930-8473	Sequence 8473, Ap

101	27	87.1	347	4	US-10-425-114-47805	Sequence 47805, A	174	26	83.9	60	6	US-11-093-088-44	Sequence 44, Appl
102	27	87.1	351	4	US-10-275-595A-28	Sequence 28, Appl	175	26	83.9	61	4	US-10-424-599-279574	Sequence 279574, A
103	27	87.1	356	4	US-10-425-115-359329	Sequence 359329, A	176	26	83.9	61	4	US-10-767-701-48124	Sequence 48124, A
104	27	87.1	381	4	US-10-276-272A-10	Sequence 10, Appl	177	26	83.9	61	4	US-10-425-115-294863	Sequence 294863, A
105	27	87.1	388	4	US-10-437-963-102898	Sequence 102898, A	178	26	83.9	61	4	US-10-425-115-323415	Sequence 323415, A
106	27	87.1	389	4	US-10-276-272A-4	Sequence 4, Appl	179	26	83.9	62	4	US-10-424-599-148416	Sequence 148416, A
107	27	87.1	393	5	US-10-739-930-6015	Sequence 6015, Ap	180	26	83.9	65	6	US-10-125-258-43	Sequence 43, Appl
108	27	87.1	401	4	US-10-094-240-20	Sequence 20, Appl	181	26	83.9	65	6	US-11-092-429-43	Sequence 43, Appl
109	27	87.1	401	4	US-10-056-405-20	Sequence 20, Appl	182	26	83.9	65	6	US-11-092-430-43	Sequence 43, Appl
110	27	87.1	407	4	US-10-767-701-47158	Sequence 47158, A	183	26	83.9	65	6	US-11-093-225-43	Sequence 43, Appl
111	27	87.1	407	4	US-10-425-115-283373	Sequence 283373, A	184	26	83.9	65	6	US-11-092-027-43	Sequence 43, Appl
112	27	87.1	408	4	US-10-437-963-117365	Sequence 117365, A	185	26	83.9	65	6	US-11-082-427-43	Sequence 43, Appl
113	27	87.1	422	4	US-10-424-599-277445	Sequence 277445, A	186	26	83.9	65	6	US-11-093-088-43	Sequence 43, Appl
114	27	87.1	422	5	US-10-739-930-9013	Sequence 9013, Ap	187	26	83.9	68	4	US-10-424-599-190908	Sequence 190908, A
115	27	87.1	425	4	US-10-424-599-191171	Sequence 191171, A	188	26	83.9	68	4	US-10-424-599-218467	Sequence 218467, A
116	27	87.1	425	4	US-10-276-272A-6	Sequence 6, Appl	189	26	83.9	71	4	US-10-424-599-234678	Sequence 234678, A
117	27	87.1	428	4	US-10-425-115-295015	Sequence 295015, A	190	26	83.9	71	4	US-10-425-115-241132	Sequence 241132, A
118	27	87.1	444	4	US-10-437-963-102909	Sequence 102909, A	191	26	83.9	72	5	US-10-450-763-52260	Sequence 52260, A
119	27	87.1	454	5	US-10-501-282-2882	Sequence 2882, Ap	192	26	83.9	74	4	US-10-425-115-185420	Sequence 185420, A
120	27	87.1	471	6	US-11-021-951-185	Sequence 185, Ap	193	26	83.9	75	4	US-10-425-115-337684	Sequence 337684, A
121	27	87.1	478	5	US-10-486-781A-6	Sequence 6, Appl	194	26	83.9	76	4	US-10-425-115-259075	Sequence 259075, A
122	27	87.1	478	5	US-10-954-778-13	Sequence 13, Appl	195	26	83.9	82	4	US-10-425-115-350964	Sequence 350964, A
123	27	87.1	498	5	US-10-486-781A-11	Sequence 11, Appl	196	26	83.9	83	4	US-10-425-115-367965	Sequence 367965, A
124	27	87.1	581	4	US-10-282-122A-65905	Sequence 65905, A	197	26	83.9	93	4	US-10-424-599-266485	Sequence 266485, A
125	27	87.1	582	3	US-09-916-658-4	Sequence 4, Appl	198	26	83.9	93	4	US-10-437-963-178420	Sequence 178420, A
126	27	87.1	582	3	US-09-391-104-28	Sequence 28, Appl	199	26	83.9	96	4	US-10-425-115-349216	Sequence 349216, A
127	27	87.1	582	3	US-09-801-196-27	Sequence 27, Appl	200	26	83.9	97	4	US-10-424-599-182131	Sequence 182131, A
128	27	87.1	582	3	US-09-919-497-84	Sequence 84, Appl	201	26	83.9	98	4	US-10-437-963-109168	Sequence 109168, A
129	27	87.1	582	3	US-09-916-849A-2	Sequence 2, Appl	202	26	83.9	99	4	US-10-424-599-269978	Sequence 269978, A
130	27	87.1	582	4	US-10-133-797-6	Sequence 6, Appl	203	26	83.9	101	4	US-10-425-114-57111	Sequence 57111, A
131	27	87.1	582	4	US-10-131-985-43	Sequence 43, Appl	204	26	83.9	105	4	US-10-424-599-210257	Sequence 210257, A
132	27	87.1	582	4	US-10-411-010-26	Sequence 26, Appl	205	26	83.9	106	4	US-10-424-599-254314	Sequence 254314, A
133	27	87.1	582	4	US-10-447-315-9	Sequence 9, Appl	206	26	83.9	109	4	US-10-425-115-215142	Sequence 215142, A
134	27	87.1	582	4	US-10-276-272A-19	Sequence 19, Appl	207	26	83.9	111	3	US-09-933-767-303	Sequence 303, App
135	27	87.1	582	5	US-10-901-417-43	Sequence 43, Appl	208	26	83.9	111	4	US-10-004-860-303	Sequence 303, App
136	27	87.1	582	5	US-10-953-264-26	Sequence 26, Appl	209	26	83.9	111	4	US-10-023-282-303	Sequence 303, App
137	27	87.1	582	5	US-10-773-446-100	Sequence 100, App	210	26	83.9	114	4	US-10-424-599-235618	Sequence 235618, A
138	27	87.1	590	4	US-10-276-272A-2	Sequence 2, Appl	211	26	83.9	114	4	US-10-437-963-170598	Sequence 170598, A
139	27	87.1	592	4	US-10-282-122A-65055	Sequence 65055, A	212	26	83.9	117	4	US-10-424-599-280839	Sequence 280839, A
140	27	87.1	592	4	US-10-276-272A-12	Sequence 12, Appl	213	26	83.9	118	4	US-10-047-676A-17	Sequence 17, Appl
141	27	87.1	626	4	US-10-369-493-11939	Sequence 11939, A	214	26	83.9	118	4	US-10-424-599-212612	Sequence 212612, A
142	27	87.1	729	4	US-10-276-272A-15	Sequence 15, Appl	215	26	83.9	118	5	US-10-790-914-17	Sequence 17, Appl
143	27	87.1	738	4	US-10-221-097-48	Sequence 48, Appl	216	26	83.9	120	4	US-10-425-115-257063	Sequence 257063, A
144	27	87.1	814	4	US-10-425-115-214562	Sequence 214562, A	217	26	83.9	120	4	US-10-425-115-245327	Sequence 245327, A
145	27	87.1	833	4	US-10-041-018-255	Sequence 255, App	218	26	83.9	130	4	US-10-425-115-327283	Sequence 327283, A
146	27	87.1	856	4	US-10-041-018-204	Sequence 204, App	219	26	83.9	134	4	US-10-425-115-327283	Sequence 327283, A
147	27	87.1	856	4	US-10-041-018-240	Sequence 240, App	220	26	83.9	137	4	US-10-424-599-236305	Sequence 236305, A
148	27	87.1	856	4	US-10-041-018-340	Sequence 340, App	221	26	83.9	143	4	US-10-425-115-353247	Sequence 353247, A
149	27	87.1	930	4	US-10-276-272A-13	Sequence 13, Appl	222	26	83.9	152	4	US-10-425-115-240443	Sequence 240443, A
150	27	87.1	1024	3	US-09-841-739-2	Sequence 2, Appl	223	26	83.9	159	4	US-10-437-963-106452	Sequence 106452, A
151	27	87.1	1024	3	US-09-864-921-97	Sequence 97, Appl	224	26	83.9	176	4	US-10-424-599-222299	Sequence 222299, A
152	27	87.1	1024	4	US-10-156-733-2	Sequence 2, Appl	225	26	83.9	190	4	US-10-424-599-144945	Sequence 144945, A
153	27	87.1	1024	4	US-10-449-315-2	Sequence 2, Appl	226	26	83.9	191	3	US-09-738-626-6093	Sequence 6093, Ap
154	27	87.1	1024	5	US-10-766-682-97	Sequence 97, Appl	227	26	83.9	225	4	US-10-425-115-208680	Sequence 208680, A
155	27	87.1	1070	4	US-10-221-097-49	Sequence 49, Appl	228	26	83.9	293	4	US-10-369-493-6935	Sequence 6935, Ap
156	27	87.1	1204	3	US-09-841-739-5	Sequence 5, Appl	229	26	83.9	293	4	US-10-652-857-4	Sequence 4, Appl
157	27	87.1	1204	4	US-10-449-315-5	Sequence 5, Appl	230	26	83.9	295	4	US-10-282-122A-65569	Sequence 65569, A
158	27	87.1	2697	3	US-09-961-527A-5	Sequence 5, Appl	231	26	83.9	310	5	US-10-774-355A-1555	Sequence 1555, A
159	26	83.9	28	4	US-10-767-701-48268	Sequence 48268, A	232	26	83.9	314	5	US-10-774-355A-2197	Sequence 2197, Ap
160	26	83.9	36	4	US-10-424-599-208993	Sequence 208993, A	233	26	83.9	321	5	US-10-459-065A-564	Sequence 564, App
161	26	83.9	37	4	US-10-425-115-343187	Sequence 343187, A	234	26	83.9	343	4	US-10-156-761-9520	Sequence 9520, Ap
162	26	83.9	45	5	US-10-425-115-343187	Sequence 4052, Ap	235	26	83.9	344	4	US-10-210-172-42	Sequence 42, Appl
163	26	83.9	51	4	US-10-437-963-142406	Sequence 142406, A	236	26	83.9	363	4	US-10-437-963-176802	Sequence 176802, A
164	26	83.9	53	4	US-10-424-599-197895	Sequence 197895, A	237	26	83.9	373	4	US-10-437-963-125070	Sequence 125070, A
165	26	83.9	53	4	US-10-425-114-49675	Sequence 49675, A	238	26	83.9	384	5	US-10-501-282-6210	Sequence 6210, Ap
166	26	83.9	55	4	US-10-437-963-164041	Sequence 164041, A	239	26	83.9	390	4	US-10-369-493-6541	Sequence 6541, Ap
167	26	83.9	59	4	US-10-425-115-366583	Sequence 366583, A	240	26	83.9	390	5	US-10-732-923-7871	Sequence 7871, Ap
168	26	83.9	60	6	US-10-125-258-44	Sequence 44, Appl	241	26	83.9	393	4	US-10-369-493-13098	Sequence 13098, A
169	26	83.9	60	6	US-11-093-429-44	Sequence 44, Appl	242	26	83.9	397	4	US-10-017-161-2220	Sequence 2220, Ap
170	26	83.9	60	6	US-11-092-430-44	Sequence 44, Appl	243	26	83.9	397	4	US-10-292-798-1866	Sequence 1866, Ap
171	26	83.9	60	6	US-11-093-225-44	Sequence 44, Appl	244	26	83.9	400	5	US-10-739-930-8089	Sequence 8089, Ap
172	26	83.9	60	6	US-11-092-027-44	Sequence 44, Appl	245	26	83.9	404	4	US-10-369-493-15092	Sequence 15092, A
173	26	83.9	60	6	US-11-092-427-44	Sequence 44, Appl	246	26	83.9	414	4	US-10-369-493-11566	Sequence 11566, A
										414	4	US-10-282-122A-48315	Sequence 48315, A

247 26 83.9 426 3 US-09-738-626-6036 Sequence 6036, Ap
248 26 83.9 426 4 US-10-627-476-424 Sequence 424, App
249 26 83.9 431 5 US-10-495-148-21 Sequence 21, Appl
250 26 83.9 431 5 US-10-732-923-11170 Sequence 11170, A
251 26 83.9 437 5 US-10-501-282-5896 Sequence 5896, Ap
252 26 83.9 442 4 US-10-437-963-145134 Sequence 145134, A
253 26 83.9 444 4 US-10-369-493-9766 Sequence 9766, Ap
254 26 83.9 446 5 US-10-732-923-23883 Sequence 23883, A
255 26 83.9 459 4 US-10-369-493-18271 Sequence 18271, A
256 26 83.9 459 5 US-10-732-923-23570 Sequence 23570, A
257 26 83.9 465 4 US-10-424-599-254007 Sequence 254007, A
258 26 83.9 466 5 US-10-732-923-11191 Sequence 11191, A
259 26 83.9 470 4 US-10-437-963-155526 Sequence 155526, A
260 26 83.9 483 4 US-10-369-493-5486 Sequence 5486, Ap
261 26 83.9 483 4 US-10-369-493-5487 Sequence 5487, Ap
262 26 83.9 504 6 US-11-097-143-21684 Sequence 21684, A
263 26 83.9 518 4 US-10-032-585-7864 Sequence 7864, Ap
264 26 83.9 526 4 US-10-369-493-3924 Sequence 3924, Ap
265 26 83.9 536 4 US-10-424-599-212613 Sequence 212613, A
266 26 83.9 548 4 US-10-282-122A-63246 Sequence 63246, A
267 26 83.9 581 6 US-11-097-143-15831 Sequence 15831, A
268 26 83.9 618 5 US-10-450-763-56476 Sequence 56476, A
269 26 83.9 641 5 US-10-450-763-55856 Sequence 55856, A
270 26 83.9 661 4 US-10-425-115-330488 Sequence 330488, A
271 26 83.9 681 4 US-10-335-977-5995 Sequence 5995, Ap
272 26 83.9 690 4 US-10-425-114-61393 Sequence 61393, A
273 26 83.9 698 4 US-10-437-963-132561 Sequence 132561, A
274 26 83.9 712 4 US-10-335-977-5996 Sequence 5996, Ap
275 26 83.9 717 4 US-10-335-977-5997 Sequence 5997, Ap
276 26 83.9 719 4 US-10-369-493-22359 Sequence 22359, A
277 26 83.9 754 6 US-11-097-143-23787 Sequence 23787, A
278 26 83.9 860 4 US-11-097-143-21294 Sequence 21294, A
279 26 83.9 888 4 US-10-282-122A-63048 Sequence 63048, A
280 26 83.9 891 6 US-11-097-143-26673 Sequence 26673, A
281 26 83.9 919 5 US-10-200-545-95 Sequence 95, Appl
282 26 83.9 960 4 US-10-437-963-129061 Sequence 129061, A
283 26 83.9 976 5 US-10-732-923-1219 Sequence 1219, Ap
284 26 83.9 994 4 US-10-437-963-129064 Sequence 129064, A
285 26 83.9 1082 4 US-10-282-122A-49664 Sequence 49664, A
286 25 80.6 6 3 US-09-867-847-7 Sequence 7, Appl
287 25 80.6 6 3 US-09-867-847-11 Sequence 11, Appl
288 25 80.6 6 3 US-09-867-847-19 Sequence 19, Appl
289 25 80.6 6 3 US-09-867-847-20 Sequence 20, Appl
290 25 80.6 6 3 US-09-972-475-9 Sequence 9, Appl
291 25 80.6 6 3 US-09-915-092-1 Sequence 1, Appl
292 25 80.6 6 3 US-09-915-092-9 Sequence 9, Appl
293 25 80.6 6 3 US-09-915-092-10 Sequence 10, Appl
294 25 80.6 6 3 US-09-915-092-28 Sequence 28, Appl
295 25 80.6 6 3 US-09-956-625-25 Sequence 25, Appl
296 25 80.6 6 3 US-09-747-408-1 Sequence 1, Appl
297 25 80.6 6 3 US-09-747-408-3 Sequence 3, Appl
298 25 80.6 6 3 US-09-747-408-10 Sequence 10, Appl
299 25 80.6 6 3 US-09-747-408-11 Sequence 11, Appl
300 25 80.6 6 4 US-10-463-729-9 Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-867-847-13
; Sequence 13, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-13

Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
DB 1 KVFVFA 6

RESULT 2

US-09-867-847-21
; Sequence 21, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-21

Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
DB 1 KVFVFA 6

RESULT 3

US-09-915-092-3
; Sequence 3, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-3

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6
      |||||

RESULT 4
US-09-915-092-11
; Sequence 11, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-11

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6
      |||||

RESULT 5
US-09-747-408-4
; Sequence 4, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6
      |||||

RESULT 6
US-09-747-408-12
; Sequence 12, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6
      |||||

RESULT 7
US-10-728-028-3
; Sequence 3, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-3

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
| | | | |
Db 1 KVFVFA 6

RESULT 8

US-10-728-028-11
; Sequence 11, Application US/10728028
; Publication No. US20050048000A1

; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNERULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: US28 THEROP
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-11

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
| | | | |
Db 1 KVFVFA 6

RESULT 9

US-10-825-958-11
; Sequence 11, Application US/10825958
; Publication No. US20050090439A1

; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-11

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
| | | | |
Db 1 KVFVFA 6

RESULT 10

US-10-825-958-19
; Sequence 19, Application US/10825958
; Publication No. US20050090439A1

; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-19

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
| | | | |
Db 1 KVFVFA 6

RESULT 11

US-10-424-599-174685
; Sequence 174685, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174685
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12875C.1.pep
US-10-424-599-174685

Query Match 100.0%; Score 31; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 11 KVFVFA 16

RESULT 12
US-10-424-599-164908
; Sequence 164908, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164908
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11992C.1.pep
US-10-424-599-164908

Query Match 100.0%; Score 31; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 34 KVFVFA 39

RESULT 13
US-10-424-599-203722
; Sequence 203722, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 203722
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25988C.1.pep
US-10-424-599-203722

Query Match 100.0%; Score 31; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFA 6
|||
Db 5 KVFVFA 10

RESULT 14
US-10-437-963-118848
; Sequence 118848, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118848
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22120C.1.pep
US-10-437-963-118848

Query Match 100.0%; Score 31; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 80 KVFVFA 85

RESULT 15
US-10-437-963-118846
; Sequence 118846, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118846
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(372)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_22119C.1.pep
US-10-437-963-118846

Query Match 100.0%; Score 31; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 121 KVFVFA 126

RESULT 16

US-10-437-963-138916
; Sequence 138916, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Bing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138916
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_4025C.1.pep
US-10-437-963-138916

Query Match 100.0%; Score 31; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 80 KVFVFA 85

RESULT 17

US-10-437-963-118773
; Sequence 118773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118773
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22052C.1.pep

US-10-437-963-118773

Query Match 96.8%; Score 30; DB 4; Length 420;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 355 KVFVFA 360

RESULT 18

US-10-424-599-266901
; Sequence 266901, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 266901
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(54)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83031C.1.pep
US-10-424-599-266901

Query Match 90.3%; Score 28; DB 4; Length 54;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 18 KVFVFA 23

RESULT 19

US-10-425-115-327241
; Sequence 327241, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 327241
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_61513C.1.pep
US-10-425-115-327241

Query Match 90.3%; Score 28; DB 4; Length 115;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|||
Db 72 KVFVFS 77

RESULT 20

US-10-425-115-290464
; Sequence 290464, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 290464
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27992C.1.pap
US-10-425-115-290464

Query Match 90.3%; Score 28; DB 4; Length 126;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|||
Db 99 KVFVFA 104

RESULT 21

US-10-425-115-193086
; Sequence 193086, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 193086
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_10767C.1.pap
US-10-425-115-193086

Query Match 90.3%; Score 28; DB 4; Length 159;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
:||||
Db 89 RVVFFA 94

RESULT 22

US-10-767-701-37567
; Sequence 37567, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37567
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C3123_1.pap
US-10-767-701-37567

Query Match 90.3%; Score 28; DB 4; Length 240;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
:||||
Db 155 KVFVFS 160

RESULT 23

US-10-369-493-6279
; Sequence 6279, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6279
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6279

Query Match 90.3%; Score 28; DB 4; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
:||||
Db 291 RVVFFA 296

RESULT 24

US-10-994-726-438
; Sequence 438, Application US/10994726
; Publication No. US20050147999A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481D1

; CURRENT APPLICATION NUMBER: US/10/994,726
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 09/830,230
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 438
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-438

Query Match 90.3%; Score 28; DB 5; Length 490;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 23 RVVFA 28

RESULT 25
US-09-877-476-2
; Sequence 2, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-877-476-2

Query Match 90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 26
US-09-877-476-28
; Sequence 28, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ ID NO:4) and 3' 330 amino acids from A. thaliana
; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176
US-09-877-476-28

Query Match 90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 27
US-09-877-476-30
; Sequence 30, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 107 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa = Pro or Gln
US-09-877-476-30

Query Match 90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 28
US-09-877-476-36
; Sequence 36, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

```

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
US-09-877-476-36

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
        ||:||||
Db      356 KFLFFA 361

RESULT 29
US-10-276-977-7
; Sequence 7, Application US/10276977
; Publication No. US2004049806A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
; APPLICANT: KUNST, LJERKA
; APPLICANT: SMITH, MARK A.
; APPLICANT: MOON, HANGSIK
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A PLANT VERY LONG CHAIN
; TITLE OF INVENTION: FATTY ACID BIOSYNTHETIC ENZYME
; FILE REFERENCE: 56120-5004US
; CURRENT APPLICATION NUMBER: US/10/276,977
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/IB01/01140
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,789
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-276-977-7

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
        ||:||||
Db      356 KFLFFA 361

RESULT 30
US-10-758-524-2
; Sequence 2, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID BLONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08

```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from A. thaliana PAE1 (SEQ ID
; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated AC399
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa = Pro or Gln
; US-10-758-524-30

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      356 KFLFFA 361

RESULT 33
US-10-758-524-36
; Sequence 36, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana PAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
; US-10-758-524-36

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      356 KFLFFA 361

RESULT 34
US-10-282-122A-47052
; Sequence 47052, Application US/10282122A
; Publication No. US20040029198A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana PAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
; US-10-758-524-36

Query Match          90.3%; Score 28; DB 4; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      41 RFVFFA 46

RESULT 35
US-10-994-726-437
; Sequence 437, Application US/10994726
; Publication No. US20050147999A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481D1
; CURRENT APPLICATION NUMBER: US/10/994,726
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 09/830,230
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 437
; LENGTH: 508

; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47052
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
; US-10-282-122A-47052
```

```
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-437

Query Match          90.3%; Score 28; DB 5; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 41 RVVFFA 46

RESULT 36
US-10-732-923-18725
; Sequence 18725, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18725
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18725

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 359 KFLFFA 364

RESULT 37
US-10-732-923-18726
; Sequence 18726, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18726
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18726

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 358 KFLFFA 363

RESULT 38
US-10-732-923-18737
; Sequence 18737, Application US/10732923
; Publication No. US20050108791A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18737
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica rapa
US-10-732-923-18737

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 358 KFLFFA 363

RESULT 39
US-10-282-122A-51929
; Sequence 51929, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51929
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51929
```

```
Query Match      90.3%; Score 28; DB 4; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFPVFFA 6
Db      314 KFMFFA 319

RESULT 40
US-10-369-493-2154
; Sequence 2154, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2154
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1089)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2154

Query Match      90.3%; Score 28; DB 4; Length 1089;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFPVFFA 6
Db      13 KFPVFFS 18

RESULT 41
US-10-425-115-236339
; Sequence 236339, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 236339
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_147123C.1.pep
US-10-425-115-236339

Query Match      87.1%; Score 27; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KFPVFF 5
Db      23 KFPVFF 27

RESULT 42
US-10-425-115-200545
; Sequence 200545, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 200545
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_114485C.1.pep
US-10-425-115-200545

Query Match      87.1%; Score 27; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFPVFF 5
Db      25 KFPVFF 29

RESULT 43
US-10-424-599-232761
; Sequence 232761, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232761
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52207C.1.pep
US-10-424-599-232761

Query Match      87.1%; Score 27; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFPVFF 5
Db      11 KFPVFF 15

RESULT 44
US-10-425-115-206883
; Sequence 206883, Application US/10425115
```

```
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 206883
/ LENGTH: 48
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_120267C.1.pep
US-10-425-115-206883

Query Match      87.1%; Score 27; DB 4; Length 48;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      15 KPAFFA 20

RESULT 45
US-10-437-963-176215
/ Sequence 176215, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 176215
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_73986C.1.pep
US-10-437-963-176215

Query Match      87.1%; Score 27; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
DB      13 KVFVFF 17

RESULT 46
US-10-425-114-38807
/ Sequence 38807, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.

/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 38807
/ LENGTH: 57
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700684806_FLI.pep
US-10-425-114-38807

Query Match      87.1%; Score 27; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
DB      29 KVFVFF 33

RESULT 47
US-09-764-877-1136
/ Sequence 1136, Application US/09764877
/ Patent No. US20020147140A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC005
/ CURRENT APPLICATION NUMBER: US/09/764,877
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - refer to PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 4031
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1136
/ LENGTH: 62
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (55)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: SITE
/ LOCATION: (60)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1136

Query Match      87.1%; Score 27; DB 3; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
DB      31 KVFVFF 35

RESULT 48
US-10-242-515-1136
/ Sequence 1136, Application US/10242515
/ Publication No. US20040009488A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC005C1
/ CURRENT APPLICATION NUMBER: US/10/242,515
/ CURRENT FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: 09/764,877
/ PRIOR FILING DATE: 2001-01-17
```

```
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1136
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1136

Query Match      87.1%; Score 27; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
      |||||
Db      31 KVFVF 35

RESULT 49
US-10-424-599-146372
; Sequence 146372, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146372
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103191C.1.pap
US-10-424-599-146372

Query Match      87.1%; Score 27; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
      |||||
```

```
Db      18 KVFVF 22

RESULT 50
US-10-425-115-248149
; Sequence 248149, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 248149
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_157899C.1.pap
US-10-425-115-248149

Query Match      87.1%; Score 27; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
      |||||
Db      67 KVFVF 71

RESULT 51
US-10-425-115-229605
; Sequence 229605, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 229605
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140993C.1.pap
US-10-425-115-229605

Query Match      87.1%; Score 27; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
      |||||
Db      1 KVFVF 5

RESULT 52
US-10-425-115-259222
```

; Sequence 259222, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259222
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167996C.1.pep
US-10-425-115-259222

Query Match 87.1%; Score 27; DB 4; Length 80;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
DB 66 KFTFFA 71

RESULT 53
US-10-425-115-215979
; Sequence 215979, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215979
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_128569C.1.pep
US-10-425-115-215979

Query Match 87.1%; Score 27; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 5
|||
DB 30 KVFVFF 34

RESULT 54
US-10-424-599-195261
; Sequence 195261, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215979
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_128569C.1.pep
US-10-425-115-215979

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195261
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18348C.1.pep
US-10-424-599-195261

Query Match 87.1%; Score 27; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
|||
DB 66 KVFVFF 70

RESULT 55
US-10-450-763-44156
; Sequence 44156, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44156
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-44156

Query Match 87.1%; Score 27; DB 5; Length 82;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
DB 11 EFVFFA 16

RESULT 56
US-10-425-115-275005
; Sequence 275005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 275005
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays

; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_182395C.1.pep
US-10-425-115-275005

Query Match 87.1%; Score 27; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
|||

Db 49 KPVFF 53

RESULT 57

US-10-424-599-259257
; Sequence 259257, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 259257
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_76133C.1.pep
US-10-424-599-259257

Query Match 87.1%; Score 27; DB 4; Length 88;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 6
:|:|

Db 13 RPIFF 18

RESULT 58

US-10-424-599-246138
; Sequence 246138, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246138
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(92)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64294C.1.pep
US-10-424-599-246138

Query Match 87.1%; Score 27; DB 4; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
|||

Db 71 KPVFF 75

RESULT 59

US-10-424-599-207674
; Sequence 207674, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207674
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29556C.1.pep
US-10-424-599-207674

Query Match 87.1%; Score 27; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
|||

Db 5 KPVFF 9

RESULT 60

US-10-425-115-221194
; Sequence 221194, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221194
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133318C.1.pep
US-10-425-115-221194

Query Match 87.1%; Score 27; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
|||

Db 20 KPVFF 24

RESULT 61

US-10-424-599-182454
; Sequence 182454, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 182454

; LENGTH: 103

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_135769C.1.pep

US-10-424-599-182454

Query Match 87.1%; Score 27; DB 4; Length 103;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5

DB 30 KVVFF 34

RESULT 62

US-10-437-963-201763

; Sequence 201763, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 201763

; LENGTH: 103

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_97105C.1.pep

US-10-437-963-201763

Query Match 87.1%; Score 27; DB 4; Length 103;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5

DB 43 KVVFF 47

RESULT 63

US-09-823-153-4

; Sequence 4, Application US/09823153

; Patent No. US20020025540A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; APPLICANT: Roberts, Susan

; APPLICANT: Pak, Roger

; APPLICANT: Lewis, Martin

; APPLICANT: Smith, David

; APPLICANT: Hendrick, Joseph

; APPLICANT: Vinitsky, Alexander

; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF

; FILE REFERENCE: D0004

; CURRENT APPLICATION NUMBER: US/09/823,153

; CURRENT FILING DATE: 2001-07-02

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Human Beta App

US-09-823-153-4

Query Match 87.1%; Score 27; DB 3; Length 104;

Best Local Similarity 83.3%; Pred. No. 5.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 6

DB 21 EFVFFA 26

RESULT 64

US-10-713-981-4

; Sequence 4, Application US/10713981

; Publication No. US20040121411A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; APPLICANT: Roberts, Susan

; APPLICANT: Pak, Roger

; APPLICANT: Lewis, Martin

; APPLICANT: Smith, David

; APPLICANT: Hendrick, Joseph

; APPLICANT: Vinitsky, Alexander

; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF

; FILE REFERENCE: D0004 DIV

; CURRENT APPLICATION NUMBER: US/10/713,981

; CURRENT FILING DATE: 2003-11-14

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Human Beta App

US-10-713-981-4

Query Match 87.1%; Score 27; DB 4; Length 104;

Best Local Similarity 83.3%; Pred. No. 5.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 6

DB 21 EFVFFA 26

RESULT 65

US-10-425-115-215097

; Sequence 215097, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215097
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127767C.1.pep
US-10-425-115-215097

Query Match 87.1%; Score 27; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 97 KPVFF 101

RESULT 66
US-10-424-599-207673
; Sequence 207673, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207673
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29555C.1.pep
US-10-424-599-207673

Query Match 87.1%; Score 27; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 16 KPVFF 20

RESULT 67
US-10-437-963-146282
; Sequence 146282, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146282

; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_46920C.1.pep
US-10-437-963-146282

Query Match 87.1%; Score 27; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 18 KPVFF 22

RESULT 68
US-10-424-599-278159
; Sequence 278159, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278159
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93200C.1.pep
US-10-424-599-278159

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 5 KPVFF 9

RESULT 69
US-10-425-115-208261
; Sequence 208261, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 208261
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121527C.1.pep
US-10-425-115-208261

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
Db 33 KFVFF 37

RESULT 70
US-10-425-115-286779
; Sequence 286779, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286779
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(110)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24637C.1.pep
US-10-425-115-286779

Query Match 87.1%; Score 27; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5
Db 96 KFVFF 100

RESULT 71
US-09-864-408A-4214
; Sequence 4214, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4214
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-4214

Query Match 87.1%; Score 27; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5
```

```
Db 67 KFVFF 71

RESULT 72
US-10-425-115-256025
; Sequence 256025, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256025
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165087C.1.pep
US-10-425-115-256025

Query Match 87.1%; Score 27; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5
Db 47 KFVFF 51

RESULT 73
US-10-425-115-289631
; Sequence 289631, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 289631
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27231C.1.pep
US-10-425-115-289631

Query Match 87.1%; Score 27; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5
Db 26 KFVFF 30

RESULT 74
US-10-424-599-208184
; Sequence 208184, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
```

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208184
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30014C.1.pep
US-10-424-599-208184

Query Match 87.1%; Score 27; DB 4; Length 131;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
|||:
Db 118 KFIFFS 123

RESULT 75
US-10-424-599-221174
; Sequence 221174, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221174
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41750C.1.pep
US-10-424-599-221174

Query Match 87.1%; Score 27; DB 4; Length 131;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
|||:
Db 83 KFAFFA 88

Search completed: December 29, 2005, 18:49:46
Job time : 67.2903 secs

THIS PAGE BLANK (USPTO)